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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27,
10 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file pto_PLACENTA.txt, created 24
25 January 2001, having 26,548,337 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

placenta and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the
20 predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

25 Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect,
30 particularly those with polygenic etiology.

Summary of the Invention

35 The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
5 expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified
10 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon
15 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality
20 of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least
25 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

30 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
35 Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

5 Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

10 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

15 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
20 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
25 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single
30 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
35 nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable 10 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or 15 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome- 20 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of 25 SEQ ID Nos. 13,233 - 26,232, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention, 30 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,232 or a complementary sequence or a fragment thereof . 35 wherein said probe hybridizes at high stringency to a

nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

5 13,233 - 26,232 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed
15 in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the
20 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
25 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,
30 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

35 In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In a sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

5 wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
10 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
15 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
20 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
25 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 wherein said sequence encodes a peptide.

30 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
35 encoded by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
5 ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,233 - 38,837, or fragment thereof.

10 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
15 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

20

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
25 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
30 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
35 Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
5 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a
10 portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a
15 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF
20 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another
25 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit
30 specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

35 As used herein with respect to the visual display

of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray.
The graph shows the number of sequence-verified products
that were either not expressed ("0"), expressed in one or
more but not all tested tissues ("1" - "9"), or expressed
5 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
expression of verified sequences that showed expression
with signal intensity greater than 3 in at least one
tissue, with: FIG. 7A showing the expression as measured by
10 microarray hybridization in each of the 10 measured
tissues, and the expression as measured "bioinformatically"
by query of EST, NR and SwissProt databases; with FIG. 7B
showing the legend for display of physical expression
(ratio) in FIG. 7A; and with FIG. 7C showing the legend for
15 scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3
signal intensity for arrayed sequences that were identical
to sequences in existing EST, NR and SwissProt databases or
that were dissimilar (unknown), where black denotes the
20 signal intensity for all sequence-verified products with a
BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30})
("unknown") and a dotted line denotes sequence-verified
spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

25 FIG. 9 presents a Mondrian of BAC AC008172 (bases
25,000 to 130,000), containing the carbamyl phosphate
synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30

Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

35 FIG. 1 is a flow chart illustrating in broad

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly

include several divisions thereof, including the
htgs(draft), NT (nucleotide, command line), and NR
(nonredundant) divisions. GenBank is produced by the
National Institutes of Health and is maintained by the
5 National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
eukaryotic organisms will also prove useful as genomic
10 sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
are predicted to have a biological function as specified by
15 the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
regulating message degradation after transcription into
20 mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

The particular genomic sequence to be input into
25 process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
given genomic region. In such case, the input often will
30 be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
experimental confirmation is identified. Experimental
35 confirmation can involve physical and/or bioinformatic

assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the
5 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often
10 will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the
15 functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within
20 the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

25 The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

30 FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and
35 facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or
5 interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of
10 functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20
15 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis
20 approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast,
25 corresponding, *e.g.*, syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

30 The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic
35 sequence, the query will accordingly require that the

sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query
20 can be generated that takes into account the initial
negative result.

When query 20 returns sequence meeting the query
5 criteria, the returned sequence is then passed to optional
preprocessing 24, suitable and specific for the desired
analytical approach and the particular analytical methods
thereof to be used in process 25.

Preprocessing 24 can include processes suitable
10 for many approaches and methods thereof, as well as
processes specifically suited for the intended subsequent
analysis.

Preprocessing 24 suitable for most approaches and
methods will include elimination of sequence irrelevant to,
15 or that would interfere with, the subsequent analysis.
Such sequence includes repetitive sequence, such as Alu
repeats and LINE elements, vector sequence, artificial
sequence, such as artificial polylinkers, and the like.
Such removal can readily be performed by identification and
20 subsequent masking of the undesired sequence.

Identification can be effected by comparing the
genomic sequence returned by query 20 with public or
private databases containing known repetitive sequence,
vector sequence, artificial sequence, and other artifactual
25 sequence. Such comparison can readily be done using
programs well known in the art, such as CROSS_MATCH, or by
proprietary sequence comparison programs the engineering of
which is well within the skill in the art.

Alternatively, or in addition, undesirable,
30 including artifactual, sequence can be identified
algorithmically without comparison to external databases
and thereafter removed. For example, synthetic polylinker
sequence can be identified by an algorithm that identifies
a significantly higher than average density of known
35 restriction sites. As another example, vector sequence can

be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,

where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating
5 transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability
10 or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function
15 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as
20 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for
25 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)
30 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene
35 finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
5 and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling,
10 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such
15 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored
20 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further
25 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27
30 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three
35 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
5 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving
10 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such
15 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process
20 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in
25 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the
30 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression
35 of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of
verifying gene expression in which expression of predicted
ORFs is measured and confirmed using a novel type of
nucleic acid microarray, the genome-derived single exon
5 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene
calling, particularly gene prediction, algorithms in
process 200, and as further identified as suitable by
process 300, are amplified from genomic DNA using the
10 polymerase chain reaction (PCR). Although PCR is
conveniently used, other amplification approaches can also
be used.

Amplification schemes can be designed to capture
the entirety of each predicted ORF in an amplicon with
15 minimal additional (that is, intronic or intergenic)
sequence. Because ORFs predicted from human genomic
sequence using the methods of the present invention differ
in length, such an approach results in amplicons of varying
length.

20 However, most predicted ORFs are shorter than 500
bp in length, and although amplicons of at least about 100
or 200 base pairs can be immobilized as probes on nucleic
acid microarrays, early experimental results using the
methods of the present invention have suggested that longer
25 amplicons, at least about 400 or 500 base pairs, are more
effective. Furthermore, certain advantages derive from
application to the microarray of amplicons of defined size.

Therefore, amplification schemes can
alternatively, and preferably, be designed to amplify
30 regions of defined size, preferably at least about 300, 400
or 500 bp, centered about each predicted ORF. Such an
approach results in a population of amplicons of limited
size diversity, but that typically contain intronic and/or
intergenic nucleic acid in addition to putative ORF.

35 Conversely, somewhat fewer than 10% of ORFs

predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

10 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic
15 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased
20 commercially or synthesized by standard techniques.

 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves
25 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later
30 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

 Such predetermined sequence is usefully at least
35 about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for
5 amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the
10 organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual,
15 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

20 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather,
25 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes
30 not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single
35 exon probe) is disposed in an array upon a support

substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see
5 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene,
10 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,
15 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

20 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination
25 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or
30 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

35 As is well known in the art, microarrays

typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can
5 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
10 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
15 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
20 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
25 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
30 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
35 provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
5 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
10 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
15 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

20 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
25 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
30 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific"
35 libraries targeted at a particular biological question,

R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure
5 expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective
10 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be
15 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the
20 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA
25 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

30 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present
35 invention depends upon a successful amplification from

genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
5 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,
10 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric
15 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
20 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present
25 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the
30 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically
35 include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
5 such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
10 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
15 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
20 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
25 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-
30 spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
35 probes. For human genes, the near-complete sequence of

human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

5 In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70,
10 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single
15 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression
20 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such
25 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention
30 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon
35 microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound

noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased

commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
5 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
10 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

15 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
20 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
25 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
30 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
35 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
5 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
10 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-
15 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
20 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

25 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

30 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered
35 set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local
5 alignment search tool"). The results of such query – including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to
10 inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data
15 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or
20 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or
25 displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence
30 annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic
35 works of Piet Mondrian, visual display 80 is alternatively

described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given
5 the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left
10 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

15 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
20 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
25 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
30 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
35 fulcrum point about which a chosen range of sequence is

anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or

approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

- 5 For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

- 10 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

- Alternatively, or in addition, the color, hue, 15 density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be 20 indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 25 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

- As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, 30 field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

- Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 35 can include as few as one such series of rectangles and as

many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show
5 predictions of a plurality of different functions.
However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis,
10 such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the
15 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional
20 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an
25 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

30 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84
35 identifies the sequence included within the probe

immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity
5 has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links
10 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be
15 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical
20 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of
25 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of
30 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to
35 depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,232 of these ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was
5 effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in
10 pregnancy.

One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In
15 chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus
20 cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

25 Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one
30 end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself
35 in variety of phenotypic defects that vary in severity

among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes
5 and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis,
10 caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over \$1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought
15 that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease,
20 neurodegenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must coincide in the same individual or even the same cell for the disease to develop and/or progress.

25 A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all
30 such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, it is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may
35 be detected in placenta.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be
5 expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based
10 upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof.

In one embodiment, the gene expression profile is
15 generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from
20 individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

25 In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the
30 massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated
35 gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and
Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
5 46(3):425-8 (1999)), in drug discovery screens (see, for
example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
10 Expression Profile Analysis of Human Breast Cancer
Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
15 appreciated that even those probes that show no change in
expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
20 failure of the agent to change a gene's expression level is
evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
25 lead compound discovery or in subsequent screening of lead
compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

30 WO 99/58720 provides methods for quantifying the
relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
35 percentage of the individual gene expression measurements

from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999);
5 Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified
10 nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA
15 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
20 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

25 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity
30 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and
35 WO 00/15779. As is well understood, where the probes are

to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

5 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or
10 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged
15 therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
20 in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a
25 genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF.
30 Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase
35 hybridization, however — that is, for use in a

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human cot1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as
5 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes
10 of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one
15 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more
20 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand
25 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art
30 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to
35 provide single-stranded nucleic acid probes that have

sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverly, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 13,233 - 26,232. Such amino acid sequences are set out in SEQ ID NOS: 26,233 - 38,837. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

5 After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets:
10 GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
15 DNA.

 The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
20 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

 The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
25 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

 ORFs predicted by any two of the three programs
30 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single
35 gene if fewer than 7 exons were found within the 25 kb

window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto,

CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
5 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)
10 length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
15 size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

20 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
25 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
30 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR
35 and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material
5 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
10 similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-
15 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally
20 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt
25 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe
30 sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

35 All of the probe sequences (as amplified) were

then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

Exon Microarrays

The two genome-derived single exon microarrays
5 prepared according to Example 1 were hybridized in a series
of simultaneous two-color fluorescence experiments to (1)
Cy3-labeled cDNA synthesized from message drawn
individually from each of brain, heart, liver, fetal liver,
placenta, lung, bone marrow, HeLa, BT 474, or HBL 100
10 cells, and (2) Cy5-labeled cDNA prepared from message
pooled from all ten tissues and cell types, as a control in
each of the measurements. Hybridization and scanning were
carried out using standard protocols and Molecular Dynamics
equipment.

15 Briefly, mRNA samples were bought from commercial
sources (Clontech, Palo Alto, CA and Amersham Pharmacia
Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were
incorporated during separate reverse transcriptions of 1 µg
of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
20 and 2 µg random 9mer primers as follows. After heating to
70°C, the RNA:primer mixture was snap cooled on ice. After
snap cooling on ice, added to the RNA to the stated final
concentration was: 1X Superscript II buffer, 0.01 M DTT,
100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
25 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
30 column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
35 Speedvac, resuspended in 30 µl hybridization solution

containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
--

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates

				activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to
5 rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being
10 absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the
15 highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20
20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
25 AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in
30 the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
35 chromosome RNA-binding motif (Chai et al., *Genomics*

49(2):283-89 (1998))(AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability
5 of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

10 EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray
15 as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for
20 multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the
25 paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate
30 synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully
35 identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be
5 from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show
10 identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes.
15 Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very
20 good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following
25 colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and
30 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
35 Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique
5 exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon
10 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
15 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,232 single exon probes, each fragment corresponding to an extension product from one of
20 the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232 . The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
25 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
30 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
35 expression is based on a statistical confidence that the

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give
5 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the
10 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining
15 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)
20 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
25 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
30 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus
35 presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,233 - 26,232 was individually
5 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were
10 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted
15 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective
20 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be
25 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the
30 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide
35 sequences. These are set out as PEPTIDE SEQ ID NOS.:. The

peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs
5 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the
10 exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
15 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
20 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
25 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
30 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ — which is probative evidence that the query sequence has previously
35 been shown to be expressed — the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
5 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
10 a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,232) and probe exon (SEQ ID NOs.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

15 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST
20 query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

25 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

30 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring
Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and
35 functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
463	13658	26695	5				
912	14087	27162	9.88				
1070	14236		3.01				
1330	14487	27555	10.9				
1645	14797	27982	1.82				
1666	14818	27901	4.94				
1764	14913	28008	1.03				
1788	14937	28030	1.67				
1794	14943	28036	8.53				
1939	15082	28183	1.57				
2034	15175	28285	2.66				
2234	15368	28497	3.39				
2353	15484	28616	2.53				
3255	16429	29447	3.75				
3637	16702	29713	1.48				
3604	16768	29783	10.5				
3651	16814		0.84				
3747	16908	29912	0.98				
4057	17213		0.94				
4314	17457	30445	1.55				
4377	17520	30500	6.88				
4396	17539	30519	0.87				
4398	17539	30520	0.87				
4457	17597		1.89				
4512	17651	30639	0.61				
4958	18088	31084	1.86				
5002	18131		0.6				
5157	18276	31244	5.14				
5168	18290	31255	1.24				
5371	18574	31442	1.76				
5371	18574	31443	1.76				
5538	18735		4.12				
5714	18907		7.26				
5766	18735		3.31				

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Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5858	19048	32354	4.22				
6146	25820	32668	1.61				
6174	19350	32696	1.92				
6549	19708		1.01				
6678	19838	33226	1.28				
6679	19838	33227	1.25				
7275	20358	33812	1.42				
7275	20358	33813	1.42				
7569	20641	34117	1.18				
7569	20641	34118	1.18				
8251	21333	34851	1.44				
8682	21752	35296	1.14				
9061	22140	35684	0.76				
9061	22140	35685	0.76				
9734	22799	36373	3.82				
9968	23007	36602	0.56				
10096	23124	36725	1.51				
10226	23264	36853	0.88				
10643	23677	37286	0.74				
10643	23677	37287	0.74				
10922	24005		2.32				
11280	24346		1.78				
11348	24410	38063	2.79				
11641	24721	38414	1.73				
11749	23935	37561	1.36				
11749	23935	37562	1.36				
11792	24782		2.09				
12057	25038	38746	1.58				
12623	25419		2.06				
12967	25628	31960	1.5				
6177	19353	32700	16.82	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8195	21277	34800	1.5	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9944	22983	36575	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9944	22983	36576	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7139	20274	33714	0.82	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7139	20274	33715	0.82	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10536	23670	37279	0.93	9.6E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor 1H1 polypeptide 2 (Gtf2h2) genes, complete cds
10636	23670	37280	0.93	9.6E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor 1H1 polypeptide 2 (Gtf2h2) genes, complete cds
2731	15849	28959	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prMM) envelope glycoprotein (E) polypeptide mRNA, partial cds
2731	15849	28960	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prMM) envelope glycoprotein (E) polypeptide mRNA, partial cds
2990	16196	29182	3.08	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8290	21372	34893	1.08	9.3E+00	AF130890.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9204	22282	35822	3.03	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP88)
7625	20685	34171	0.6	9.2E+00	Q61767	SWISSPROT	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(5)-STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5411	18613	31588	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5411	18613	31587	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9630	22885		1	9.0E+00	P09241	SWISSPROT	RH-ODOPSIN
5160	19336	32681	5.15	8.9E+00	BE971806.1	EST_HUMAN	601651039R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6510	19675	33044	2.03	8.7E+00	AB019783.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6510	19675	33045	2.03	8.7E+00	AB019783.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
453	19649	28686	1.79	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9654	21087	34611	2.09	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11443	24504		1.96	8.0E+00	P41820	SWISSPROT	BREIFELDIN A RESISTANCE PROTEIN
8345	21426		0.98	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7601	20576		1.85	7.5E+00	AL445085.1	NT	Thermoplasma acidophilum complete genome; segment 13/5
8566	21637	35174	1.42	7.5E+00	P36441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8566	21637	35175	1.42	7.5E+00	P36441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5921	19108	32421	3.6	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285506 5'
8953	22032	35673	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8953	22032	35674	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3042	16218	29238	3.41	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
3042	16218	29239	3.41	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
7174	20307	33760	1.07	7.2E+00	BE178080.1	EST_HUMAN	RCO-HT0613-203000-031-407 HT0613 Homo sapiens cDNA
7299	20381	33838	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7299	20381	33839	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9798	22838		9.23	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11698	24746	38437	2.44	7.1E+00	P05850	SWISSPROT	HYPOTHELICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
10187	23224	36818	2.76	7.0E+00	P48810	SWISSPROT	ARGININE KINASE (AK)
11528	24584	38261	1.52	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8478	21559	35093	3.17	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10559	23594	37200	1.12	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10579	23614	37219	0.6	6.9E+00	P34228	SWISSPROT	SKT5 PROTEIN
6092	21174	34888	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Scores melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:291860 5'
8092	21174	34889	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Scores melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:291860 5'
9333	22409		1.82	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10413	23448	37053	3.6	6.8E+00	Q03570	SWISSPROT	HYPOTHELICAL 167.0 KDA PROTEIN C39C10.5 IN CHROMOSOME III
5398	19800		0.86	6.8E+00	Q89028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6875	19834	33223	0.86	6.6E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
9234	26228		0.55	6.8E+00	P51925	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10279	23314	36912	2.14	6.6E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10279	23314	36913	2.14	6.6E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10843	23876	37496	0.47	6.6E+00	H29330.1	EST_HUMAN	ym6006.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:52737 3'
11393	24454		1.48	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9382	22457	36020	7	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10512	23547	37158	0.52	6.5E+00	BE866001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5'
9943	22982	36574	1.34	6.2E+00	AY010901.1	NT	Schizosaccharomyces commune unknown mRNA
10787	23920	37444	0.7	6.2E+00	6754621	NT	Mus musculus mimosinase 2, alpha B1 (Man2b1), mRNA
7181	20313	33756	1.6	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10021	23059	36855	0.49	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1468000 nt, position (6/7)
10732	23765	37373	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10732	23765	37374	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6650	19809	33197	7.14	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlck3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11933	24919		3.02	5.0E+00	BE088630.1	EST_HUMAN	601645276F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3830451 5'
3613	16777		1.15	5.8E+00	7681557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7312	20394	33855	0.74	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor I gsr mRNA, complete cds
7312	20394	33856	0.74	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor I gsr mRNA, complete cds
7742	20803		1.34	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLII)
11289	24355	37096	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11289	24355	37097	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11765	23951	37581	2.52	5.8E+00	Q56276	SWISSPROT	LYCOPENE BETA CYCLASE
6381	19550	32906	0.74	5.6E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
8982	23021		0.56	5.5E+00	P19983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11018	24097		1.48	5.6E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11763	23949	37578	2.32	5.5E+00	P11890	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7069	20122	33536	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7069	20122	33537	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7484	20559		1.04	5.4E+00	Q99435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8013	21063	34575	0.74	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8054	21137		1.82	5.4E+00	Q91082	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELIN LV-1N; LIPOVITELIN LV-1C;
8999	22078	35618	0.83	5.4E+00	P40379	SWISSPROT	LIPOVITELIN LV-2]
8999	22078	35619	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10242	23277	36870	1.45	5.4E+00	Q17094	SWISSPROT	REP1 PROTEIN
10242	23277	36871	1.45	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4908	18036	31024	1.47	5.3E+00	L43128.1	NT	RHODOPSIN
6617	19777		0.7	5.3E+00	P41779	SWISSPROT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
8270	21352		3.39	5.3E+00	P54098	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8184	22262		0.72	5.3E+00	AB034990.1	NT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
11928	24914	38616	1.51	5.3E+00	Q27905	SWISSPROT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
5580	18775		1.16	5.2E+00	BE184840.1	EST_HUMAN	PROBABLE ANTIBACTERIAL PEPTIDE POLYPEPTIDE PRECURSOR
10583	23618		0.96	5.2E+00	AF248070.1	NT	QV4-HT0881-270400-188-108 HT0881 Homo sapiens cDNA
11470	24529		1.63	5.2E+00	Q10138	SWISSPROT	Drosophila orientalis R1B retrotransposable element reverse transcriptase gene, partial cds
9162	22240	35784	0.94	5.1E+00	O16005	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
10030	23068	36667	1.33	5.1E+00	P09182	SWISSPROT	RHODOPSIN
8415	19534	32946	0.74	5.0E+00	BF310443.1	EST_HUMAN	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
10397	23432		0.7	5.0E+00	BF308561.1	EST_HUMAN	601894910F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:412414 5'
							601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10845	23678	37289	2.89	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11569	24624	38304	7.24	5.0E+00	Z63860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10437	23472		0.78	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RatRat gene, and sodium phosphate transporter (NPT3) gene, complete cds
4172	17322		12.39	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
8348	21429	34953	0.8	4.8E+00	BF367809.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8738	21817		4.92	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310100-002-004 BT0547 Homo sapiens cDNA
300	13517	26550	3.04	4.7E+00	BF240562.1	EST_HUMAN	60187664F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098716 5'
301	13517	28550	1.85	4.7E+00	BF240562.1	EST_HUMAN	60187664F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098716 5'
3347	16520	29534	1.02	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7862	21012	34522	0.59	4.6E+00	U67569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9397	22471	36036	1.1	4.6E+00	BE646437.1	EST_HUMAN	7885g10 x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
9397	22471	36037	1.1	4.6E+00	BE646437.1	EST_HUMAN	KIA0645 PROTEIN, contains element PTR5 repetitive element
10600	23635		0.63	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
7947	20997		0.7	4.5E+00	AF126177.1	NT	Issatchenia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
11904	24892	38593	1.87	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
12058	25039	39747	1.53	4.5E+00	BF698941.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3105	16281	29298	0.84	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brr67 Homo sapiens cDNA clone IMAGE:4215284 5'
3105	16281	29297	0.84	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brr67 Homo sapiens cDNA clone IMAGE:4215284 5'
6331	19502		1.58	4.4E+00	X13414.1	NT	Murine I gene for MHC class II (Ia) associated invariant chain
6245	19419		0.77	4.3E+00	AF059879.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7596	20668	34142	2.53	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
7792	20848	34341	0.68	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
11101	24174	37809	14.74	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5634	18928		4.1	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5711	18904	32199	1.07	4.2E+00	P51828	SWISSPROT	LA-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
5880	19070		0.71	4.2E+00	O27830	SWISSPROT	POTATIVE ATP-DEPENDENT HELICASE MTH1802
6911	20226	33857	1.87	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8911	20226	33658	1.67	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9160	22238	35783	5.3	4.2E+00	A1809013.1	EST_HUMAN	W87g03.x1 Scarsa_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360892 3'
10122	23160	36759	1.03	4.2E+00	P31368	SWISSPROT	NUBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10382	23387		0.47	4.2E+00	P40868	SWISSPROT	HEXOSE TRANSPORTER HXT8
7281	20344	33796	0.98	4.1E+00	BE253988.1	EST_HUMAN	60110727:NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7839	20894	34398	7.66	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7980	21010		0.64	4.1E+00	AB041623.1	NT	Pathopeden yessensis mRNA for calcineurin A, complete cds
7983	21013	34523	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7983	21013	34524	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8101	21183	34703	2.88	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9740	22805	36381	0.61	4.1E+00	P11283	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9873	22913	36408	2.25	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10370	23405		0.55	4.1E+00	AJ235273.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4
10514	23549		0.52	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
11124	24195		2.15	4.1E+00	P08716	SWISSPROT	HYPOTHETICAL PROTEIN HMLF1
11214	24283		12.25	4.1E+00	BE886880.1	EST_HUMAN	601607510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
3635	16799		0.72	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5575	20130	33546	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5575	20130	33547	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33546	0.98	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33547	0.98	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7339	20419	33881	1	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9074	22153	35697	0.49	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10148	23186	36783	0.65	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10368	23403	37014	0.9	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10464	23499	37111	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10464	23499	37112	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11762	23948	37577	1.59	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11843	24832	38524	2.98	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11843	24832	38525	2.98	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]
12133	25113	38817	1.34	4.0E+00	P35811	SWISSPROT	ERYTHROCYTE ADDUCIN ALPHA SUBUNIT
3591	16755	29770	5	3.9E+00	X64518.1	NT	N tabacum chitinase gene 50 for class I chitinase C
4441	17681		0.87	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5775	18987	32270	2.92	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5775	18987	32271	2.92	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6772	19927	33322	0.93	3.9E+00	AF298209.1	NT	Dicotyledonous dicotyledon non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6829	19982	33389	0.7	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H-LA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7013	20149	33570	4.43	3.9E+00	P39289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7519	20592	34068	4.25	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8512	21593	35128	2.44	3.9E+00	X65865.1	NT	X laevis mRNA for M4 muscarinic receptor
11674	23902	37624	2.77	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2693	15813		1.53	3.8E+00	AE001592.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6520	19685	33057	1.05	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
8827	21707	35244	1.12	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9699	23037		0.6	3.8E+00	AJ390961.1	NT	Streptococcus oralis partial xpi gene for xanthine phosphoribosyltransferase, strain NCTC7864
12120	25100		11.65	3.8E+00	9631204	NT	Melanoplus sanguinalipes antitoxin, complete genome
4129	17282	30277	12.78	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7316	20398		0.83	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8378	22454	36017	1.04	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11715	24755	38430	2.11	3.7E+00	BF68279.1	EST_HUMAN	602120551F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:4277748 5'
11715	24755	38451	2.11	3.7E+00	BF68279.1	EST_HUMAN	602120551F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:4277748 5'
12260	25196		1.87	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
608	13795	26814	0.78	3.6E+00	AV781095.1	EST_HUMAN	AV781055 MDS Homo sapiens cDNA clone MDSBLUE10 5'
5363	18572	31440	0.78	3.6E+00	BF316316.1	EST_HUMAN	601901668F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
8749	21828	35364	0.86	3.6E+00	D12387.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line, Homo sapiens cDNA clone tb08
8749	21828	35365	0.86	3.6E+00	D12387.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line, Homo sapiens cDNA clone tb08
8847	21826	35464	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome

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8847	21928	35485	3.67	3.6E+00	AE004447.1	NT	<i>Pseudomonas aeruginosa</i> PAD1, section 8 of 829 of the complete genome
9884	22804	36488	0.51	3.6E+00	U72775.1	NT	<i>Ciconia episcopus</i> cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
9884	22804	36489	0.51	3.6E+00	U72775.1	NT	<i>Ciconia episcopus</i> cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11093	24167						<i>Ciconia episcopus</i> cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
3319	18492	29609	3.21	3.6E+00	M86795.1	NT	<i>Escherichia coli</i> glycerophosphate dehydrogenase (gpd) gene, partial cds; and the translation start site has been verified (gpe), the translation start site has been verified (gpg), and repressor protein (gpr) genes, complete cds
6123	18302		1.04	3.5E+00	AF221538.1	NT	<i>Cryptosporidium felis</i> heat shock protein 70 (HSP70) gene, partial cds
6341	19511	32888	0.93	3.5E+00	L42898.1	NT	<i>Borrelia burgdorferi</i> (strain 25015) outer surface protein (ospC) gene, partial cds
8681	21761		0.56	3.5E+00	R19745.1	EST_HUMAN	1940c08.r1 Soares infant brain IN1B Homd sapiens cDNA clone IMAGE:34940 5'
9232	22310	36851	0.99	3.5E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9232	22310	36852	0.99	3.5E+00	AA190998.1	EST_HUMAN	488b04.s1 Stragene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element contains element MSR1 repetitive element;
9884	22743	36313	1	3.5E+00	AA190998.1	EST_HUMAN	488b04.s1 Stragene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element contains element MSR1 repetitive element;
10739	23772	37383	0.98	3.5E+00	AL161553.2	NT	<i>Arabidopsis thaliana</i> DNA chromosome 4, contig fragment No. 63
1542	14694	27773	3.81	3.4E+00	AJ133723.1	NT	<i>Bos taurus</i> mRNA for Ran-binding protein 2, partial
2844	15767	28882	1.07	3.4E+00	AF254577.1	NT	<i>Brassica napus</i> RP85d mRNA, complete cds
7818	20591	34085	2.33	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7880	20632	34437	0.76	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8876	21955					SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9274	22350	35901	0.77	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNK1) gene, complete cds
9312	22388	35939	0.54	3.4E+00	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
10471	23506	37119	3.35	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
11822	24811	38608	2.06	3.4E+00	AF013167.1	NT	<i>Saccharomyces cerevisiae</i> MSS1 gene, complete cds
6193	19399	32719	0.97	3.4E+00	L77570.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
6193	19399	32720	0.97	3.3E+00	Q08669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8077	21159	34676	1.03	3.3E+00	AF111168.2	NT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
10681	23715	37321	1.04	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10681	23715	37321	1.04	3.3E+00	AF001511.1	NT	<i>Bacillus halodurans</i> genomic DNA, section 5/4
513	13707	28736	1.79	3.2E+00	AP001511.1	NT	<i>Bacillus halodurans</i> genomic DNA, section 5/4
					X98422.1	NT	D. rerio zp-50 POU gene

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4136	13707	28735	0.78	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4850	17983	30971	0.95	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (GEACAM1), mRNA
5686	18880	32170	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5686	18880	32171	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5719	18912	32207	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5719	18912	32208	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6436	19603	32966	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6436	19603	32967	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7781	20837	34330	0.86	3.2E+00	P04276	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7952	21002	34513	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7952	21002	34514	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9230	22308		5.26	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9730	22795	36369	1.31	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (LDV1) gene, complete cds
10345	23350	38981	2.06	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC6 gene for guanylyl cyclase C, complete cds
12219	25169		2.95	3.2E+00	L39338.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5996	19181	32503	2.29	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7547	20619	34095	0.91	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7904	20956		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pale) gene, complete cds
8279	21361	34880	0.51	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8801	21880	35417	5.14	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE 1 DEIODINASE) (DIO1) (TYPE 1 D1) (SD1)
8801	21880	35418	5.14	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE 1 DEIODINASE) (DIO1) (TYPE 1 D1) (SD1)
						SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9469	22575		3.7	3.1E+00	Q14957	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9526	22591	36162	0.55	3.1E+00	Q01149	SWISSPROT	Chlorella vulgaris chloroplast, complete genome
10100	23138	36739	0.78	3.1E+00	7624769	NT	HYPOTHETICAL 96.3 KD PROTEIN F92C9.5 IN CHROMOSOME III
10193	23230		0.56	3.1E+00	Q10125	SWISSPROT	DEOXYTHYMPUSINE SYNTHASE (DHS)
10543	23578	37187	4.09	3.1E+00	P48365	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN), MATRIX PROTEIN (ENVELOPE PROTEIN M), MAJOR ENVELOPE PROTEIN E, NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
						SWISSPROT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
11751	23937		2.45	3.1E+00	P33516	SWISSPROT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds
11771	24763		2.49	3.1E+00	S56980.1	NT	
13019	26670		1.17	3.1E+00	U77666.1	NT	

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2899	16078	26095	0.95	3.0E+00	8023984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5454	18654	31633	1.28	3.0E+00	X53086.1	NT	S. aureus genes encoding Sau861 DNA methyltransferase and Sau861 restriction endonuclease
6686	19844	33234	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.98.2)
6686	19844	33235	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.98.2)
7306	20398		11.21	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7346	20428		0.7	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9108	22187		1.62	3.0E+00	X67836.1	NT	B. rapae DNA for myrosinase
10501	23536	37146	0.58	3.0E+00	Q59605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11259	24328	37967	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11259	24328	37968	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11885	24873	38570	1.37	3.0E+00	P34194	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
2067	15208	28324	2.69	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 94 of the complete genome
7049	20102	33519	1.65	2.9E+00	Z36879.1	NT	F. pringii gdcSP4 gene for P-protein of the glycine cleavage system
7360	20439	33899	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7360	20439	33900	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7614	20684	34160	6.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8082	21135	34655	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8082	21135	34656	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8289	21371	34892	0.81	2.9E+00	BF344171.1	EST_HUMAN	6020774.13F1 NCL_OGAP_Brt64 Homo sapiens cDNA clone IMAGE:4153059 5'
9438	22612		0.82	2.9E+00	AJ002153.2	NT	Segulus oedipus gene for seminal vesicle secreted protein semenogelin I
1466	14639	27722	4.77	2.8E+00	A1180398.1	NT	Bufo terrestris mature K (matK) gene, partial cds; chloroplast gene for chloroplast product
1662	14814		3.14	2.8E+00	AL161662.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7460	20535	34010	5.05	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9813	22853		0.6	2.8E+00	BE566182.1	EST_HUMAN	601342756F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10928	20535	34010	1.53	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
240	13462	26490	13.96	2.7E+00	6678306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
240	13462	26491	13.96	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6669	18893	32148	1.41	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8339	21420		0.74	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
9188	22246		2.18	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9632	21075	34587	0.61	2.7E+00	AW088191.1	EST_HUMAN	xx88e12x1 NCI_CGAP_Bn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10718	23751		1.94	2.7E+00	BE003527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4796	17931	30917	5.51	2.6E+00	AF088749.1	NT	mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5695	18859	32143	2.04	2.6E+00	6755601.1	NT	mus musculus SRY-box containing gene 13 (Sox13), mRNA
5695	18859	32144	2.04	2.6E+00	6755601	NT	mus musculus SRY-box containing gene 13 (Sox13), mRNA
5947	19133		2.55	2.6E+00	Y17062.1	NT	Mycobacterium fortuitum furA II gene
7727	26220		1.18	2.6E+00	AJ224639.1	NT	Homo sapiens Surf-9 and Surf-6 genes
7879	20931		11.26	2.6E+00	AF235602.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8249	21331	34847	1.17	2.6E+00	AJ132180.1	NT	fabu bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
8249	21331	34848	1.17	2.6E+00	AJ132180.1	NT	fabu bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
9858	22898	36481	2.85	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10563	23598		1.91	2.6E+00	9055193	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Opsf3), mRNA
11281	24347	37984	2.2	2.6E+00	AF143875.1	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
12917	26054		3.3	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1492	14845	27728	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1492	14845	27727	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5834	19120	32431	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5834	19120	32432	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6586	19120	32431	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6586	19120	32432	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6868	20020	33428	0.77	2.6E+00	D30062.1	NT	Vibrio cholerae ctaA gene and ctaB gene for cholera toxin, complete cds
7936	20968	34494	1.19	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0009-110900-205-g07 FT0009 Homo sapiens cDNA
7985	21034	34547	0.62	2.6E+00	4502902	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9304	22380	35931	1.55	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10057	23095	36697	0.71	2.5E+00	BE297796.1	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11832	24821		1.39	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
12216	25167		1.86	2.5E+00	AF288665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds, and ELN gene, partial cds
3076	16254	29276	0.89	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5027	18156	31134	4.93	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6134	19313	32652	4.09	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7538	20611	34085	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7538	20611	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
8334	21416	34941	2.06	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	21416	34942	2.06	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8406	21487		2.8	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8852	21931		1.72	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031289-011-405 PT0004 Homo sapiens cDNA
9026	22107	35648	8.99	2.4E+00	P24091	SWISSPROT	ENDOCHITININASE B PRECURSOR (CHNB)
10244	23278	36874	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	23279	36875	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313	23348	36954	2.31	2.4E+00	X92511.1	NT	H sapiens CTGF gene and promoter region
10449	23484		7.28	2.4E+00	P08069	SWISSPROT	XYLOOSE KINASE (XYLOKININASE)
10528	23563	37169	1.64	2.4E+00	BE326702.1	EST_HUMAN	h6306.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10528	23563	37170	1.64	2.4E+00	BE326702.1	EST_HUMAN	h6306.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10818	23851	37474	1.06	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11335	24398	38047	1.36	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees; glpPKD operon and downstream
11640	24720	38413	2.44	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1282	14438	27607	9.98	2.3E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4237	17383		1.41	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5957	19143		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
7612	20682	34166	2.76	2.3E+00	6978554	NT	PROLYLCARBOXYPEPTIDASE
7771	26221		2.37	2.3E+00	P07199	SWISSPROT	Rattus norvegicus ATPase, Car++ transporting, ubiquitous (Atp2a3), mRNA
7958	21008	34518	1.28	2.3E+00	X80285.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
9310	22386	36938	0.62	2.3E+00		NT	M. mazel dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9371	22446	36008	1.86	2.3E+00	Q11127	SWISSPROT	Polypterus ornamentalis mitochondrion, complete genome
11041	24120	37763	2.72	2.3E+00	Q07078	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
12076	25056	36763	2.14	2.3E+00	BF541987.1	EST_HUMAN	ANNEXIN VII (SYNEXIN)
12076	25056	36764	2.14	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088173 5'
12448	26315	32091	7.41	2.3E+00	BF895237.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088173 5'
4126	17280	30276	1.06	2.2E+00	AF020528.1	NT	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
4432	17572	30553	4.12	2.2E+00	D67071.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
							Rat gene for glucocorticoid, exon1 (non-coding exon)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4432	17572	30554	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5458	18658	31637	11.22	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5458	18658	31637	11.22	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5975	19160	32478	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5975	19160	32478	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6187	19363	32711	9.38	2.2E+00	BE260383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
6484	19661	33013	2.87	2.2E+00	Q00336	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6730	19886	33278	3.14	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7097	18524		3.4	2.2E+00	AA594574.1	EST_HUMAN	h85502 st NCI CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1058379 3'
7470	20545	34017	0.83	2.2E+00	AA137027.1	EST_HUMAN	z18704.t1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7783	20839	34332	11.91	2.2E+00	AA449012.1	EST_HUMAN	z405910.t1 Soares_t01 Soares_t01 Homo sapiens cDNA clone IMAGE:785834 5'
7868	20920	34427	0.66	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8284	21376	34896	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2863207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8284	21376	34897	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2863207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9542	22607		12.49	2.2E+00	BE741878.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9788	26860		2.12	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A
10259	23294	36890	1.12	2.2E+00	A1280373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2Ndb-HP8b9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10259	23294	36891	1.12	2.2E+00	A1280373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2Ndb-HP8b9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10301	23336	36941	3.04	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10873	23707	37316	2.6	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11726	23912	37536	3.3	2.2E+00	P07811	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11915	24902	38605	6.04	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
583	16016	26785	13.2	2.1E+00	AF132812.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3678	16841		1.19	2.1E+00	AW449396.1	EST_HUMAN	UI-H-B13-aid-e-08-q-U1.st NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6260	19434		0.97	2.1E+00	P76357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6947	20260	33698	3.51	2.1E+00	O70169	SWISSPROT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7169	20302	33745	0.77	2.1E+00	4503430	NT	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7191	20058	33466	5.88	2.1E+00	N28575.1	EST_HUMAN	y08a10.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
8694	21774		2.43	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
1223	14383	27444	1.32	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000871 5'
1223	14383	27445	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1366	14520	27595	1.37	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1606	14759		3.06	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2216	16360	28480	7.2	2.0E+00	Z78278.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2219	16350	28481	7.2	2.0E+00	Z78278.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4218	17365	30353	1.71	2.0E+00	AW664496.1	EST_HUMAN	R. norvegicus mRNA for collagen alpha1 type I
4218	17365	30354	1.71	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677
7722	20786		0.96	2.0E+00	P07568	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8214	21296	34815	4	2.0E+00	AB008878.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8214	21296	34816	4	2.0E+00	AB008878.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE
8214	21296	34817	4	2.0E+00	AB008878.1	NT	GLYCOPROTEINS E1 AND E2
9122	22201	35743	3.04	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
12815	26022	31670	6.76	2.0E+00	5834843	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5715	18908	32202	4.28	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5715	18908	32203	4.28	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6225	19400	32750	1.2	1.9E+00	BE969695.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
6792	19947		0.92	1.9E+00	AW845689.1	EST_HUMAN	Gallus gallus mitochondrion, complete genome
8888	20040		1.91	1.9E+00	Q63927	SWISSPROT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (Itp1), mRNA
8853	21733	35272	2.21	1.9E+00	P02467	SWISSPROT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (Itp1), mRNA
8853	21733	35273	2.21	1.9E+00	P02467	SWISSPROT	MRD-CT0063-077089-002-gp2 CT0063 Homo sapiens cDNA clone IMAGE:3946881 5'
8859	21638		3.32	1.9E+00	BF360208.1	EST_HUMAN	CTD-BINDING SR-LIKE PROTEIN RA4
9095	22174		1.86	1.9E+00	O51781	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							CM3-MT0114-010800-323-H12-MT0114 Homo sapiens cDNA
							ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8830	22870	36452	0.63	1.8E+00	AA669125.1	EST_HUMAN	ab94a04.s1 Stratigene lung (#937210) Homo sapiens cDNA clone IMAGE:854674 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element ;
10780	23823	37447	0.87	1.8E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3182	16337	29348	1.69	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3190	16365	28370	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3190	16365	29371	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5988	19173		1.63	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6230	19405	32755	2.02	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6528	19692		1.28	1.8E+00	BF683327.1	EST_HUMAN	602138470F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:4298272 5'
6878	20031	33441	1.15	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7204	20069	33479	1.22	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7411	20489		0.8	1.8E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1 & GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8308	21390	34913	0.68	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8308	21390	34914	0.68	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8308	21390	34914	0.68	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8055	22134	35678	2.28	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9376	22451	36013	0.78	1.8E+00	R31042.1	EST_HUMAN	Y772e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9482	22519	36081	0.82	1.8E+00	AW880004.1	EST_HUMAN	QY6-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
9886	23034	36628	0.47	1.8E+00	P06828	SWISSPROT	FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1]
10054	23092	36884	0.94	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10480	23525		4.71	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10777	23810		0.75	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12575	25994		4.97	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12687	25444		6.01	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
13005	25987	31854	1.45	1.8E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
1132	14297	27352	1.68	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2345	15478	28609	4.9	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2445	16573	28702	1.49	1.7E+00	AI141067.1	EST_HUMAN	oz43405.x1 Sceres_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4581	17718	30701	0.98	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5730	18923	32216	1.73	1.7E+00	BE003546.1	EST_HUMAN	CMO-BT0282-171299-127-e08 BT0282 Homo sapiens cDNA
5730	18923	32217	1.73	1.7E+00	BE003546.1	EST_HUMAN	CMO-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
6141	19319	32681	3.02	1.7E+00	Q97TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
6682	19840	33230	0.67	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE) PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)
7367	20446	33908	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7367	20446	33909	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8036	21121	34641	1.1	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8222	21304	34825	1.08	1.7E+00	6755715	NT	Mus musculus T cell acute lymphocytic leukemia 1 (Tal1), mRNA
8252	21334	34852	0.67	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCL CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4214689 5'
8739	21818	36362	0.76	1.7E+00	AF245513.1	EST_HUMAN	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8828	21907	35519	0.66	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
8901	21980	35620	0.66	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9014	22093	35633	1.03	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9350	25859	35981	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9350	25859	35982	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9806	22846		1	1.7E+00	AF161390.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10376	23410		0.54	1.7E+00	AW953581.1	EST_HUMAN	EST368761 MAGC resequences, MAGC Homo sapiens cDNA
10857	23890	37509	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890484 5'
10857	23890	37510	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890484 5'
11898	24884	38582	1.87	1.7E+00	W22424.1	EST_HUMAN	6787 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12623	26356	32066	1.94	1.7E+00	AI678443.1	EST_HUMAN	tu82807.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11
2090	15230	28352	19.63	1.6E+00	AF196339.1	NT	MSR1 repetitive element;
2101	15241	28362	4.14	1.6E+00	AF077374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2107	15246	28367	1.26	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2357	15488		0.97	1.6E+00	X98373.1	NT	Mus musculus ST6GalNAcII gene, exon 2
3028	16202	29225	1.22	1.6E+00	W59426.1	EST_HUMAN	B. napus gene encoding endo-polygalacturonase
							z123701.r1 Sceres_fetal_heart_NHH18W Homo sapiens cDNA clone IMAGE:341889 5' similar to
							gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);

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3857	17017		1.08	1.6E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4142	17294		6.06	1.6E+00	BF570077.1	EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4472	17612	30590	1.25	1.6E+00	AF165827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4472	17612	30591	1.25	1.6E+00	AF165827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5184	18306	31270	0.59	1.6E+00	AF127897.1	NT	Samitri boliviensis olfactory receptor (SBO27) gene, partial cds
5194	18316	31284	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5194	18316	31285	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5948	19134	32447	2.38	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6035	19218	32540	0.78	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6599	19759	33147	0.91	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6849	20002	33411	1.05	1.6E+00	AW284981.1	EST_HUMAN	UI-H-B12-ahr-b-04-Q-U1.s1 NCLCGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7394	20472	33938	2.37	1.6E+00	BE697287.1	EST_HUMAN	RCO-C70415-200700-032-c10 C70415 Homo sapiens cDNA
8219	21301		1.3	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8574	21655	35196	3.3	1.6E+00	AJ287131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SQL & CYP_b genes
9101	22180	35724	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9101	22180	35725	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9272	22348	35898	0.49	1.6E+00	BE388331.1	EST_HUMAN	601263925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9659	25857	34615	1.05	1.6E+00	X62046.1	NT	M. musculus COL3A1 gene for collagen alpha1
9659	25857	34616	1.05	1.6E+00	X62046.1	NT	M. musculus COL3A1 gene for collagen alpha1
9786	22826		0.7	1.6E+00	AF043466.1	NT	Thermotoga bacter ethandicus D-xylase-binding protein (xylF) gene, complete cds
9935	22974	36566	1.49	1.6E+00	T41290.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
10388	23423	37029	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0018-090200-100-407 LT0018 Homo sapiens cDNA
10388	23423	37030	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0018-090200-100-407 LT0018 Homo sapiens cDNA
10552	23587	37195	0.52	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11010	24089	37726	1.77	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
11082	19218	32540	4.8	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
12006	24991	38695	3.68	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
33	13271	26275	2.96	1.6E+00	U53449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
241	13463	26492	2.44	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
636	13821		1.81	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagridin) (Adam15), mRNA
2481	15608	28732	1.56	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2684	15709	28828	2.02	1.5E+00	6878360	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tlmt1), mRNA

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3208	15608	28732	1.75	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3462	16629	29649	0.77	1.5E+00	AE001945.1	NT	Delnecoccus radicularis R1 section 82 of 229 of the complete chromosome 1
5846	19036	32342	0.71	1.5E+00	AI855301.1	EST_HUMAN	tt12f10.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1;
5846	19036	32343	0.71	1.5E+00	AI855301.1	EST_HUMAN	tt12f10.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1;
6536	19699	33072	2.49	1.5E+00	R17879.1	EST_HUMAN	tg10a02.r1 Soares infant brain T1B1 Homo sapiens cDNA clone IMAGE:31693 5'
7278	20361	33853	1.68	1.5E+00	BE78336.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7311	20393	33854	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7311	20393	33854	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575	34048	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak26f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7768	20826	34317	0.77	1.5E+00	AI003254.1	EST_HUMAN	an07b11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684833 3' similar to gb:395936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8313	21395	34920	0.9	1.5E+00	BE887446.1	EST_HUMAN	601609889F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8367	21448	34971	0.5	1.5E+00	AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8846	21925	35463	1.09	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
9218	22296		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9334	22410	35963	0.51	1.5E+00	BF217818.1	EST_HUMAN	601882682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9684	22733	36303	0.85	1.5E+00	R61928.1	EST_HUMAN	y03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9835	22875	36469	1.6	1.5E+00	AW376697.1	EST_HUMAN	QV3-OT0192-261099-008-009 CT0192 Homo sapiens cDNA
10064	23102	36705	6.49	1.5E+00	BF376754.1	EST_HUMAN	RCb-TN0078-150900-034-005 TN0078 Homo sapiens cDNA
10258	23293		1.85	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183865 5'
10399	23434	37040	2.26	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10399	23434	37041	2.26	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11684	24693	38373	3.4	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243.s1 547 (synonym: hfor1) Homo sapiens cDNA clone DKFZp547P243 3'
11834	24823		7.68	1.5E+00	X07380.1	NT	Maize mitochondrial rRNA-Ser gene and rRNA-Phe pseudogene
11829	24915	38617	1.39	1.5E+00	AI400798.1	EST_HUMAN	tg94409.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
11829	24915	38618	1.39	1.5E+00	AI400798.1	EST_HUMAN	tg94409.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12615	26085	31662	1.61	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12765	25508		3.92	1.5E+00	AI445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
12888	25588		2.17	1.5E+00	6878492	NT	Rattus norvegicus 5'-Lipoxygenase (ALOX5), mRNA
13220	25794	31888	1.31	1.5E+00	BF223835.1	EST_HUMAN	7q82006.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
30	13268	26271	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
30	13268	26272	2.27	1.4E+00	7661686	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15482		0.97	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (gha) gene, complete cds
2411	15541		9.39	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2734	15551	28984	1.7	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2833	15947	29055	3.22	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2833	15947	29056	3.22	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3414	16883		0.79	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4370	17513	30493	1.13	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-H08 NN1005 Homo sapiens cDNA
4370	17513	30494	1.13	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-H08 NN1005 Homo sapiens cDNA
4708	17543		1.51	1.4E+00	BF681547.1	EST_HUMAN	602T56687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287566 5'
5317	18434		0.94	1.4E+00	Q07969	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5488	18687	31705	1.73	1.4E+00	AW054976.1	EST_HUMAN	w45g07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5845	18839		8.04	1.4E+00	AB032883.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6409	19578	32839	3.07	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6424	28214		3.93	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6542	19705	33078	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6542	19705	33079	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6961	20189	33614	0.8	1.4E+00	AW893057.1	EST_HUMAN	CM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA
7438	20515	33988	1.89	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7454	20531	34005	1.14	1.4E+00	AW467750.1	EST_HUMAN	haz305.x1 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7614	20588	34062	0.7	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ)
7514	20588	34063	0.7	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ)
8530	21611		0.72	1.4E+00	P07693	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8994	22073		5.4	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9295	22371	35020	1.65	1.4E+00	R20459.1	EST_HUMAN	yx33112.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9388	22472	36038	3.83	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9432	22502	36072	0.65	1.4E+00	AF134944.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10412	23447	37052	0.88	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10457	23492	37102	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10457	23492	37103	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10744	23777	37390	0.96	1.4E+00	D63441.1	NT	Pandora colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10744	23777	37391	0.96	1.4E+00	D63441.1	NT	Pandora colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10852	23895	37504	1.15	1.4E+00	Q07283	SWISSPROT	TRICHOHYALIN
11499	24557	38232	4.92	1.4E+00	AB006882.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11691	24699	38379	3.46	1.4E+00	BE982107.2	EST_HUMAN	801655184R1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3845805 3'
11691	24699	38380	3.48	1.4E+00	BE982107.2	EST_HUMAN	801655184R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3845805 3'
11711	24751	38444	2.3	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11711	24751	38445	2.3	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12359	26012		2.01	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12765	26204		2.99	1.4E+00	11545838	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen ser70-2 (SE70-2), mRNA
684	13776		1.06	1.3E+00	Z73640.1	NT	M. musculo gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
825	14100	27164	2.79	1.3E+00	AJ271192.1	NT	Centharrellus sp. partial 26S rRNA gene, isolate 1161
1153	14317		23.81	1.3E+00	Y18213.1	NT	Homo sapiens putative palHbA pseudogene for hair keratin, exons 2 to 7
1325	14482	27549	14.36	1.3E+00	4507988	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1325	14482	27550	14.36	1.3E+00	4507988	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1387	14542		0.98	1.3E+00	U61730.2	NT	Cdx lacryme-joli dihydrodipicolinate synthase (dapa) gene, complete cds
1641	14783		2.35	1.3E+00	AE002338.2	NT	Ghlamydia muridarum, section 86 of 86 of the complete genome
2316	15448		2.38	1.3E+00	AB030447.1	NT	Cyathus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP)
2615	15739		1.81	1.3E+00	BE968735.2	EST_HUMAN	and MASP-related protein, complete cds
3005	16180	29201	0.86	1.3E+00	6755821	NT	Mus musculus alpha-spectrin 1, erythroid (Sptal), mRNA
3686	16949	29857	1.14	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5631	18825	31900	1	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOXYGENASE P3 COMPONENT)
5827	19017	32322	0.58	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6142	19320	32662	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-08 CT0289 Homo sapiens cDNA
6142	19320	32663	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-08 CT0289 Homo sapiens cDNA
6547	19709	33085	1.14	1.3E+00	M33496.1	NT	D melanogaster no-on-transient A gene product, complete cds
6990	20042		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6928	20243		0.58	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
6978	20206	33634	1.04	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7092	20186	33610	1.16	1.3E+00	BE538819.1	EST_HUMAN	601661420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447865 5'
7249	20332	33779	0.96	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7616	20686	34162	0.78	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8494	21575	35112	1.78	1.3E+00	AJ009912.1	NT	Sus scrofa alp gene
8642	21722	35259	2.28	1.3E+00	BE963378.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
8758	21837	35378	1.05	1.3E+00	BE974280.1	EST_HUMAN	601660250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3960532 3'
8907	21986		1.87	1.3E+00	8910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8990	22089	35609	0.89	1.3E+00	AJ927628.1	EST_HUMAN	wc85607.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9347	22423	35978	0.51	1.3E+00	H42981.1	EST_HUMAN	y086c03.s1 Soares breast 3NBHb1 Homo sapiens cDNA clone IMAGE:183078 3'
9347	22423	35977	0.51	1.3E+00	H42981.1	EST_HUMAN	y086c03.s1 Soares breast 3NBHb1 Homo sapiens cDNA clone IMAGE:183078 3'
9715	22780		5.02	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9724	22789	36359	2.47	1.3E+00	X72019.1	NT	S. alba phr-1 mRNA for photolyase
9724	22789	36360	2.47	1.3E+00	X72019.1	NT	S. alba phr-1 mRNA for photolyase
9823	22863	36444	1.21	1.3E+00	AF069250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9847	22887		0.47	1.3E+00	AW024390.1	EST_HUMAN	w03703.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2528477 3' similar to gb:M31522
9871	22911	36496	1.05	1.3E+00	Q00754	SWISSPROT	TRANSCRIPTION FACTOR ITF-1 (HUMAN);
9952	22961	36584	1.21	1.3E+00	AJ927629.1	EST_HUMAN	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
10031	23089	36668	0.68	1.3E+00	AJ23962.1	NT	w05507.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
10031	23089	36669	0.68	1.3E+00	AJ23962.1	NT	Lactococcus lactis cremoris NCDO-hv1 chromosomal inversion junction DNA
10070	23108	36711	3.93	1.3E+00	BE963379.2	EST_HUMAN	Lactococcus lactis cremoris NCDO-hv1 chromosomal inversion junction DNA
10130	23188		0.57	1.3E+00	AJ56944.1	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
10353	23388	36996	0.5	1.3E+00	AF061251.1	NT	IQ77a12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723
10353	23388	36997	0.5	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10418	23453	37059	1.68	1.3E+00	AE004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10435	23470	37076	1.59	1.3E+00	IM28953.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10811	23844		0.98	1.3E+00	AL163302.2	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10838	23871	37493	0.47	1.3E+00	AJ900846.1	EST_HUMAN	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10851	23884		0.53	1.3E+00	8923937	NT	Homo sapiens chromosome 21 segment HS21C102
							w032e10.x1 NCI_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN
							O16881 THIOREDOXIN REDUCTASE ;
							Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10854	23887	37506	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	23887	37507	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10861	23884	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yc68c03.st Soares breast 3Nb-HBst Homo sapiens cDNA clone IMAGE:183076 3'
10861	23884	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yc68c03.st Soares breast 3Nb-HBst Homo sapiens cDNA clone IMAGE:183076 3'
10832	24014		4.05	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	2.4	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11169	24240	37872	1.77	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
11619	24670		1.43	1.3E+00	AW274791.1	EST_HUMAN	xp06c03.x1 NCI CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'
11831	24820	38511	2.73	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11923	24909	38610	2.28	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.6kb fragment
11994	24978		1.35	1.3E+00	L31891.1	NT	Arabidopsis thaliana 3-ketoacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12504	25347		3.81	1.3E+00	AF187673.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12696	25465	32022	2.76	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158452 5'
12707	25689		1.96	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	25549		1.93	1.3E+00	AF187036.1	NT	Sturnira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
13200	25783		1.34	1.3E+00	U38978.1	NT	Naphthalenesulfonate-degrading bacterium BN6 2,3-dihydroxybiphenyl dioxygenase (bphCII) gene, complete cds
13231	25981		1.63	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21G083
687	13953	28881	8.73	1.2E+00	AA676248.1	EST_HUMAN	z122408.st Soares_fetal_liver_spleen_1NF1S ST Homo sapiens cDNA clone IMAGE:431535 3'
846	14024	27082	1.92	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFH-RP-III)
846	14024	27083	1.92	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFH-RP-III)
846	14024	27084	1.92	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFH-RP-III)
901	14076		1.21	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PR03077 (PRO3077), mRNA
1187	14349	27407	7.6	1.2E+00	AF080245.2	NT	Eleis oleifera sesquiterpene synthase mRNA, complete cds
1232	14391	27453	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1232	14391	27454	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2068	16207	28323	1.02	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16364	29359	1.06	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3234	16408	29421	7.01	1.2E+00	AL161663.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	29422	7.01	1.2E+00	AL161663.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3358	16530		3.57	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3437	16605	28625	0.61	1.2E+00	AF188740.1	NT	Homo sapiens LFX3 gene, intron 2
3804	16964	28987	9.16	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4084	17249	30254	1.87	1.2E+00	BF37570.1	EST_HUMAN	MRO-FT0176-050900-203-g06_1 FT0175 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4413	16605	29625	1.08	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4564	17731		1.91	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4945	17781	30763	0.94	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4882	17817	30803	2.03	1.2E+00	AF158495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4712	17847		6.8	1.2E+00	Y09200.1	NT	T. dinnatum chloroplast rbcL gene, partial
5554	18751	31788	1.13	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5672	18866	32152	2.34	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0181-140200-013-c05 ST0191 Homo sapiens cDNA
5917	19105		0.55	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
5995	19180	32502	0.77	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF161 (ZNF161) gene, complete cds
8280	19454	32802	2.45	1.2E+00	X74885.1	NT	O. hydral y1 repeat cluster DNA, fragment D
6342	19512	32869	3.81	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-303 BN0090 Homo sapiens cDNA
8420	19589	32953	1.28	1.2E+00	X86084.1	NT	C. glutamicum pla gene and ackA gene
6420	19589	32954	1.28	1.2E+00	X89084.1	NT	C. glutamicum pla gene and ackA gene
6453	19630	32991	36.06	1.2E+00	AA759254.1	EST_HUMAN	sh84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374.3'
							yy93b12.s1 Soares melanocyte 2Nbr-IM Homo sapiens cDNA clone IMAGE:273599 3' similar to.
6566	19726	33105	0.73	1.2E+00	N33295.1	EST_HUMAN	gb U87936 HUMAAALU472 Human carcinoma cell-derived Alu RNA transcript, (fRNA); gb J04870
6830	19760	33178	0.62	1.2E+00	P17671	SWISSPROT	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6634	19763	33182	1.94	1.2E+00	AW813276.1	EST_HUMAN	ECODYSONE-INDUCIBLE PROTEIN E75-A
7055	20108	33524	1.72	1.2E+00	AB028010.1	NT	MR3-ST0181-140200-013-c05 ST0191 Homo sapiens cDNA
7067	20120	33534	2.81	1.2E+00	AJ002141.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
							Mus musculus DSPP gene
7180	20312	33755	0.68	1.2E+00	AA167810.1	EST_HUMAN	zc38t05.11 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632001 5' similar to
7403	20481		0.71	1.2E+00	AJ271735.1	NT	gb D10522 Human mRNA for 80K-L protein, complete cds. (HUMAN);
7542	20547	34092	1.85	1.2E+00	AV734585.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
7828	20883	34385	2.81	1.2E+00	X74207.1	NT	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
7987	21047	34560	0.6	1.2E+00	BE787846.1	EST_HUMAN	L. lactis pyrD and pyrF genes
8787	21846	35387	3.19	1.2E+00	AB033030.1	NT	801481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
							Homo sapiens mRNA for KIAA1204 protein, partial cds
8863	21942	35477	0.82	1.2E+00	P38427	SWISSPROT	ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT
9077	22156		0.7	1.2E+00	7706271	NT	(TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE
9226	22304	35847	1.81	1.2E+00	AW37210.1	EST_HUMAN	GLUCOSYL TRANSFERASE)
9440	22514	36078	0.51	1.2E+00	H48399.1	EST_HUMAN	Homo sapiens CGI-30 protein (LOC51611), mRNA
							MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
							yy80a06.17 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:202066 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9698	22653	36224	3.79	1.2E+00	Z32850.1	NT	R communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9805	22845	36423	2.13	1.2E+00	D11745.1	EST_HUMAN	HUMHMO1A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
10136	23173	36771	3.6	1.2E+00	X56832.1	NT	H sapiens ENO3 gene for muscle specific enolase
10532	23567		0.82	1.2E+00	AB009668.1	NT	Homo sapiens hldho gene, exon 1
11432	24493	38158	1.69	1.2E+00	M38686.1	NT	Mus musculus Id gene, exon 1
11627	24707	38400	1.51	1.2E+00	AW817817.1	EST_HUMAN	PMD-ST0284-161199-001-d01 ST0284 Homo sapiens cDNA
11666	24743		7.69	1.2E+00	BE160761.1	EST_HUMAN	PM1-H10422-160200-007-g10 HT0422 Homo sapiens cDNA
11744	23930	37558	3.13	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12101	25081	38788	1.68	1.2E+00	M10408.1	NT	Mutze mitochondrial F-O-A1Pase protolipid (subunit 9) gene
12471	25884	31768	17.76	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12491	25339		1.74	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 8/14
13218	25793		2.66	1.2E+00	AA077909.1	EST_HUMAN	7H11A06 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H11A06
476	13671	28703	1.11	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1802	14951	28045	1.23	1.1E+00	AW985383.1	EST_HUMAN	QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1948	15091	28192	1.21	1.1E+00	AW578889.1	EST_HUMAN	U1HF-BR0p-alk-f02-0-U1et NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3074834 3'
2017	15157		2.74	1.1E+00	AF137273.1	NT	Gallus gallus alpha 1 (V) collagen mRNA, complete cds
3409	16579	29594	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3409	16579	29595	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3575	19740	29757	1.02	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3670	16833	29844	0.99	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3812	16972	29974	1.16	1.1E+00	AE003866.1	NT	SW-F531_HUMAN Q12888 P63-BINDING PROTEIN 53BP1 ;
3812	16972	29975	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3920	17079		0.92	1.1E+00	X85374.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
4054	17210	30220	1.03	1.1E+00	8922841	NT	H-parahaemolyticus hphIM(A), hphIM(G), hphIR and menB genes
4130	17283	30278	0.72	1.1E+00	8755205	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4331	17474		6.82	1.1E+00	5835331	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
5107	18235	31204	3.45	1.1E+00	U18466.1	NT	R. unkonis complete mitochondrial genome
5180	18302	31286	2.06	1.1E+00	X78426.1	NT	African swine fever virus, complete genome
5422	18023	31598	1.49	1.1E+00	6978530	NT	E. faecalis pfp5 gene
5731	18924	32218	14.33	1.1E+00	BE960184.1	EST_HUMAN	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5750	18942	32243	1.32	1.1E+00	AI138582.1	EST_HUMAN	60165276R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828835 3'
6217	19392	32740	0.9	1.1E+00	11419739	NT	q885603.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
							Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6404	19573	32935	0.59	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6537	19700	33073	0.72	1.1E+00	RO6037.1	EST_HUMAN	ye86d03.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:124924 5'
6866	20009	33419	0.78	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 88 (EP88 gene)
7447	20524	33997	0.58	1.1E+00	X65981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7632	20701	34178	0.67	1.1E+00	BF683714.1	EST_HUMAN	602136678F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301322 5'
7659	20728	34201	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7659	20728	34202	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7680	20746	34226	8.36	1.1E+00	AL161988.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7754	25853	34305	1.04	1.1E+00	11987980	NT	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8326	21407	34634	3.2	1.1E+00	BF693966.1	EST_HUMAN	60208282F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8416	21497	35029	0.91	1.1E+00	AJ478339.1	EST_HUMAN	tn36111.x1 NC1_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
8835	22014	35554	0.86	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COX1-like gene
9015	22094	35634	0.87	1.1E+00	S80750.1	NT	VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
9126	22206	35748	0.53	1.1E+00	AJ079946.1	EST_HUMAN	α3405.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9637	21080		0.75	1.1E+00	BE384878.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9828	22868	36450	0.51	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
9863	22923		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9974	23013	36607	1.03	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psae, psaf, adhesin (psaA), chaperone (psab), and usher (psac) genes, complete cds
10038	23076	36676	1.85	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
10141	23178	36777	4.09	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10202	23239	36829	20.74	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10719	23752	37358	1.21	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10831	23894	37486	0.56	1.1E+00	AJ878921.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2818282 5' similar to gb:D10522
10866	23970	37600	1.97	1.1E+00	11067364	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN); Homo sapiens KIAA0828 gene product (KIAA0828), mRNA
10947	24029		3.14	1.1E+00	AF068942.1	NT	Klebsoridium fluitans cytochrome o oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11343	24406	38055	3.72	1.1E+00	L16877.1	NT	Homo sapiens cytochrome P450C9 (CYP2C9) gene, 5' flank and exon 1
11361	18486		2.74	1.1E+00	8822973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11386	24427	38083	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11369	24427	38084	2.03	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11637	24717	38409	3.99	1.1E+00	AF009699.1	EST_HUMAN	w78e11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11870	24858	38552	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
11870	24858	38553	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12441	25312		1.82	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12647	26371	32070	3.58	1.1E+00	AF216993.1	NT	Taenia solium Immunogenic protein Ts78 mRNA, partial cds
12689	25980		1.86	1.1E+00	AF234169.1	NT	Dictyostellum discoideum isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
101	13337		1.84	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
116	13347	26374	2.1	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
431	13626		-2.78	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
590	13761	26800	1.44	1.0E+00	AJ251660.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
694	13877	26910	7.14	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
696	13878		2.29	1.0E+00	AF125984.1	NT	Aedes aegypti muclin-like protein MUC1 mRNA, complete cds
1417	16037		1.35	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1795	14944	28037	1.33	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2554	15679	28803	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2554	15679	28804	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2621	15744		0.95	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WIP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;
2940	16117	29129	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2940	16117	29130	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3032	16208		0.95	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C9F12.08C IN CHROMOSOME I
3269	16443	29463	1.16	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WIP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;
3459	16626		0.73	1.0E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NmlU) gene, exons 5 and 6
3688	13337		0.75	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3772	16933	29939	1.81	1.0E+00	AJ223816.1	NT	Agericus bisporus mRNA for tyrosinase

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4180	17350	30322	1.12	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4390	17533		0.72	1.0E+00	8922246	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5396	18598	31568	2.3	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5971	19157	32472	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5971	19157	32473	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6077	19259	32588	1.74	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6241	19415	32763	4.85	1.0E+00	P04501	SWISSPROT	FIBRIN PROTEIN
6248	19422	32768	1.67	1.0E+00	AW452782.1	EST_HUMAN	UIH-B8-alk-d-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3086989 3'
6618	19778	33167	2.04	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6671	19830	33219	0.83	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6767	19923		1.07	1.0E+00	P46508	SWISSPROT	SRB-11 PROTEIN
6795	19950	33349	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6795	19950	33350	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6916	20231	33864	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding yolkopsin
7288	20371	33828	1.16	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7647	20716		9.68	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7889	20941	34447	1.51	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7903	20955	34462	6.02	1.0E+00	AA775191.1	EST_HUMAN	ac79008.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:868791 3'
8019	21070		0.72	1.0E+00	BF679213.1	EST_HUMAN	602163792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8148	21230	34749	1.65	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3948005 5'
8148	21230	34750	1.65	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3948005 5'
8335	18495		1.48	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8545	21626	35163	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8545	21626	35164	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8872	21762		1.07	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8708	21788	35321	0.64	1.0E+00	Q8Y6T6	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8708	21788	35322	0.64	1.0E+00	Q8Y6T6	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8735	25858		1.82	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181089-011-008 HT0229 Homo sapiens cDNA
8776	21855	35397	1.15	1.0E+00	U427720.2	NT	Simian Immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8922	22001	35540	1.8	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9471	22528	36091	1.95	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889421 5'
9682	22731	36301	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9882	22731	36302	1.82	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9810	22850	36428	1.81	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK Homo sapiens cDNA clone GKCCYA11 5'
9815	22855	36434	1.32	1.0E+00	U44982.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9816	22856	36436	1.32	1.0E+00	U44982.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
10318	23353	36961	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBF) mRNA
10318	23353	36962	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBF) mRNA
10408	23443	37050	0.89	1.0E+00	A1077920.1	EST_HUMAN	oy15d07.st Soares_senescart_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665601 3'
10533	23688	37176	3.99	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW C04 5'
10594	23727	37333	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10594	23727	37334	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10728	23761	37368	1.22	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11216	24285	37924	1.37	1.0E+00	SG0825.1	NT	PBR1=proline-rich protein (htron 3) [human, Genomic, 898 nt]
11342	24405	38054	1.46	1.0E+00	AA701494.1	EST_HUMAN	zh93b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element;
11825	24814		1.62	1.0E+00	L47613.1	NT	Pleca glauca EMB13 mRNA
12329	25238		6.49	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12676	25451		2.67	1.0E+00	AW976184.1	EST_HUMAN	EST388283 IMAGE resequencing, MAGN Homo sapiens cDNA
3693	16855		1.04	9.9E-01	AF174855.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
6752	18944	32246	8.8	9.9E-01	P49667	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5990	19175	32498	0.83	9.8E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9461	22518		1.68	9.8E-01	U65667.1	NT	Lycopodium esculentum putative M1 copy 1 nematode-resistance gene
9765	22893		2.14	9.8E-01	Q28542	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536	13729	26753	1.17	9.8E-01	P22867	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL-GLUTAMATE SYNTHASE) (AGS) (NAGS)
2370	15501		1.26	9.8E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
2862	15976		1.29	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3903	17062	30061	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838481 3'
3903	17062	30062	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7349	20429	33890	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7349	20429	33891	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7823	20878	34378	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7823	20878	34379	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8916	21985	35534	0.94	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10853	23887		1.02	9.8E-01	AA825565.1	EST_HUMAN	cd55d04.t1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11242	24311	37948	1.84	9.8E-01	BE288705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11242	24311	37949	1.84	9.8E-01	BE288705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12564	26377					NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7309	20391	33851	2.73	9.8E-01	U52111.2	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8701	21781	35314	1.9	9.8E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8707	21787	35320	1.54	9.8E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039	22118	35661	0.73	9.8E-01	BE799922.1	EST_HUMAN	601562169F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'
11444	24505		3.56	9.8E-01	BF511209.1	EST_HUMAN	U-H-BJ4-ack-e-07-Q-U.t1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
13208	25789		3.17	9.8E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4558	17696	30675	0.74	9.8E-01	AF167925.1	NT	Borinus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4558	17696	30676	0.74	9.8E-01	AF167925.1	NT	Borinus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4580	17717	30700	1.28	9.8E-01	AW799674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5872	19062	32369	3.51	9.8E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5872	19062	32370	3.51	9.8E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6886	20038	33447	0.6	9.8E-01	Z87341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7512	20586	34059	0.63	9.6E-01	AF197881.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8586	21687		1.52	9.6E-01	X85276.1	NT	P. falciparum complete gene map of plasid-like DNA (IR-A)
9052	22131	35875	0.92	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps27 gene, complete cds
11348	24408	38000	1.42	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein e4 Y isoform gene, complete cds
11808	24798	38496	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11808	24798	38497	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
12225	25174		1.31	9.6E-01	11421722	NT	Homo sapiens centromere protein 2 (CEP2), mRNA
12915	26081	31656	1.68	9.6E-01	U91423.1	NT	Sphyma liburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2545	15870	28794	1.81	9.5E-01	7705591	NT	Homo sapiens GGI-125 protein (LOC51003), mRNA
3882	17041	30038	2.1	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3882	17041	30039	2.1	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9202	22280	35919	0.71	9.5E-01	A190182.1	EST_HUMAN	qds7d07.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1733561 3'
9308	22382	35933	1.04	9.5E-01	AW881102.1	EST_HUMAN	RC1-C70295-241189-011-502 C70295 Homo sapiens cDNA
11520	24578	38254	1.56	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11737	23923	37548	1.57	9.5E-01	AW293799.1	EST_HUMAN	UI-H-B12-ahp-f03-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3271	16445		6.72	9.4E-01	AF165900.1	NT	Barotella claudigiae RNA polymerase beta subunit (pob) gene, partial cds
3289	16463		2.17	9.4E-01	AF080695.1	NT	Pimpla brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9086	22145	35692	0.79	9.4E-01	M90724.1	NT	Human Fe-gamma-receptor IIA (FCGR2A) gene, exon 4
12496	25343		1.86	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3869829 5'
12014	25975		1.4	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1769	14918		1.24	9.3E-01	AF242382.1	NT	Homo sapiens phytoeyl-CoA hydroxylase (PHYH) gene, exon 5
2698	15818	28934	3.62	9.3E-01	BE071172.1	EST_HUMAN	RC5-B70503-271199-011-B01 BT0503 Homo sapiens cDNA
4146	17298	30289	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4146	17298	30289	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5709	18002	32197	1.6	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5795	18988	32289	3.48	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7488	20581		1.08	9.3E-01	AF270848.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8257	21339	34856	1.88	9.3E-01	AA847040.1	EST_HUMAN	600903.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1385357
9013	22092		1.1	9.3E-01	AF081981.1	NT	Xenopus laevis CCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9137	22216	35760	0.89	9.3E-01	AL161534.2	NT	Aralidopsis thaliana DNA chromosome 4, contig fragment No. 34

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13039	26683	31661	2.09	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA
13049	25683		1.22	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rL34 mRNA, complete cds
3311	16484	28503	3.92	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4969	18128		0.61	9.2E-01	BF129973.1	EST_HUMAN	601817814F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4041363 5'
5836	18025		1.58	9.2E-01	7105410	NT	Mus musculus soluble carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6109	19293	32824	4.97	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884681 5'
6770	18925	33320	0.65	9.2E-01	M84703.1	NT	N crassa valyl-tRNA synthetase (cyl-20/un-3) gene
9860	22900	36484	0.98	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9949	22988	36592	1.31	9.2E-01	6871877	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10472	23507	37120	3.6	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10627	23661	37269	1.64	9.2E-01	BF583251.1	EST_HUMAN	768903.x1 NCI_CGAP_K1811 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
10883	23967	37606	1.76	9.2E-01	BE563811.1	EST_HUMAN	P04340 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5:
12022	25006	38707	1.5	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888714 5'
							601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1654	14807	27892	1.52	9.1E-01	T96875.1	EST_HUMAN	ye52101.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2193	15328		1.49	9.1E-01	8923056	NT	Alu repetitive element:
							Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3275	16449	29468	1.28	9.1E-01	T28418.1	EST_HUMAN	AB200368 Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB20036 5'
3275	16449	29469	1.28	9.1E-01	T28418.1	EST_HUMAN	AB200368 Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB20036 5'
8296	19469	32824	1.54	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6635	19794	33183	3.25	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7750	20810	34300	17.46	9.1E-01	AA806623.1	EST_HUMAN	cb71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336962 3'
7816	20987	34473	2.81	9.1E-01	U72995.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10379	23414	37023	0.8	9.1E-01	P38432	SWISSPROT	P80-COILIN
12595	26054		19.67	9.1E-01	AF090113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3277	16451	29472	0.8	9.0E-01	7661625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
3439	16607		0.73	9.0E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4219	17668	33367	0.68	9.0E-01	8022310	NT	Homo sapiens hypothetical protein FLJ10251 (FLJ10251), mRNA
4498	17638	30620	1.43	9.0E-01	AF099810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
5127	18252	31218	13.05	9.0E-01	AF0117729.1	NT	Oryzobolus cuniculus Rad51 (RAD51) mRNA, complete cds
7551	20623	34100	0.82	9.0E-01	L42847.1	NT	Danio rerio LIM class homeodomain protein (limf) mRNA, complete cds
7579	20651		1.42	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9549	22614	36183	0.68	9.0E-01	AF086761.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
10035	23073	36873	0.48	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
12113	25093	38797	1.41	9.0E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HBAR (H-bar) gene, complete cds
5814	19004	32309	2.5	8.9E-01	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6378	19547		1.28	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA
6590	25827	33134	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6590	25827	33135	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
8621	21701	35237	0.92	8.9E-01	AF269667.1	NT	Orf100 nana cytochrome-c oxidase subunit I (cox) gene, partial cds; mitochondrial gene for mitochondrial product
12080	25060	38766	2.72	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12423	25300		4.02	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4664	17799	30788	2.11	8.8E-01	O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5489	18688	31706	0.66	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
7701	20766	34250	0.69	8.8E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10436	23471	37077	1.07	8.8E-01	7656078	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11337	24400	38049	2.23	8.8E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12092	26072	38779	7.56	8.8E-01	AA808055.1	EST_HUMAN	cc38h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains 5'U repetitive element; contains element MER22 repetitive element
12240	26158		2.13	8.8E-01	D90811.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719843
477	13672	26704	2	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2475	15602	28727	0.98	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2938	16115	29127	5.32	8.7E-01	AA686863.1	EST_HUMAN	nm035111.s1 NCL_CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
5120	18246		4.12	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put>
8229	21311	34831	0.66	8.7E-01	AW697935.1	EST_HUMAN	RC4-NN0057-120500-013-607 NN0057 Homo sapiens cDNA
9130	22209	35762	0.66	8.7E-01	AI239456.1	EST_HUMAN	q138e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9130	22209	35763	0.66	8.7E-01	AI239456.1	EST_HUMAN	q138e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9639	22978	36569	2.07	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
10511	23546	37168	1.08	8.7E-01	BF570189.1	EST_HUMAN	60218554T11 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10511	23546	37157	1.08	8.7E-01	BF570169.1	EST_HUMAN	60218554T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309903 3'
11070	24145	37782	5.87	8.7E-01	BF363970.1	EST_HUMAN	QY0-NN1021-100900-337-403 NN1021 Homo sapiens cDNA
12034	25017	38720	3.32	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'
12034	25017	38721	3.32	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'
12652	25940		2.8	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
487	13681		2.39	8.6E-01	X17012.1	NT	Rat IGF1 gene for insulin-like growth factor II
881	14057	27123	3.14	8.6E-01	W69089.1	EST_HUMAN	z444603.r1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2344	15475	28608	1.31	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3710	16871	29875	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3901	17060	30059	1.31	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6019	19202	32521	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6019	19202	32522	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6508	25825	33042	0.7	8.6E-01	S78772.1	NT	polyprotein [Coxsackie B4 virus CB4, host-mice, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6848	20001	33409	1.96	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6848	20001	33410	1.96	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7696	20761		0.84	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8112	21194		1.82	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8232	21314	34834	0.56	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9887	22927		0.54	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12856	25983		2.11	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2509	15635		1.46	8.5E-01	AJ011824.1	NT	Arabidopsis thaliana (ecotype Columbia) spl2 gene, exons 1-5
6866	20018	33427	1.1	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7684	20759	34243	2.36	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8180	21262	34784	0.57	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8613	21693	35230	0.92	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8613	21693	35231	0.92	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8702	21782	35315	0.68	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10558	23593	37198	1.49	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10558	23593	37199	1.49	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12577	26056		5.29	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP-1), mRNA
12585	25394		6.39	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4873	18006	30389	0.68	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5611	25808	31871	2.75	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5611	25808	31872	2.75	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7991	21041	34553	0.57	8.4E-01	AF051142.1	NT	Manesbra brassicae phenolase binding protein 2 precursor (PBP2) mRNA, complete cds
10163	23200		3.42	8.4E-01	AJ248267.1	NT	Pyrococcus abyssi complete genome; segment 5/6
760	13941	26986	2.17	8.3E-01	M83437.1	NT	Tiermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3164	16339	29347	3.45	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3912	17071	30069	0.69	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4120	17274	30273	3.17	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthesis gene cluster
6383	18585	31454	2.32	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9870	22910		4	8.3E-01	AJ791852.1	EST_HUMAN	nm011212, y6 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR11 THR repetitive element;
10316	23351	36058	1.32	8.3E-01	AF088070.1	NT	Drosophila melanogaster Ust1 homolog mRNA, complete cds
10423	23458	37063	3.9	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10911	23994	37627	2.18	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10930	24012		1.65	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11584	24637	38317	9.95	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2111	15249	28369	2.72	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2166	15292		1.32	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2744	15961		0.95	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
4009	17166	30174	0.68	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4247	17393	30381	0.7	8.2E-01	Z72594.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
4247	17393	30382	0.7	8.2E-01	Z72594.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
5217	18338	31311	1.19	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6781	18338	33332	0.59	8.2E-01	X65283.1	NT	G. gallus mRNA for C-Serrat-1 protein
6781	18338	33333	0.59	8.2E-01	X65283.1	NT	G. gallus mRNA for C-Serrat-1 protein
6913	20228	33661	0.76	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SC1125 protein
7037	20173	33595	3.19	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7419	25844	33986	4.48	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8639	21719	35256	0.55	8.2E-01	BE263145.1	EST_HUMAN	601144885F2 NH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10231	23266	36866	0.81	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
10264	23269	36897	1.51	8.2E-01	AF052659.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10428	23483	37070	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10428	23483	37071	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10596	23631	37238	3.78	8.2E-01	Q9J170	SWISSPROT	MCUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10596	23631	37240	3.78	8.2E-01	Q9J170	SWISSPROT	MCUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11942	24928	38631	4.72	8.2E-01	L10127.1	NT	McLusium contagiosum virus type 1 ORF1 and ORF2 DNA
12030	25013	38715	5.12	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12035	25018	38722	3.97	8.2E-01	H87388.1	EST_HUMAN	JW14402.1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252185.5'
12607	25408	32046	3.01	8.2E-01	AJ001281.1	NT	similar to gb:M36072.80S RIBOSOMAL PROTEIN L7A (HUMAN);
2817	15931	33309	1.38	8.1E-01	AF181839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3547	16712	29723	2.77	8.1E-01	AF055086.1	NT	Homo sapiens MHC class 1 region
4730	17865	30347	0.63	8.1E-01	4506290	NT	Homo sapiens MHC class 1 region
5825	19015	32321	0.63	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6445	19612	32975	0.89	8.1E-01	U16780.1	NT	(MELANOCORTIN-1 RECEPTOR) (MC1-R)
6759	19915	33309	2.17	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6759	19915	33310	2.17	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7681	20746	34227	0.7	8.1E-01	Q47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
							CYTOCHROME B
8095	21177	34693	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8095	21177	34694	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8808	21887	35428	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8808	21887	35429	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8869	22048	35691	1.14	8.1E-01	AW242647.1	EST_HUMAN	xx01103.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2892469.3' similar to SW:1.YAR_MOUSE
10330	23365	36974	0.58	8.1E-01	P06425	SWISSPROT	C08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22.b1 PTR5 repetitive element;
10623	23667	37267	0.52	8.1E-01	N84541.1	EST_HUMAN	PROBABLE E4 PROTEIN
10769	23802		0.54	8.1E-01	AE001228.1	NT	KK972F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872.5' similar to EST(C-ONE C-0PE11)
							Treponea pallidum section 42 of 87 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11772	24764	38459	2.62	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-010 TN0080 Homo sapiens cDNA
11772	24764	38460	2.62	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-010 TN0080 Homo sapiens cDNA
12303	26221	32102	2.22	8.1E-01	AE001711.1	NT	Thermoboga maritima section 23 of 136 of the complete genome
181	13404		2.62	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15
299	13516	26549	10.2	8.0E-01	AJ271510.1	NT	Bos taurus tub and rif genes
2093	15233		1.95	8.0E-01	AJ132772.1	EST_HUMAN	602072473F1 NCI CGAP Bim67 Homo sapiens cDNA clone IMAGE:4215091 5'
3146	16322	29334	1.32	8.0E-01	BF530962.1	NT	Salmonella enteritidis olfactory receptor (SBO27) gene, partial cds
3387	16557	29572	1.29	8.0E-01	AF127897.1	NT	Mus musculus gene for ovalucal glycoprotein, complete cds
4655	17791	30775	6.77	8.0E-01	AB008163.1	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5096	18224	31196	1	8.0E-01	X63739.2	NT	Mus musculus myosin IXb (Myo9b), mRNA
8179	21261		2.66	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h08 NN1012 Homo sapiens cDNA
8722	21802	35338	1.21	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3'
10635	23659		0.48	8.0E-01	BE833329.1	EST_HUMAN	QV3-OT0065-280600-250-008 OT0065 Homo sapiens cDNA
10827	23660	37483	0.48	8.0E-01	BE833329.1	EST_HUMAN	Gallus gallus PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds
11198	24267	37902	1.43	8.0E-01	Q82783	SWISSPROT	CREB-BINDING PROTEIN
486	13681	26697	0.75	7.9E-01	D11476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
733	13915		0.92	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1635	14787		28.32	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1687	14839		1.06	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2337	15465	28603	9.03	7.9E-01	AB004816.1	NT	Oryzotagus curticulcus mRNA for mitsugumin29, complete cds
2338	15469	28604	4.11	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3605	16769	29784	3.57	7.9E-01	AF228684.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4416	17557		0.87	7.9E-01	BE263612.1	EST_HUMAN	60192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4734	17669	30852	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4734	17669	30853	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5210	18331		0.88	7.9E-01	Z47210.1	NT	Mus musculus embigin homolog (Drosophila) (Enah), mRNA
5235	18357	31325	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dxbB, cap3A, cap3B and cap3C genes and orfs
5235	18357	31326	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dxbB, cap3A, cap3B and cap3C genes and orfs
5283	18402		0.68	7.9E-01	AF139718.1	NT	Chrysomya bezziana peritrophin-48 precursor, gene, complete cds
6475	19642	33003	0.68	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8300	21382	34903	2.66	7.9E-01	X90996.1	NT	P.sativum GR gene
9747	22811	36390	3.24	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10255	23290	36887	5.43	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10299	23331	36834	1.17	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKGDRE12 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10728	23762	37369	0.78	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10845	23878	37498	0.61	7.9E-01	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11256	24325		1.75	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11487	24546	38218	1.84	7.9E-01	P18022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
889	14074		1.49	7.8E-01	P24785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2348	15480	28812	6.99	7.8E-01	AW959587.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4823	17956	30942	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5149	18271		0.89	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6184	19370	32721	2.28	7.8E-01	AF116856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6348	19518	32876	2.28	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6501	19761	33136	0.84	7.8E-01	AL445068.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
8688	21768	35299	1.13	7.8E-01	BF108927.1	EST_HUMAN	7164d06.x1 Soares NSF_F8_0T_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526176 3'
9434	22508	36074	1.53	7.8E-01	Y10159.1	NT	D.discoideum recGAP gene
9533	22598	36170	0.56	7.8E-01	Q28452	SWISSPROT	Homo sapiens nucleoporin 214KD (NUP214), mRNA
10328	23364		1.28	7.8E-01	Q28452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12571	26033		1.92	7.8E-01	L29280.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
146	13371	28403	5.78	7.7E-01	AF194345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
744	13925						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-II>
2776	15892	28003	1.72	7.7E-01	AF050167.1	NT	CITRATE SYNTHASE
3438	16806		1.34	7.7E-01	Q38915	SWISSPROT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNAc-T7) (GALNAc-T7), mRNA
3689	16851	29859	0.89	7.7E-01	8393408	NT	Homo sapiens PRO1976 mRNA, complete cds
4516	17655	30843	3.86	7.7E-01	AF118085.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4516	17655	30844	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18872	32169	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18872	32169	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5678	18872	32169	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	19258	32587	1.41	7.7E-01	R08800.1	EST_HUMAN	Y24502.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:127755 3'
10049	23087	36689	1.41	7.7E-01	R08800.1	EST_HUMAN	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12452	25317		0.68	7.7E-01	AB021134.1	NT	Archaeoglobus fulgidus, complete genome
			7.14	7.7E-01	11497621	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6224	18389	32748	5.26	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6224	18399	32749	5.26	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6647	19806	33193	0.66	7.6E-01	P37838	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6900	18509	31501	0.74	7.6E-01	AI253399.1	EST_HUMAN	ac14612.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6900	18509	31526	0.74	7.6E-01	AI253399.1	EST_HUMAN	ac14612.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7196	20061	33472	0.84	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8255	21337	34855	1.54	7.6E-01	AF148793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8318	21400	34924	2.38	7.6E-01	6857752	NT	Mus musculus adillan (Adillan) mRNA
8318	21400	34925	2.38	7.6E-01	6857752	NT	Mus musculus adillan (Adillan) mRNA
8520	21601	35137	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8520	21601	35138	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9167	22245	35789	1.33	7.6E-01	P30372	SWISSPROT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9479	22536	36100	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9479	22536	36101	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11639	24719	38411	2.29	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11639	24719	38412	2.29	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12010	24995		2.78	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25157		8.21	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
526	13719		1.31	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
597	13787	26807	1.08	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
7690	20755	34240	0.8	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (gph) mRNA, complete cds
12621	26354		5.2	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialoporphoprotein precursor (DSPP) gene, complete cds
1154	14318	27372	1.61	7.4E-01	AI598146.1	EST_HUMAN	bt14609.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
2419	15548	28676	0.97	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
3620	16980	29983	0.97	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4010	17167	30175	0.71	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTX01 Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4429	17569	30551	8.12	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8027	21110	34628	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8027	21110	34628	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8834	21913	35451	1.01	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
8910	21989		1.45	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, transcribed alternative untranslated exon
9288	22374	35925	6.96	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3934174 5'
9357	22432	36990	1.24	7.4E-01	AA187898.1	EST_HUMAN	z967h01.s1 Stragatene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to
10613	22647	37256	0.7	7.4E-01	11424933	EST_HUMAN	SW:TCPO_MOUSE P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
12170	25133		3.69	7.4E-01	6753217	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12287	25213		1.7	7.4E-01	A1472841.1	EST_HUMAN	Mus musculus complement component 1 inhibitor (C1hh), mRNA
4083	17238		0.73	7.3E-01	AP000062.1	NT	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4738	17873	30856	0.8	7.3E-01	AE001166.1	NT	Aeropyrum pernix genomic DNA, section 577
4822	17955	30941	2.38	7.3E-01	AF225421.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
6741	19897	33287	5.5	7.3E-01	L35772.1	NT	Homo sapiens HT017 mRNA, complete cds
6741	19897	33288	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (OD72) gene
7243	20841	33771	0.93	7.3E-01	AJ011418.1	NT	Mus musculus antigen (OD72) gene
7617	20687	34163	0.69	7.3E-01	Z14133.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7718	20782	34288	7.25	7.3E-01	M26511.1	NT	D.melanogaster Cnc mRNA for clathrin heavy chain
7718	20782	34289	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
11714	24754	38448	3.29	7.3E-01	AA678019.1	EST_HUMAN	V.alginolyticus sucrose (scrB) gene, complete cds
11714	24754	38448	3.29	7.3E-01	AA678019.1	EST_HUMAN	z25508.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
854	14031		1.96	7.2E-01	L29281.1	NT	z25508.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
2012	15152	28257	3.43	7.2E-01	X79140.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2532	15657	28781	1.96	7.2E-01	AB009805.1	NT	N.tabacum NtIF-4A13 mRNA
3135	16311	29323	1.27	7.2E-01	AF168100.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3541	16705	29717	2.36	7.2E-01	AF065606.1	NT	Fowlpox virus, complete genome
3702	16883	29866	1.35	7.2E-01	AB002307.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3875	17132	30136	1.57	7.2E-01	BF338350.1	EST_HUMAN	Human mRNA for KIAA0309 gene, partial cds
4173	17323		0.73	7.2E-01	AF108093.1	NT	602035589F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4882	18022	31007	2.68	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5225	18347	31317	1.07	7.2E-01	AF198778.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel a>
5225	18347	31318	1.07	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel a>
5308	18425	31395	0.65	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7382	20441	33903	0.59	7.2E-01	U69833.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8648	21728	35285	1.31	7.2E-01	AF236081.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9163	22241		0.54	7.2E-01	AF743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD08 5'
10548	23583	37192	2.25	7.2E-01	BF870061.1	EST_HUMAN	602118331F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4276381 5'
10977	24056	37690	3.28	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome b mRNA, complete cds
12530	18491	31530	1.51	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polypeptide precursor (DVA) mRNA, complete cds
12737	25488		4.37	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 87
12784	26075		1.46	7.2E-01	Y10168.1	NT	B.thurifragilis PK1 & cap genes, putative
710	13892	28928	11.37	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
3130	16306	29320	16.1	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4324	17467	30453	3.07	7.1E-01	7305360	NT	Mus musculus otogelin (Olog), mRNA
4324	17467	30454	3.07	7.1E-01	7305360	NT	Mus musculus otogelin (Olog), mRNA
6059	19251	32579	1.73	7.1E-01	BF881034.1	EST_HUMAN	602155438F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4296344 5'
6059	19251	32580	1.73	7.1E-01	BF881034.1	EST_HUMAN	602155438F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4296344 5'
7088	20182	33606	6.48	7.1E-01	U98232.1	NT	Drosophila melanogaster 6-pyruvyltetrahydropteridin synthase (pr) gene, complete cds
8934	22013	35552	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-409 BT0567 Homo sapiens cDNA
8934	22013	35553	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-409 BT0567 Homo sapiens cDNA
10058	23087	36700	1.6	7.1E-01	BE904405.1	EST_HUMAN	601498330F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3898495 5'
10621	23655	37265	1.1	7.1E-01	M12861.1	NT	Human T-cell receptor gamma chain J2 gene
12505	25956		2.84	7.1E-01	AA421492.1	EST_HUMAN	zu08h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14415	27479	0.86	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14415	27480	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2521	15947	28770	1.29	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:289708 3' similar to contains Alu repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2521	15647	28771	1.29	7.0E-01	N82412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5169	18291		2.32	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6073	19255		0.89	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8573	21654		6.52	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1685 section 143 of 400 of the complete genome
9517	22582	36150	0.68	7.0E-01	U63868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
9517	22582	36151	0.68	7.0E-01	U63868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
11382	24443	38102	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11382	24443	38103	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13133	25937	31772	1.47	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
992	14164	27224	6.3	6.9E-01	U68074.1	NT	Candida albicans equalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
992	14164	27225	6.3	6.9E-01	U68074.1	NT	Candida albicans equalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1338	14495	27666	2.91	6.9E-01	AA693530.1	EST_HUMAN	nm28a09.s1 NCL CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3291	16465	28484	1.71	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3531	16698	29707	16.79	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
5311	18428	31398	97.22	6.9E-01	BE782751.1	EST_HUMAN	601465694F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3668043 5'
5602	18091	32405	0.82	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds
6112	19292	32627	0.85	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6500	19666	33029	1.12	6.9E-01	BE298188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3332328 5'
7979	21028	34542	0.98	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8163	21250	34769	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8168	21250	34770	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9572	22447		0.66	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9898	22936	36520	0.56	6.9E-01	AF208319.1	NT	Musa acuminata peckate lyase 1 (PL1) mRNA, complete cds
9898	22936	36521	0.56	6.9E-01	AF208319.1	NT	Musa acuminata peckate lyase 1 (PL1) mRNA, complete cds
10619	23653	37263	0.78	6.9E-01	BF242307.1	EST_HUMAN	601805500F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109419 5'
11536	24592	38268	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11536	24592	38269	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12148	25949		3.77	6.9E-01	Q99658	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
979	14152	27212	1.84	6.8E-01	AF017784.1	NT	Glial fibrillary acidic protein gene, complete cds
2738	15856		1.41	6.8E-01	D90617.1	NT	Synechocystis sp. PCC6803 complete genome, 27127, 3418852-3573470
2890	14798	27883	1.43	6.8E-01	AA854475.1	EST_HUMAN	q175a05.s1 Soares parathyroid tumor_NHHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4684	17829	30815	1.32	6.8E-01	J00782.1	NT	Rat(hooded) prolactin gene : exon III and flanks
4980	18109	31085	0.82	6.8E-01	4758521	NT	Homo sapiens hevN (HEVIN) mRNA
9838	22878	36460	1.08	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10587	23602		5.72	6.8E-01	AA687936.1	EST_HUMAN	nt13907.s1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546_ma1
11344	24407	38056	2.4	6.8E-01	AJ276675.1	NT	Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
11344	24407	38057	2.4	6.8E-01	AJ276675.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
11378	24437	38008	1.91	6.8E-01	AJ276675.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
11378	24437	38097	1.91	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11579	24633	38312	1.57	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
				6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (T4) (eIF-4C) mRNA, complete cds
11906	24893	38594	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11906	24893	38595	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
309	13525	28559	30.38	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
349	13580	26588	25.24	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1951	15104		1.14	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2214	15348	28477	1.98	6.7E-01	AA451884.1	EST_HUMAN	Zx12g12.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788310 3' similar to contains element TAR1 repetitive element;
2235	16058	28498	5.15	6.7E-01	AF188073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3060	16236	29256	5.81	6.7E-01	6678680	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4575	17712	30695	0.82	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5626	18820	31894	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5626	18820	31895	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6083	19265	32994	0.79	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6453	19620	32983	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6453	19620	32984	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6784	19910	33304	0.59	6.7E-01	BE966241.2	EST_HUMAN	601650177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6754	19910	33305	0.59	6.7E-01	BE966241.2	EST_HUMAN	601650177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7468	20543		3.97	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 187 of 528 of the complete genome
7495	20570	34042	0.94	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10348	23383		1.01	6.7E-01	M34048.1	NT	Human placental protein 14 (PP14) gene, complete cds
11196	24265	37900	2.06	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11748	23932	37558	2.75	6.7E-01	O14357	SWISSPROT	N-ACETYL-GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPII
11959	24944	38649	2.48	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2570	15695	28819	0.97	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2765	15680	28889	1.13	6.6E-01	AF189339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3578	16743	29760	1.16	6.6E-01	4508880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3748	16909	29913	4.58	6.6E-01	Y07669.1	NT	Calicans random DNA marker, 282bp
4226	17373		2.48	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6462	19629	32990	3.82	6.6E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7272	20355	33808	0.62	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 528 of the complete genome
7272	20355	33809	0.62	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 528 of the complete genome
7882	20916	34421	3.7	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
8784	21843	35384	0.58	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9865	22905		2.34	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10207	23243		0.51	6.6E-01	AU118198.1	EST_HUMAN	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
840	13825	26848	2.02	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
840	13825	26849	2.02	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3516	16685	29686	5.5	6.5E-01	A5041226.1	NT	Mus musculus gene for Tob2, complete cds
4148	17300	30292	1.73	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4397	17540	30521	7.71	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5174	18286	31258	2.88	6.5E-01	U28821.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5569	25807	31785	1.86	6.5E-01	P19480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
5865	20017	33425	1.3	6.5E-01	D88348.1	NT	Chicken mRNA for 118-kDa melanosomal matrix protein, complete cds
7760	20819	34309	0.74	6.5E-01	X04789.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7846	20901	34404	0.99	6.5E-01	A1789882.1	EST_HUMAN	wc6a02.x1 NC1_CGAP_P728 Homo sapiens cDNA clone IMAGE:2321842 3'
10042	23080		0.89	6.5E-01	T78904.1	EST_HUMAN	y421b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3'
10542	23877	37185	2.53	6.5E-01	AF118676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10869	23954						
10928	24008	37583	2.55	6.5E-01	H87583.1	EST_HUMAN	yw1706.r1 Soares_placenta_80c6weeks_2NBHP80csw Homo sapiens cDNA clone IMAGE:252515 5'
11030	24109	37643	2.98	6.5E-01	AA601287.1	EST_HUMAN	not15c07.s1 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
			3.39	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11899	24887	38586	5.43	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b
12568	25386		8.59	6.5E-01	BE465050.1	EST_HUMAN	genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12840	25889		3.83	6.5E-01	Z74145.1	NT	h74a10.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
262	13481	28513	8.59	6.4E-01	U48948.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
3545	16710	29721	4.42	6.4E-01	U48854.2	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3864	17122	30129	1.46	6.4E-01	AB046827.1	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
4614	17751	30731	0.74	6.4E-01	Y12488.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4614	17751	30732	0.74	6.4E-01	Y12488.1	NT	M.musculus wtn gene
8812	21891	35432	1.58	6.4E-01	AE001247.1	NT	M.musculus wtn gene
10221	23257		0.5	6.4E-01	11418320	NT	Trapanema pallidum section 63 of 87 of the complete genome
10294	23329	36633	7.31	6.4E-01	U82828.1	NT	Homo sapiens hypothetical protein FLJ10140 (FLJ10140), mRNA
10309	23344	36949	1.31	6.4E-01	BF570405.1	EST_HUMAN	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12693	25461		19.53	6.4E-01	AV759212.1	EST_HUMAN	602150289F1 NIH_JMGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
447	13643	26682	3.76	6.3E-01	P05228	SWISSPROT	AV759212 MDS Homo sapiens cDNA clone MDSGCC09 5'
548	13741	26765	1.85	6.3E-01	U32689.1	NT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFHRP-II)
2230	15364	28493	3.29	6.3E-01	U81136.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2646	15769	28884	3.65	6.3E-01	U75331.1	NT	Shigella flexneri multi-antigen resistance locus
3081	16257	28885	3.65	6.3E-01	U75331.1	NT	Galus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
6189	19363	32713	0.84	6.3E-01	BE093906.1	EST_HUMAN	Galus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
6733	19889	33281	1.01	6.3E-01	L27798.1	NT	Lycopodium esculentum p68a gene, complete CDS
6733	19889	33282	1.01	6.3E-01	L27798.1	NT	PMO-BT0757-010500-002-a03 BT0757 Homo sapiens cDNA
							Streptococcus dysgalactiae (mag) gene, complete cds
							Streptococcus dysgalactiae (mag) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8718	21798		3.44	6.3E-01	BE02044.1	EST_HUMAN	601876889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958351 5'
9087	22168	35712	0.79	6.3E-01	S62827.1	NT	glycoprotein Ila (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9421	22495	36082	0.65	6.3E-01	BF216994.1	EST_HUMAN	601894050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4702596 5'
9620	22675	36245	3.14	6.3E-01	8627521	NT	Varidra virus, complete genome
9620	22675	36246	3.14	6.3E-01	8627521	NT	Varidra virus, complete genome
10142	23180		0.68	6.3E-01	AE002328.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10641	23675	37285	1.59	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10747	23780	37393	1	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10781	23814		0.48	6.3E-01	AW755395.1	EST_HUMAN	PMO-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
11315	24378	38024	1.78	6.3E-01	AA877715.1	EST_HUMAN	nc9008.s1 NCLCGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916 HLARK.
11620	24671	38359	6.18	6.3E-01	AB04160.1	EST_HUMAN	CM-BT043-090289-046 BT043 Homo sapiens cDNA
11708	24748	38442	1.55	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INOT-IDS2 INTERGENIC REGION
11888	24878	38573	2.12	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN YMA12-APN1 INTERGENIC REGION
12086	25066	38772	1.47	6.3E-01	8838361	NT	Beta vulgaris mitochondrion, complete genome
12262	26130	31546	15.92	6.3E-01	8910283	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12358	26257		1.6	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
12582	26029		4.27	6.3E-01	X83528.1	NT	C. limicola pscD gene
5991	19178	37497	2.15	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7664	20731		3.59	6.2E-01	AF022293.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rd) mRNA, partial cds
7715	25852	34286	1.16	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltracrin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8487	21578	35114	4.87	6.2E-01	HT2255.1	EST_HUMAN	ys01508.s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:213542 3'
9057	22136	35681	0.7	6.2E-01	AF034411.1	NT	Lyopericon esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinolate dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9548	21091	34606	1.47	6.2E-01	BE562697.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680010 5'
9710	22769		2.58	6.2E-01	M24481.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTB3) mRNA, complete cds
10283	23318	36919	6.83	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10426	23461	37087	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10426	23461	37088	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10756	23789	37405	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOLE PROTEASE P3C; HELICASE (20 LIKE PROTEIN); COAT PROTEIN]

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10756	23789	37408	5.75	6.2E-01	P27410	SWISSPROT	NONSTRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2488	15936		6.27	6.1E-01	0678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5653	18847	32129	1.33	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CcMyoD (hlt-1) alternatively spliced genes, complete cds
7009	20146	33664	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7009	20146	33665	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7160	20283	33738	0.67	6.1E-01	AW105653.1	EST_HUMAN	cd60h03.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gbX12671_mn1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7254	20337	33787	0.69	6.1E-01	Q63789	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8428	21509	35041	3.47	6.1E-01	AF033335.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8995	22074	35612	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8995	22074	35613	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8615	22670	36239	20.44	6.1E-01	AF238117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9615	22670	36240	20.44	6.1E-01	AF238117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10047	23085	36888	1.06	6.1E-01	AE004462.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
10252	23287	36883	0.92	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10833	23666	37489	0.47	6.1E-01	AF025893.1	NT	Sus scrofa neural cell adhesion molecule (NCAM) gene, 3' UTR and microsatellite repeat region
12033	25016	38718	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12033	25016	38719	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
13062	25695		1.16	6.1E-01	X95287.1	NT	M. megal orfA, orfB, and orfC of archaeal ABC-transporter system
507	13701	26730	1.79	6.0E-01	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
575	13767		4.74	6.0E-01	5802899	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1303	14547	27623	1.83	6.0E-01	AF065263.1	NT	Human respiratory syncytial virus strain CH63-53b attachment protein (G) gene, complete cds
3917	17078	30073	0.87	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4305	17448		1.26	6.0E-01	AF058895.1	NT	Homo sapiens Natch3 (NOTCH3) gene, exons 26, 27, and 28
5395	18567	31567	1.96	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5555	18753	31791	2.5	6.0E-01	AW139713.1	EST_HUMAN	U1H.B1.aeb-e-10-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
5669	19828	33216	2.74	6.0E-01	U36813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6900	19955	33355	0.68	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)

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6856	20288	33705	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6855	20288	33706	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7509	20583	34056	6.49	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8315	21397	34922	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8315	21397	34923	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10028	23066	36664	1.57	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10480	23515		1.04	6.0E-01	Q01487	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN3)
10594	23628		0.61	6.0E-01	BE837779.1	EST_HUMAN	RC2-FN0094-180700-017-d08 FN0094 Homo sapiens cDNA
11312	24376	38021	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11312	24376	38022	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11846	24835	38528	2.74	6.0E-01	A120823.1	EST_HUMAN	ff08f07.x1 NC1_CGAP_P728 Homo sapiens cDNA clone IMAGE2095921 3'
12663	25440	32052	2.08	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12781	25523		1.48	6.0E-01	AA700087.1	EST_HUMAN	z98g05.s1 Soares fetal liver spleen_1NF5_S1 Homo sapiens cDNA clone IMAGE462776 3'
12953	25956		1.44	6.0E-01	5903138	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12998	25933	31766	5.48	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
13032	25880		8.12	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1025	14193	27254	1.09	6.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3343	16519	29530	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3343	16516	29531	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3916	17075	30072	0.62	5.9E-01	U74341.1	NT	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
4337	17480		3.95	5.9E-01	AF182756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
5289	18407	31374	0.68	5.9E-01	AF026566.1	NT	Ovis aries SRY gene promoter region
6594	19754	33140	1.95	6.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7416	20494	33982	3.08	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7568	20628		0.63	5.9E-01	X68801.1	NT	G.gallus gene for skeletal alpha-actinin, exon EF2
8188	21270	34795	0.48	5.9E-01	D80911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1676593-1719643
8839	21918	35456	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9743	22807	36395	1.01	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW31/Ox major outer membrane protein (omp1) gene, complete cds
10117	23155		0.64	5.9E-01	P06463	SWISSPROT	E6 PROTEIN
10391	23426	37033	1.28	5.9E-01	P55294	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)

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10908	23991	37824	2.24	5.9E-01	Q9X0I8	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10916	23999	37832	1.71	5.9E-01	AF187944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11203	24272	37908	2.76	5.9E-01	AF037175.1	EST_HUMAN	PM1-DT0041-190100-002-H03 DT0041 Homo sapiens cDNA
11469	24528	38201	1.98	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/IEI CD48 antigen (Cd48) gene, partial cds
12302	25220	32101	1.78	5.9E-01	L42320.1	NT	Oryzopsis cuniculatus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12549	25372		1.92	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12798	25533		4.82	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1958	15101	28201	1.28	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
4092	17247	30252	1.11	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4078131 5'
4637	17773	30763	3.59	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4917	18047		2.22	5.8E-01	AF110848.1	NT	Megascella scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5490	18889		1.02	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5648	18842	32123	0.81	5.8E-01	Q10899	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313	19485	32840	1.69	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA* (T Fujihara) Homo sapiens cDNA clone GEN:500E06 5'
6442	19609	32972	0.58	5.8E-01	D50801.1	NT	Shigella sonnei DNA for 28 ORF's, complete cds
6952	20265		2.37	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8071	21153		2.87	5.8E-01	H41571.1	EST_HUMAN	Yn91503.a1 Soares adult brain N2b9HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:578187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8278	21360	34878	0.66	5.8E-01	A1280051.1	EST_HUMAN	qh85510.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8278	21360	34879	0.66	5.8E-01	A1280051.1	EST_HUMAN	qh85510.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21466	34991	2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP88
8385	21466	34992	2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP88
9092	22171	35716	10.4	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9172	22250	35793	1.23	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
9173	22251	35794	0.97	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE T46F2.2 IN CHROMOSOME X
9795	22835		0.79	5.8E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827288 5'
11237	24306	37643	7.26	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11291	24357		3.35	5.8E-01	BF700092.1	EST_HUMAN	602127677F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11407	24468		1.44	5.8E-01	BF700092.1	EST_HUMAN	602127677F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3108	16284		0.73	5.7E-01	6755253	NT	Mus musculus plesmacytoma variant translocation 1 (Pv1), mRNA
3295	16469	26488	1.46	5.7E-01	Q9W1J2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3593	16757		2.84	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6485	19652	33014	4.41	5.7E-01	BF036413.1	EST_HUMAN	801454862F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3888590 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6850	20003	33412	0.92	5.7E-01	AA194201.1	EST_HUMAN	z38c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7000	18519	31512	1.15	5.7E-01	AL111440.1	NT	Bolytic chinea strain T4 cDNA library under conditions of nitrogen deprivation
7941	20891	34501	1.88	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8157	21239		0.55	5.7E-01	AJ251635.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tape1, Tsc4 and Tsc5 genes, alternative transcripts
10004	23042	36634	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10004	23042	36635	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10803	23836	37461	0.91	5.7E-01	BF540982.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4086610 5'
12255	26192		1.28	5.7E-01	BE716051.1	EST_HUMAN	MR3-HT0736-180700-003-402 HT0736 Homo sapiens cDNA
13025	26675		1.31	5.7E-01	BE959722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839783 3'
3449	16617	29635	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3449	16617	29636	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3989	17146	30152	0.59	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4354	17497	30476	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
9003	22082	35625	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9003	22082	35626	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9575	22717	36285	1.13	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25123		7.84	5.6E-01	BE988280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913457 5'
12772	25204	38362	1.39	5.6E-01	AA489535.1	EST_HUMAN	ng'fg10.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7 repetitive element;
12661	17146	30152	2.38	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12690	25460		2.66	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13167	25738		3.64	5.6E-01	BF573828.1	EST_HUMAN	602132028F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1238	14397	27459	6.04	5.5E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2766	15881	28990	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2766	15881	28991	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2985	16161	29178	1.17	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3134	16310		1.57	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N255H555Y Homo sapiens cDNA clone IMAGE:178266 3'
3306	16480	29501	2.93	5.5E-01	AF27240.1	NT	Rabbit oral papillomavirus, complete genome
3783	16844	29851	1.34	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
6249	18370		1	5.5E-01	AF063886.1	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
5269	18388	31356	1.01	5.5E-01	U86097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7405	20483	33950	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7405	20483	33951	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7439	20516		0.74	5.5E-01	AB015598.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8678	21786	35291	0.47	5.5E-01	BE163243.1	EST_HUMAN	QV3-HT0458-170200-090-b05 HT0458 Homo sapiens cDNA
9689	23008		0.56	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10588	23623	37230	0.83	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Stralagene (calf#936206) Homo sapiens cDNA clone HFBCQ35
11406	24467	38132	1.64	5.5E-01	BF128607.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE-4054003 3'
147	13372	26404	8.11	5.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
147	13372	26405	8.11	5.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
598	13789	26808	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsIA (gsIA) genes, complete cds; and unknown genes
598	13789	26809	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsIA (gsIA) genes, complete cds; and unknown genes
1300	14486	27522	2.21	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-cb4 NN0040 Homo sapiens cDNA
2173	15308		2.8	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2328	15461	28594	2.82	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15.15' beta carotene dioxygenase (beta-diox gene)
5774	18936	32269	0.83	5.4E-01	AW842327.1	EST_HUMAN	FM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6320	19492	32850	0.93	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7170	20303	33746	0.77	5.4E-01	BE965592.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7490	20565	34035	1.96	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7490	20565	34036	1.96	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7492	20567	34039	1.47	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10195	23232		2.69	5.4E-01	BF572636.1	EST_HUMAN	60207645F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243600 5'
11334	24397	38046	2.68	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11920	24906	38607	2.76	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11920	24906	38608	2.76	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

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12039	19492	32850	1.3	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
12217	25168		2.41	5.4E-01	AI858398.1	EST_HUMAN	w37g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
528	13722	26748	2.12	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2843	15957	29055	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2843	15957	29066	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3315	16498	29506	3.8	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4327	17470		1.2	5.3E-01	U98987.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5574	18770	31813	1.55	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5574	18770	31814	1.55	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5671	18865	32150	0.95	5.3E-01	AA193672.1	EST_HUMAN	zr42g08.r1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5671	18865	32151	0.95	5.3E-01	AA193672.1	EST_HUMAN	zr42g08.r1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5762	18954	32257	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5762	18954	32258	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9105	22184		1.59	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl.) gene, partial cds; chloroplast gene for chloroplast product
9156	22234	35779	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER28 repetitive element;
9156	22234	35780	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER28 repetitive element;
10416	23451	37056	0.65	5.3E-01	AI854210.1	EST_HUMAN	wx94b02.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;
11857	24845	38542	5.63	5.3E-01	BE663281.1	EST_HUMAN	601339867FTNIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
12145	25958		1.73	5.3E-01	AA016053.1	EST_HUMAN	cg30a05.s1 NCI_CGAP_B77 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02811 APOLOPROTEIN D PRECURSOR (HUMAN);
639	14017	27072	20.65	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1190	14352	27410	7.57	5.2E-01	Q8WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-A15)
1218	14379	27438	3.05	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1935	15078		3.88	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
							Homo sapiens chromosome 21 segment HS21C085

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2213	16347	28478	2.85	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3189	16384	29369	2.1	5.2E-01	U69642.1	NT	Chlamydia abortus strain S263 POMP91A and POMP90A precursor, genes, complete cds
3309	16483		1.05	5.2E-01	D73443.1	NT	Azotobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds
3491	16658		1.61	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3530	16805	29708	2.01	5.2E-01	AA084165.1	EST_HUMAN	am77g05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3722	16883		0.77	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast melate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3724	16885	29891	0.87	5.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
4720	17864	30848	0.61	5.2E-01	6752847	NT	Mus musculus acetylcholine receptor beta (Acb), mRNA
5770	18862	32283	0.92	5.2E-01	AA284261.1	EST_HUMAN	zc4409.17 Soares senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:325169 3'
9932	25892	36562	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9932	25862	36563	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10136	23174	36772	0.49	5.2E-01	AA194518.1	EST_HUMAN	zq05009.11 Stragene muscle 697209 Homo sapiens cDNA clone IMAGE:628783 5'
10233	23268	36858	1.32	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13128	25738		4.83	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
632	13917	26841	2.6	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
665	13851	26876	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
665	13951	26876	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
1684	14936		1.02	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
4188	17338	30331	3.87	5.1E-01	A858495.1	EST_HUMAN	w39b12.x1 NC1 CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4303	17448	30432	2.88	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5178	18301		0.6	5.1E-01	BE091798.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6352	19522	32879	1	5.1E-01	BE541068.1	EST_HUMAN	601063608F1 NIH_MGC_10 Homo sapiens cDNA clone DCAAU07 5'
6406	19575		0.9	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAU07 5'
7057	20110	33526	1.35	5.1E-01	R60873.1	EST_HUMAN	y84a09.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:146872 3'
8770	21849	33389	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-401 ST0023 Homo sapiens cDNA
8770	21849	33390	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-401 ST0023 Homo sapiens cDNA
9888	22926	36510	4.85	5.1E-01	JO5412.1	NT	Human regenerating protein (reg) gene, complete cds
9889	22926	36513	3.95	5.1E-01	W22302.1	EST_HUMAN	6551 Human retina cDNA Tsp509H-cleaved sublibrary Homo sapiens cDNA not directional
10363	23398	37009	0.99	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12368	25874		3.49	5.1E-01	BF030207.1	EST_HUMAN	601668683F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'

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12634	25427		1.31	5.1E-01	BF439982.1	EST_HUMAN	nc51110.x1 NCL_CGAP_Bri23 Homo sapiens cDNA clone IMAGE:3408218 3' similar to contains element TAR1 repetitive element;
2203	15338	28464	1.65	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
2203	15338	28465	1.65	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
							Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28472	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28473	2.09	5.0E-01	AF008210.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
2231	15365		1.56	5.0E-01	AL161533.2	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.135, partial cds
3842	17001	30004	0.85	5.0E-01	U55574.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3934	17093	30061	0.93	5.0E-01	L39483.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
3977	17134	30137	2.67	5.0E-01	AB033010.1	NT	802132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271838 5'
6782	19337		0.82	5.0E-01	BF576199.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7842	20897	34398	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7842	20897	34399	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8727	21807		1.63	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8870	21849	35484	0.66	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9637	21100	34813	2.13	5.0E-01	BF317212.1	EST_HUMAN	601803871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22864	36445	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22864	36446	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10602	23637		1.23	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
12307	25225		3.64	5.0E-01	AF026215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13063	25713		2.25	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13109	25724		4.71	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
812	13891	27045	1.83	4.9E-01	BF571482.1	EST_HUMAN	602076949F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243880 5'
1892	14844	27928	1.08	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1955	15098	28198	1.34	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5522	18719	31735	1.17	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6161	19337	32882	2.67	4.8E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6161	19337	32883	2.67	4.8E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7610	20690	34156	1.61	4.9E-01	AB040051.1	NT	Oryza sativa subsp. Japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7882	20934	34439	0.88	4.9E-01	Q10906	SW/SSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7882	20934	34440	0.88	4.9E-01	Q10906	SW/SSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9190	22288		1.98	4.8E-01	BF209791.1	EST_HUMAN	601874934.F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102593 5'
9389	22484	36028	0.96	4.8E-01	AW339805.1	EST_HUMAN	h80cd02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807266 3' similar to TR:095714
9496	26228		2.2	4.8E-01	10946863	NT	O65714 HERC2 ;
10524	23559	37166	1.05	4.9E-01	AF053980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
12197	25154		2.61	4.9E-01	AF176912.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
13086	28174		4.94	4.9E-01	AA613882.1	EST_HUMAN	Homo sapiens neurotrophin-1B-cell stimulating factor-3 gene, complete cds
13084	25714	31939	1.69	4.9E-01	AL163301.2	NT	ng22e11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144682 3'
13181	25768		1.27	4.9E-01	11431438	NT	Homo sapiens chromosome 21 segment HS21C101
4452	17592		0.59	4.8E-01	4504850	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
6624	18818	31892	9.66	4.8E-01	J02987.1	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KONK5) mRNA, and translated products
6817	19970	33376	0.69	4.8E-01	U92882.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6827	19980		4.18	4.8E-01	AA659878.1	EST_HUMAN	Mus musculus slow skeletal muscle troponin T (Tnnt1) gene, complete cds
7469	20544		1.83	4.8E-01	5031650	NT	nu85f09.e1 NCI_CGAP_ALV1 Homo sapiens cDNA clone IMAGE:1217513
7846	20900	34403	1.06	4.8E-01	AL163209.2	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
7938	20988	34497	3.69	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21C009
7838	20988	34498	3.59	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8089	21171	34686	1.81	4.8E-01	AB20744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
9446	22932		1.05	4.8E-01	BE155148.1	EST_HUMAN	M77110.y6 Soares breast 2HbHBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element ;
10212	23248		0.55	4.8E-01	BF558633.1	EST_HUMAN	PM1-HT0350-201293-004-004 HT0350 Homo sapiens cDNA
10868	24047		1.9	4.8E-01	X83502.1	NT	602184287.F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
12278	25208		1.56	4.8E-01	AL163227.2	NT	S. cerevisiae ORFs from chromosome X
12509	25918		5.78	4.8E-01	AF227565.1	NT	Homo sapiens chromosome 21 segment HS21C027
3142	16318		0.59	4.7E-01	AF192387.1	NT	Trypanosoma cruzi transposon VJP II SIRE repeat region
6844	18903	33190	8.07	4.7E-01	BF217173.1	EST_HUMAN	Felis catus feline (eukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
7186	20051	33461	0.84	4.7E-01	AI204374.1	EST_HUMAN	601883880.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
							q172609.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	21132	34652	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
8049	21132	34653	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
9276	22352	35904	0.61	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11084	24158	38052	4.37	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51087 hemagglutinin (HA) gene, partial cds
11340	24403	38052	1.94	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 8 through 16, and partial cds
11658	24737	38428	1.45	4.7E-01	AW889448.1	EST_HUMAN	RC8-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12401	25291		1.84	4.7E-01	BE887783.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12529	25361		1.25	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GGC_S1 Homo sapiens cDNA clone IMAGE:2909188 3'
3837	16937	29959	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246481 5'
3837	16937	30000	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246481 5'
5535	18732	31747	0.93	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5535	18732	31748	0.93	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5586	18793	31828	3.52	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5588	18793	31829	3.52	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18857	32140	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3943637 5'
5677	18871	32157	3.62	4.6E-01	AI247679.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN ;
5677	18871	32158	3.62	4.6E-01	AI247679.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN ;
5685	18879	32169	1.44	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOR1
5763	18955		0.85	4.6E-01	AF212124.1	NT	Ancalis schwartzii cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5850	19040		0.9	4.6E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6386	19555	32914	0.82	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from basae 1165761 to 1176238 (section 100 of 148) of the complete genome
6906	20221	33649	2.39	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempeA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6906	20221	33650	2.39	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempeA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7379	25843	33920	0.66	4.6E-01	L07320.1	NT	Murine cytomegalovirus a1 protein gene, complete cds
7906	20958	34484	0.78	4.6E-01	AA93577.1	EST_HUMAN	h104h05.a1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8515	21696	35131	14.55	4.6E-01	BF697396.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
8948	22025	35595	0.54	4.6E-01	AA932237.1	EST_HUMAN	co76b08.a1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8946	22025	35566	0.54	4.8E-01	AA832237.1	EST_HUMAN	cc78b08.s1 NCL_CGAP_K145 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP- RIBOSYLATION FACTOR 4 (HUMAN);
9501	22557	36120	0.93	4.8E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9501	22557	36121	0.93	4.8E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9868	22906	36490	0.52	4.8E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (eccB-1) gene, complete cds; nuclear gene for chloroplast product
9868	22906	36491	0.52	4.8E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (eccB-1) gene, complete cds; nuclear gene for chloroplast product
10181	23216	36809	1.15	4.8E-01	AI015634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10181	23216	36810	1.15	4.8E-01	AI015634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11238	24307	37956	2.31	4.8E-01	P38163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
11248	24317	37957	5.06	4.8E-01	BE185448.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11248	24317	37957	5.06	4.8E-01	BE185448.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11760	23946	37573	4.3	4.8E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11760	23946	37574	4.3	4.8E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
1960	15103	28203	1.15	4.5E-01	AE001631.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1960	15103	28204	1.15	4.5E-01	AE001631.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2033	16110	29124	4.83	4.5E-01	AA677086.1	EST_HUMAN	z155d02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3380	16552	29565	0.68	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2885280 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3380	16552	29566	0.68	4.5E-01	AW083761.1	EST_HUMAN	xc25c08.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2885280 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3393	16583	29578	4.46	4.5E-01	Q05763	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3485	16632	29651	1.51	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4130	17291		1.18	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4186	17336	30329	1.02	4.5E-01	AI708908.1	EST_HUMAN	ass6e09.x1 Barsleadorta HPLRB8 Homo sapiens cDNA clone IMAGE:2353480 3'
4292	18478		4.71	4.5E-01	AW873495.1	EST_HUMAN	h060g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5058	18186	31161	1.18	4.5E-01	BE963445.2	EST_HUMAN	h01657225R1 NIH_MGC_07 Homo sapiens cDNA clone IMAGE:3866023 3'
5666	18860	32145	1.57	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c08 PT0012 Homo sapiens cDNA
6740	18896		1.38	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
7571	20643	34120	0.81	4.5E-01	M37038.1	NT	Rat nuclear proteins B23.1 and B23.2

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7785	20841	34333	2.39	4.5E-01	AI858849.1	EST_HUMAN	w32e02.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8502	21583		1.11	4.5E-01	M32691.1	NT	SW/ISNF COMPLEX 170 KDA SUBUNIT.
8598	21679	35217	2.87	4.5E-01	AI848596.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
							tz50g11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
8756	21835	35378	0.85	4.5E-01	Q62728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE)
8981	22060		2.36	4.5E-01	11444786	NT	(PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
9200	22278	35817	0.96	4.5E-01	AE000218.1	NT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
10145	23183		0.96	4.5E-01	9630816	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
10713	23746	37352	26.59	4.5E-01	M80006.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10713	23746	37353	25.59	4.5E-01	M80006.1	EST_HUMAN	Bombyx mori nuclear polyhedrosis virus, complete genome
							EST02631 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCY17
							EST02631 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCY17
							xc14h01.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT8_MOUSE
11104	24176	37812	2.52	4.5E-01	AW591271.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]
11225	24294	37835	2.16	4.5E-01	11430789	NT	Homo sapiens cadherin 3, P-cadherin (placental) (CDH3), mRNA
11530	24586		1.3	4.5E-01	AV719382.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'
12164	26162		5.59	4.5E-01	BE871481.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12895	26592		1.2	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCL_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4183280 5'
12970	26630		12.42	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2094	15234		1.11	4.4E-01	6680503	NT	Mus musculus integral membrane-associated protein 1 (Imap1), mRNA
							VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
							FACTOR)
2462	15589	26715	4.16	4.4E-01	P49785	SWISSPROT	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	16560	26575	1.54	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	16560	26576	1.54	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3395	16565	26580	2.12	4.4E-01	BF058728.1	EST_HUMAN	7191402.y1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:3393795 5'
4349	17492		1.35	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5536	18733	31749	1.31	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5536	18733	31750	1.31	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5805	18995	32300	1.58	4.4E-01	S89019.1	NT	mucln [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5823	19013	32319	1.81	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
							q62h11.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q929168 Q929168
6074	19256	32584	1.12	4.4E-01	AI198413.1	EST_HUMAN	UNKNOWN PROTEIN:

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6074	19256	32585	1.12	4.4E-01	AI198413.1	EST_HUMAN	q82h11.x1 NCL_GGAP_Bn25 Homo sapiens cDNA clone IMAGE:1861126 3' similar to TR:Q29168 Q29168
6370	19539	32899	1.67	4.4E-01	AW060785.1	EST_HUMAN	UNKNOWN PROTEIN ; xc27608.x1 NCL_GGAP_Co18 Homo sapiens cDNA clone IMAGE:2885510 3' similar to TR:Q95154 Q95154
6458	19625		1.05	4.4E-01	AA776132.1	EST_HUMAN	AFLATOXIN B1-ALDEHYDE REDUCTASE ; aa85d11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:970865 3' similar to gb:M16038
7557	20629	34104	1.14	4.4E-01	AE000571.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN); Helicobacter pylori 26695 section 49 of 134 of the complete genome
8024	21107		12.3	4.4E-01	Z11679.1	NT	S. tuberosum mRNA for induced adon lip protein (partial)
8962	22041	35584	1.11	4.4E-01	AA056427.1	EST_HUMAN	Z169a03.s1 Stragene colon (#337204) Homo sapiens cDNA clone IMAGE:509836 3'
9352	22427	35985	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 081076 from USA, envelope glycoprotein (env) gene, partial cds
9385	22460	36023	0.62	4.4E-01	AW612578.1	EST_HUMAN	h05c08.x1 NCL_GGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to
9490	22547	36110	1.13	4.4E-01	O62836	SWISSPROT	SW_MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
10167	23204	36798	1.95	4.4E-01	AI268650.1	EST_HUMAN	ZINC FINGER X-CHROMOSOMAL PROTEIN
10168	23205		2.09	4.4E-01	P28922	SWISSPROT	q339709.x1 NCL_GGAP_Lu5 Homo sapiens cDNA clone IMAGE:1610921 3'
10302	23337	36942	4.94	4.4E-01	P35590	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10585	23620	37228	1.76	4.4E-01	S76404.1	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10585	23620	37227	1.76	4.4E-01	S76404.1	NT	beta-HKA=H.K-ATPase beta-subunit [rate, Genomic, 8983 nt, segment 2 of 2]
10829	23862	37486	0.48	4.4E-01	P02716	SWISSPROT	beta-HKA=H.K-ATPase beta-subunit [rate, Genomic, 8983 nt, segment 2 of 2]
11522	24578	38256	1.64	4.4E-01		NT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
12435	25308	32087	4.23	4.4E-01		NT	Terbrautina retusa mitochondrion, complete genome
12447	26084		13.47	4.4E-01	AL163282.2	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
13051	25689		1.41	4.4E-01	P54725	SWISSPROT	Homo sapiens chromosome 21 segment H521C082
424	13619	26659	2.42	4.3E-01	AF155218.1	NT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HR23A)
424	13619	26660	2.42	4.3E-01	AF155218.1	NT	Calitrix jacobus MW/LW opsin gene, upstream flanking region
1633	14785	27671	1.11	4.3E-01	AW866590.1	EST_HUMAN	Calitrix jacobus MW/LW opsin gene, upstream flanking region
2935	16112		1.34	4.3E-01	AW935289.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
3127	16303	29316	0.95	4.3E-01	AW999477.1	EST_HUMAN	QV2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
4526	13619	26659	1.27	4.3E-01	AF155218.1	NT	MFO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4526	13619	26660	1.27	4.3E-01	AF155218.1	NT	Calitrix jacobus MW/LW opsin gene, upstream flanking region
5071	18199		1.04	4.3E-01	AL161502.2	NT	Calitrix jacobus MW/LW opsin gene, upstream flanking region
5220	18342		0.94	4.3E-01	9635250	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5480	18678	31663	0.95	4.3E-01	P48634	SWISSPROT	Xestia c-nigrum granulovirus, complete genome
		31694	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
				4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6009	19194	32512	1.31	4.3E-01	BE181665.1	EST_HUMAN	QV1-HT0638-070500-191-088 HT0638 Homo sapiens cDNA
6027	19210	32530	1.99	4.3E-01	AF179825.1	NT	Salmid sclerous olfactory receptor (SSC186) gene, partial cds
6847	20000	33408	3.1	4.3E-01	AJ001878.1	NT	Columnix coturnix japonica ifnG gene
6825	20240	33876	0.67	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7005	20141		0.77	4.3E-01	Q33367	SWISSPROT	DNA GYRASE SUBUNIT B
7596	20698		1.28	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'
8622	21702		3.15	4.3E-01	U67040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-flaI) genes, complete cds
9455	22571	36137	1.02	4.3E-01	Y14804.1	NT	Erwinia amylovora rdsV gene
9928	22968	36556	2.36	4.3E-01	AW630048.1	EST_HUMAN	h174e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
9928	22968	36557	2.36	4.3E-01	AW630048.1	EST_HUMAN	h174e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
10433	23488	37076	0.99	4.3E-01	AW170559.1	EST_HUMAN	TR:O00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2. ;
11172	20240	33875	2.27	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
13162	25754		1.56	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1386	16036	27618	1.17	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
2002	15143		1.02	4.2E-01	AA781653.1	EST_HUMAN	n234e09.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3697	16858	29862	4.1	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3727	16888	29892	1.09	4.2E-01	AI280338.1	EST_HUMAN	q94b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	18477		0.73	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07876, 240493
3984	17141	30146	0.74	4.2E-01	AW835627.1	EST_HUMAN	QV0-LT0015-180200-127-H01 LT0015 Homo sapiens cDNA
4819	17952	30937	2.57	4.2E-01	AA634093.1	EST_HUMAN	n59h01.s1 NCL_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4903	18033	31022	3.8	4.2E-01	R13467.1	EST_HUMAN	y77e01.L1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:28278 5'
5832	19023	32330	1.42	4.2E-01	BF242055.1	EST_HUMAN	60187921F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5901	18080	32404	1.63	4.2E-01	AW854162.1	EST_HUMAN	RC3-C10254-060400-029-g04 C10254 Homo sapiens cDNA
6334	19505	32863	0.99	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7090	20184	33608	8.72	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7090	20184	33609	8.72	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7151	28839	33727	3.21	4.2E-01	S82504.1	NT	Brcal+breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7242	20326	33770	6.61	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7745	20805	34284	0.81	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8182	21264	34766	4.01	4.2E-01	AW657448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8182	21264	34767	4.01	4.2E-01	AW657448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8401	21482	35010	0.72	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit Vc (COX9C), nuclear gene encoding mitochondrial protein, mRNA
9511	22578	36141	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9511	22578	36142	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
10175	23212		0.81	4.2E-01	AA705007.1	EST_HUMAN	295501.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462649 3'
10714	23747	37364	1.44	4.2E-01	AW663666.1	EST_HUMAN	MP3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
11298	24364	38005	1.43	4.2E-01	AB023489.1	NT	Orizaba latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11679	24678	38368	1.87	4.2E-01	BE96485.2	EST_HUMAN	601600352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:390086 3'
1118	14283	27338	2.11	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA
1127	14282	27347	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1127	14292	27348	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1640	14782	27877	1.77	4.1E-01	AI905946.1	EST_HUMAN	PM-BT103-270499-884 BT103 Homo sapiens cDNA
2775	15890	29001	1.46	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
3008	16181	29202	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3008	16181	29203	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3375	16547	29881	0.66	4.1E-01	AA906344.1	EST_HUMAN	q94x08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3871	17030	30028	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST373384 MAGG resequences, MAGG Homo sapiens cDNA
3871	17030	30029	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST373384 MAGG resequences, MAGG Homo sapiens cDNA
4389	17532	30513	3.78	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF genes
4422	17563		0.96	4.1E-01	AA909257.1	EST_HUMAN	om33d02.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4789	17924	30912	1.36	4.1E-01	AV747880.1	EST_HUMAN	602166590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6111	19291	32826	4.84	4.1E-01	BF681383.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6857	20010	33420	0.65	4.1E-01	U02296.1	NT	602166590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
7560	20661	34137	2.48	4.1E-01	U87635.1	NT	Mus musculus NIH 3T3 chemokine rantes (Sclaf5) gene, complete cds
8225	21307	34827	1.36	4.1E-01	BF574604.1	EST_HUMAN	Methanococcus jannaschii section 77 of 150 of the complete genome
9262	22368	35918	1.51	4.1E-01	6756621	NT	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
9765	22782		0.75	4.1E-01	AF160597.1	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slpoc-pending), mRNA
10470	23503		1.56	4.1E-01	AL193078.2	NT	Voalavo gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10622	23656	37266	1.15	4.1E-01	AV649579.1	EST_HUMAN	Campylobacter jejuni NCTC11166 complete genome; segment 3/6
10725	23758	37365	0.68	4.1E-01	P18584	SWISSPROT	AV649578 G1C Homo sapiens cDNA clone GLOBED12 3'
10725	23758	37366	0.68	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10806	23839		1.14	4.1E-01	BF349382.1	EST_HUMAN	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	24153	37760	40.17	4.1E-01	X68700.1	NT	Zea mays ZIMPMS2 gene for 19 kDa zein protein
11675	23903	37625	1.88	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12810	26139		2.33	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
13153	26169		1.24	4.1E-01	AJ131016.1	NT	Homo sapiens SCL gene locus
1064	14229	27286	1.49	4.0E-01	8404868	NT	Leaqueus rubellus mitochondrion, complete genome
1370	14523	27598	1.21	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1514	14667		5.48	4.0E-01	6879258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2081	16053	28318	1.08	4.0E-01	Z86833.1	NT	Ascaris lumbricoides msc2 gene
2081	16053	28317	1.08	4.0E-01	Z86833.1	NT	Ascaris lumbricoides msc2 gene
2886	13369	26402	1.11	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA
3033	16209	28231	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3033	16209	28232	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mreY) genes, complete cds
3788	16947	29655	1.87	4.0E-01	AF088903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30088	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30089	3.21	4.0E-01	AJ277511.1	NT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4938	18098		8.59	4.0E-01	Q31849	SWISSPROT	EST382691 MAGG resequences, MAGG Homo sapiens cDNA
6031	19214	32535	1.07	4.0E-01	AW970610.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
6888	19790	33108	0.82	4.0E-01	P27285	SWISSPROT	MR4-TN0110-160900-202-g02 TN0110 Homo sapiens cDNA
8113	21195	34714	0.51	4.0E-01	BF092634.1	EST_HUMAN	Homo sapiens OC-TN2 gene, complete cds
8201	21283	34808	0.73	4.0E-01	AB018625.1	NT	EST26068 Cerabellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
9208	22296	35827	1.11	4.0E-01	AA323289.1	EST_HUMAN	G01558283F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3828082 5'
11869	24857		1.87	4.0E-01	BF030282.1	EST_HUMAN	Synachocystis sp. PCC 9413 transposase gene, complete cds
12021	25005		2.38	4.0E-01	L76080.1	NT	Homo sapiens chromosome 21 segment HS21C100
12453	26978		2.5	4.0E-01	AL163300.2	NT	S. cerevisiae chromosome X reading frame ORF YJL026w
13027	26116		1.38	4.0E-01	Z49301.1	NT	neib84e05.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' similar to SW-NTCR_BOVIN O18875 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1 ; S. cerevisiae chromosome X reading frame ORF YJL026w
13168	26036		1.21	4.0E-01	BF432020.1	EST_HUMAN	Corilla gorilla carboxyl-ester lyase (CEL) gene, complete cds
13222	26907		1.26	4.0E-01	Z49301.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
1409	14563	27638	1.84	3.9E-01	AF208618.1	NT	H. sapiens B-myb gene
2707	16825	28940	3.34	3.9E-01	AB033019.1	NT	
2770	15885	28994	5.03	3.9E-01	X62032.1	NT	

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2770	15885	28995	5.03	3.9E-01	X62032.1	NT	H. sapiens B-myb gene
3168	16341	28348	4.24	3.9E-01	AJ226906.1	NT	Sinorhizobium meliloti egl, syrB2, cysE3 genes and orf3
4180	17340	30333	1.48	3.9E-01	BF582611.1	EST_HUMAN	761d01.x1 NCI CGAP Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
5108	18234	31203	1.47	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE:3833689 5'
6055	19237	32562	4.58	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH MGC 53 Homo sapiens cDNA clone IMAGE:4082055 5'
6410	19578	32940	0.64	3.9E-01	U82885.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8140	21222	34740	0.99	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9062	22141	35688	0.83	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0108-170868-004-b08 CT0105 Homo sapiens cDNA
9071	22150		0.82	3.9E-01	BF348634.1	EST_HUMAN	902019944F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4155322 5'
9435	22509	36075	1.73	3.9E-01	AW186998.1	EST_HUMAN	xn86d04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821
9745	22809	36387	1.59	3.9E-01	AI937337.1	EST_HUMAN	wp76a02.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to
10082	23120	36722	2.88	3.9E-01	MT9879.1	NT	SW_RFX5_HUMAN P48382 BINDING REGULATORY FACTOR. ;
10190	23188		0.58	3.9E-01	11465620	NT	Human clathrin 27 gene, exons 10 and 11, and L1 and Alu repeats
10369	23404	37015	0.82	3.9E-01	D86722.1	NT	Porphyra purpurea mitochondrion, complete genome
10582	23597	37203	0.61	3.9E-01	BF361856.1	EST_HUMAN	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10582	23597	37204	0.61	3.9E-01	BF361856.1	EST_HUMAN	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
10836	23889		0.47	3.9E-01	AB037832.1	NT	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
11059	24135		1.37	3.9E-01	AV695974.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
12049	25030	38736	1.89	3.9E-01	AV702623.1	EST_HUMAN	AV695974 GK Homo sapiens cDNA clone GKBC11 6'
12221	26055		4.03	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12916	25603		1.76	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
164	13389		7.58	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
518	13711		6.1	3.8E-01	AB029291.1	NT	Mus musculus per-1 mRNA for pericentriolar material-1, complete cds
1919	15062		1.36	3.8E-01	AE003870.1	NT	Xyella fastidiosa, section 16 of 229 of the complete genome
2637	15760	28874	1.84	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2697	16069	28931	5.2	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1, member 8 (Sic1a6), mRNA
3068	16242		0.71	3.8E-01	AJ251057.1	NT	Mus musculus solute carrier family 1, member 8 (Sic1a6), mRNA
3113	16289	29305	1.81	3.8E-01	AF043863.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 88SE-MP1213)
3572	16737	29752	8.7	3.8E-01	AL161518.2	NT	Pleuronectes americanus aminopeptidase N (ampN) gene, partial cds
3628	16762		1.09	3.8E-01	AI807219.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
							wf38b12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3843	16782		0.97	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3852	17012	30012	1.07	3.8E-01	BE154080.1	EST_HUMAN	PIV3-HT03339-200400-010-G01 HT03339 Homo sapiens cDNA
4027	17183	30192	0.65	3.8E-01	8754085	NT	Mus musculus general transcription factor II (GTF2), mRNA
5727	18820	32214	1.11	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6469	19636		0.63	3.8E-01	S46925.1	NT	p10n protein [hink, Genomic, 2446 nt]
6761	19917	33312	5.74	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-a02 BT0537 Homo sapiens cDNA
6889	20214	33644	4.39	3.8E-01	AI374601.1	EST_HUMAN	ta94f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element;
7079	20132	33549	1.38	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7885	20750		4.27	3.8E-01	X61597.1	NT	Mus musculus gene for kallikrein-binding protein
8493	21574	35111	0.54	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8754	21833	35373	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8926	21905	35444	1.08	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9017	22096	35636	1.29	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9761	22699		4.35	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120639 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;
11034	24113		1.38	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11699	24698	38388	1.57	3.8E-01	U82971.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), callitrichin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
11824	24813		2.87	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-512 HT0841 Homo sapiens cDNA
11992	24977	38681	2.5	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11992	24977	38682	2.5	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12436	25309		2.61	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12588	26082		2	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12696	25463		1.71	3.8E-01	BE826256.1	EST_HUMAN	QV3-ET0083-190700-271-a05 ET0083 Homo sapiens cDNA
13105	25720		1.48	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
13188	25772	31933	1.78	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2551	15676	28799	12.91	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3549	16714	29726	10.67	3.7E-01	AF053336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3974	17131	30135	1.09	3.7E-01	AA319482.1	EST_HUMAN	EST1715 Adrenal gland tumor Homo sapiens cDNA 5' end
4344	17487	30470	9.09	3.7E-01	AI218707.1	EST_HUMAN	ck39e07.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4440	17580	30559	1.31	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509	17648	30636	2.61	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5280	18399	31368	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5280	18399	31368	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5883	19072	32380	1.27	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6071	19253	32582	1.25	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6639	19798	33187	0.7	3.7E-01	M10808.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6680	19819		0.8	3.7E-01	L10353.1	NT	Mus saxicola haploglobin mRNA, complete cds
7283	20375	33832	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7985	21015	34627	0.69	3.7E-01	T69802.1	EST_HUMAN	yaf0a07.3 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66324 5'
8524	21605	35143	1.96	3.7E-01	11438739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8524	21605	35144	1.96	3.7E-01	11438739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8560	21641	35180	0.68	3.7E-01	AA902912.1	EST_HUMAN	ok43b1.1 s1 NCL CGAP_L162 Homo sapiens cDNA clone IMAGE:1516701 3'
9402	22478		1.34	3.7E-01	AJ271386.1	NT	Callus gallus mRNA for beta-carotene 15,15-dioxygenase (BCDO gene)
10373	23408		0.5	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exon region
10414	23449	37054	4.21	3.7E-01	A1338411.1	EST_HUMAN	ql46507.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:1950897 3'
10783	23816	37437	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
10783	23816	37438	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
11097	24170	37805	1.8	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11285	24351	37989	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11285	24351	37990	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11754	23940	37568	2.73	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EG 2.7.7.31)
12004	24989		1.42	3.7E-01	AA973540.1	EST_HUMAN	cc46403.s1 NCL CGAP_L165 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698
12086	25047		3.5	3.7E-01	6677678	NT	TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12137	25654		1.17	3.7E-01	J04892.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12314	26229		3.94	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12410	25289		1.82	3.7E-01	D86976.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12821	25548		2.94	3.7E-01	AL121164.1	EST_HUMAN	Human mRNA for KIAA0223 gene, partial cds
12902	26697	31071	6.99	3.7E-01	Y18000.1	NT	DKFZp782K075.r1 762 (synonym: hmd2) Homo sapiens cDNA clone DKFZp782K075 5'
271	13489	28520	0.77	3.6E-01	AJ009608.1	NT	Homo sapiens NF2 gene
1020	14191		9.07	3.6E-01	U89241.1	NT	Braconia nebulosa mRNA for MAP4K alpha2 protein
1342	14498	27570	3.97	3.6E-01	T80255.1	EST_HUMAN	Human mbp gene, partial cds
1342	14498	27571	3.97	3.6E-01	T80255.1	EST_HUMAN	y03a05.r1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:24443 5'
1988	15109	28209	6.55	3.6E-01	AW590184.1	EST_HUMAN	y03a05.r1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:24443 5'
1986	15109	28210	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33302.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
							hg33302.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	15147	28253	6.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2113	15261		1.15	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgr1 gene
2343	15474		2.33	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2463	15580		2.8	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for acilin
2556	15681	28806	2.66	3.6E-01	AW812033.1	EST_HUMAN	RC6-ST0171-181089-011-g07 ST0171 Homo sapiens cDNA
2694	15814	28929	1.69	3.6E-01	P24208	SWISSPROT	PROTEIN-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2884	16475		8.47	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (suc3) mRNA, complete cds
3558	16723	29738	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3558	16723	29739	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4528	17686	30652	1.2	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4863	17996	30981	0.69	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP2K alpha2 protein
5123	18249	31215	3.18	3.6E-01	AW338393.1	EST_HUMAN	ha02g04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5209	18330	31302	0.92	3.6E-01	BE067699.1	EST_HUMAN	MR4-BT0358-270300-005-g10 BT0358 Homo sapiens cDNA
5498	18697	31713	0.84	3.6E-01	AJ006605.1	NT	Homo sapiens lipo gene intron 5
6211	19386	32735	0.96	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6607	19797	33155	1.63	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
7298	20380		3.85	3.6E-01	R84090.1	EST_HUMAN	y74a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
7435	20512	33985	1.52	3.6E-01	AW027174.1	EST_HUMAN	w72c10.x1 Soares thymus NHFTn Homo sapiens cDNA clone IMAGE:2613010 3' similar to TR:O15117
8418	21500	35032	0.75	3.6E-01	P98167	SWISSPROT	O15117 PYN BINDING PROTEIN, [1];
8474	21555	35087	18.45	3.6E-01	AL161583.2	NT	SCO-SPONDIN
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
9179	22257	35789	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9179	22257	35800	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9203	22281	35820	3.04	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9203	22281	35821	3.04	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9393	22493	36032	1.23	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9599	22654	36225	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9599	22654	36226	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9699	22631		0.98	3.6E-01	X92825.1	NT	C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
10067	23105	36708	16.64	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4T5
11187	24255	37891	2.42	3.6E-01	BE902390.1	EST_HUMAN	601876478F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3958997 5'
11370	24431	38088	3.27	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11729	23915	37540	4.44	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12173	26205		3.16	3.6E-01	Y19210.1	NT	Homo sapiens HH55 gene for hair keratin, exons 1 to 9
12261	25197		7.87	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12420	25297		3.63	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12828	25552		1.98	3.6E-01	11432898	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to 10 (AF10), mRNA
13130	26141		1.4	3.6E-01	AW160228.1	EST_HUMAN	X60a11.x1 NCLCGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
13146	25745		1.38	3.6E-01	Z54173.1	NT	Pyrococcus sp. pol gene
214	13437	26487	3.71	3.5E-01	6678833	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
695	13878	26911	1.03	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
743	13924	26985	1.53	3.5E-01	7708138	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
743	13924	26986	1.53	3.5E-01	7708138	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
801	13981	27033	4.66	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4053951 3'
1670	14822	27905	1.28	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2871	16068	28908	1.34	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
3795	16956		0.73	3.5E-01	BF214381.1	EST_HUMAN	601845470F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4076680 5'
4378	17521	30501	2.82	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5049	18176	31153	4.34	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5
5323	13349	26376	0.8	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
5449	18649	31627	1.1	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5449	18649	31628	1.1	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5667	18861	32146	1.29	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6367	19537		1	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6538	19701	33074	0.79	3.5E-01	AA431833.1	EST_HUMAN	zw78103.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:762428 5' similar to TR:G1066835
6580	19742	33124	0.69	3.5E-01	U37150.1	NT	G1066835 F10F2.1;
6803	19938	33358	0.9	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
7201	20066		3.38	3.5E-01	X88505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7713	20778	34284	0.59	3.5E-01	P47281	SWISSPROT	S.scrofa mRNA for CD31 protein (PECAM-1)
7713	20778	34285	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8262	21344		2.12	3.5E-01	11448042	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8265	21347	34862	0.82	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8662	21742		0.77	3.5E-01	AF061591.1	NT	RC4-ET0024-260600-014-d07 ET0024 Homo sapiens cDNA
9127	22206	36749	1.17	3.5E-01	4507810	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9937	22976	36567	1.75	3.5E-01	Q02284	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10090	23128	36731	4.78	3.5E-01	Z26825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
10172	23209	36802	1.12	3.5E-01	BE174794.1	EST_HUMAN	Xlaeis gene for albumin including HP1 enhancer
10672	24052	37885	2.62	3.5E-01	X81084.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11274	24342	37981	1.97	3.5E-01	AJ243178.1	NT	C.griseus rhodopsin gene for opsin protein
11274	24342	37982	1.97	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11810	24800	38499	1.33	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11892	24880	38577	1.44	3.5E-01	N77597.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
11980	24985	38667	1.53	3.5E-01	LO5145.1	NT	y280H12.r1 Soares_multiple_sclerosis_2NblmMSP Homo sapiens cDNA clone IMAGE:280375 5'
12271	26209		1.51	3.5E-01	AF297488.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12344	26249		6.66	3.5E-01	XG4565.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
12507	26348		2.91	3.5E-01	AE001774.1	NT	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12710	26472		1.5	3.5E-01	AE001691.1	NT	Thermoboga maritima section 86 of 136 of the complete genome
13196	26026	31673	3.16	3.5E-01	H80814.1	EST_HUMAN	Thermoboga maritima section 3 of 136 of the complete genome
13196	26026	31674	3.16	3.5E-01	H80814.1	EST_HUMAN	y664f11.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:219597 6'
725	13907		1.78	3.4E-01	AJ242956.1	NT	y664f11.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:219597 5'
998	14169	27230	8.2	3.4E-01	Y09798.2	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1000	14171	27232	2.06	3.4E-01	AW380120.1	EST_HUMAN	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene
1357	14512	27585	2.35	3.4E-01	Y00554.1	NT	QV3-HT0261-241199-019-g10 HT0261 Homo sapiens cDNA
2474	15601	28728	2.54	3.4E-01	D90908.1	NT	Azobacter vinelandii nifA gene for NifA protein (positive regulatory element)
							Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3065	16241	29261	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3085	16241	29262	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3218	16392	29403	1.09	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3230	16404	29416	6.1	3.4E-01	U83905.1	NT	Canis familiaris tod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3424	16583	29608	0.78	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3620	16784	29800	4.47	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3890	17049		1.89	3.4E-01	BF448010.1	EST_HUMAN	7184a01.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9JU16
4163	17313		1.48	3.4E-01	AA584186.1	EST_HUMAN	Q9JU16 DJ18C9.1
4767	17902	30884	1.79	3.4E-01	BE069912.1	EST_HUMAN	nc011b10.s1 NCI_CGAP_Phat Homo sapiens cDNA clone IMAGE:1100347 3'
5086	18194		4.3	3.4E-01	A1240973.1	EST_HUMAN	MR4-B70403-230200-202-c01 BT0403 Homo sapiens cDNA
5802	18992	32295	2.64	3.4E-01	AL161594.2	NT	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5832	19118		4.92	3.4E-01	AA08513.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6130	19309		2.17	3.4E-01	L02871.1	NT	zn12d11.s1 Striatogen HNT neuron (#637233) Homo sapiens cDNA clone IMAGE:547221 3'
6154	19330	32676	0.96	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6234	19409	32757	1.8	3.4E-01	AW204905.1	EST_HUMAN	6016718111 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3638828 3'
6364	19534	32893	1.71	3.4E-01	AL120544.1	EST_HUMAN	UI-H-BH-aef-e-12-0-JLs1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6882	20034		1.39	3.4E-01	N95226.1	EST_HUMAN	DKFZp761A249.t1 T61 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A249 5'
7086	20180	33604	1.07	3.4E-01	A1468082.1	EST_HUMAN	Z653e12.s1 Soares_Fetal_Lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7205	20070	33480	0.6	3.4E-01	BF678702.1	EST_HUMAN	Im63g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb-S37431
8030	21172		0.48	3.4E-01	AE000493.1	NT	LAMININ RECEPTOR (HUMAN);
8432	21513	35044	0.68	3.4E-01	Y14930.1	NT	602085233F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8694	21764		1.38	3.4E-01	AA337083.1	EST_HUMAN	Escherichia coli K-12 MG1685 section 383 of 400 of the complete genome
8780	21839	35380	0.71	3.4E-01	L04690.1	NT	Homo sapiens TORAV28 gene, allele A4, partial
9053	22132	35676	1.87	3.4E-01	P26013	SWISSPROT	EST141768 Endometrial tumor Homo sapiens cDNA 5' end
9413	22487	36052	4.12	3.4E-01	P26013	SWISSPROT	Cricetus griseus cholesteryl 7-alpha-hydroxylase gene, complete cds
9621	22678		0.57	3.4E-01	AB017610.1	NT	Bovine enterovirus strain K2577, complete genome
9645	21088	34602	4.58	3.4E-01	U19492.1	NT	INTEGRIN BETA-8 PRECURSOR
							INTEGRIN BETA-8 PRECURSOR
							Ephydalia fluviatilis mRNA for PLC-gamma5, complete cds
							Saccharomyces cerevisiae Mat1p (MAF1) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9845	21088	34603	4.68	3.4E-01	U19492.1	NT	Seccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9897	22837	36522	0.86	3.4E-01	U68769.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
10093	23131	36735	2.44	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 18, 17 and 18
10695	23728		0.73	3.4E-01	AE004086.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11287	24338		3.26	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11307	24372	38014	2.1	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11350	24412	38068	1.86	3.4E-01	AF043981.1	NT	Rufus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11561	24616	38295	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11561	24616	38296	1.91	3.4E-01	M25858.1	NT	Human von Willebrand factor gene, exons 36 and 37
11791	24781	38478	1.68	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for e-globin/MUC18, complete cds
11817	24806	38502	3.23	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12078	25058	38765	1.59	3.4E-01	BF081948.1	EST_HUMAN	768d12.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3480646 3'
12110	25090	38763	1.65	3.4E-01	Q27548	SWISSPROT	INOSINE-URIDINE PREFERING NUCLEOSIDE HYDROLASE (U-NUCLEOSIDE HYDROLASE)
12150	25120		2.03	3.4E-01	U68804.1	NT	Citrus variegation virus putative replicase gene, partial cds
12284	25188		1.55	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
12387	25912		1.16	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
12489	25338		10.71	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
12517	25944		2.38	3.4E-01	BE218652.1	EST_HUMAN	h42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.03
12579	26052		1.79	3.4E-01	9838361	NT	PTR5 repetitive element
12700	25486	32023	1.36	3.4E-01	AJ297191.1	NT	Beta vulgaris mitochondrion, complete genome
12954	26160		1.96	3.4E-01	AJ288948.1	NT	Mus musculus SIL_MAP_17_CYP_a_SQL & CYP_b genes
13055	25691		2.26	3.4E-01	AF019413.1	NT	Gleesridium cellucliticum partial spoIVB gene and spoOA gene, strain ATCC 35319
15	13253	26253	6.72	3.3E-01	X07990.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P 450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heilcase (SK2W), RD, complement factor B (Bf), and complement component C2 (C2) genes.>
108	13253	26253	3.19	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
461	13656	26694	1.41	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
650	13836	26863	1.97	3.3E-01	7662485	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1227	14397	27450	2.57	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1335	14492	27562	3.39	3.3E-01	BF588980.1	EST_HUMAN	Homo sapiens KIAA1100 protein (KIAA1100), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1636	14788	27873	1.26	3.3E-01	8753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1674	14828		1.43	3.3E-01	8754477	NT	Mus musculus kappa B and Rss recognition component (Krc), mRNA
1777	14926		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2477	15604		6.23	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (urate phosphoribosyl transferase and orotidine-5'- decarboxylase) (UMPS) mRNA
3014	16190	29215	1.61	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3080	16256		1.09	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3121	16297	29311	0.78	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3584	16749	29786	1.04	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3911	17070	30068	2.72	3.3E-01	O84845	SWISSPROT	EXOEXORIBONUCLEASE V BETA CHAIN
3921	17080	30076	0.82	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3)
4072	17228	30235	1.19	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4108	17262	30262	1.81	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4487	17827		2.37	3.3E-01	D31692.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4812	17945		1.91	3.3E-01	AI539114.1	EST_HUMAN	4p78b12.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4843	17978	30966	1.02	3.3E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
4960	18089	31085	1.14	3.3E-01	D84003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2888766
5439	18639	31617	2.55	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5439	18639	31618	2.55	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5907	19096	32411	0.88	3.3E-01	BF213873.1	EST_HUMAN	60184809F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6067	19249	32576	1.37	3.3E-01	BE819650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6067	19249	32577	1.37	3.3E-01	BE819650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6162	19338	32684	1.29	3.3E-01	P08691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6932	20247	33680	0.59	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6932	20247	33681	0.69	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7029	20165	33586	4.63	3.3E-01	AI628131.1	EST_HUMAN	4p84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7029	20165	33587	4.63	3.3E-01	AI628131.1	EST_HUMAN	4p84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7961	21011	34521	1.9	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 6' similar to TEGT

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8759	21838	35379	23.1	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
8926	22005	35544	0.73	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9314	22300	35941	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1)(MEK KINASE 1) (MEKK 1)
9578	22720	36289	1.16	3.3E-01	BE828481.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9578	22720	36289	1.16	3.3E-01	BE828481.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9711	22780	36330	2.9	3.3E-01	N69866.1	EST_HUMAN	za67h01.a1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9752	22850	36280	2.81	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10196	23233		2.08	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG1-C) gene, exons 1-3, complete cds
10885	23897	37620	0.74	3.3E-01	AE000631.1	NT	Helicobacter pylori 26695 section 109 of 134 of the complete genome
10960	24041	37676	3.35	3.3E-01	XG3953.1	NT	D. mauritiana Adh gene
10960	24041	37676	3.35	3.3E-01	XG3953.1	NT	D. mauritiana Adh gene
11279	24345		2.1	3.3E-01	BF526493.1	EST_HUMAN	602070802F1 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4213585 5'
11507	24595	38242	9.35	3.3E-01	BE218361.1	EST_HUMAN	h571g02.1 NCI CGAP L224 Homo sapiens cDNA clone IMAGE:3176978 3'
11626	24706	38399	3.7	3.3E-01	P47863	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-28) (CBP30)
12018	25002		2.8	3.3E-01	AA806621.1	EST_HUMAN	h571g02.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12036	13253	26253	2.33	3.3E-01	X07880.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
12250	25190	38357	1.85	3.3E-01	8598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
13044	26686		22.03	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (217)
469	13694		2.5	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
736	13918		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1188	14350		23.03	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1311	14467	27505	1.48	3.2E-01	Z60202.1	NT	P. vulgaris arcs-1 gene
1421	14575	27648	6.74	3.2E-01	Q48924	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1663	14815		1	3.2E-01	AF209730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1815	14964	28057	1.3	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1825	14974	28059	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST368264 MAGE resequences, MAGD Homo sapiens cDNA
1825	14974	28070	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST368264 MAGE resequences, MAGD Homo sapiens cDNA
1891	15035	28142	1.25	3.2E-01	AL111655.1	NT	Bacillus cinereus strain T4 cDNA library under conditions of nitrogen deprivation
2227	15361	28490	3.22	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2606	15729		2.83	3.2E-01	7710079	NT	Mus musculus Pbx1-injected 1 homeobox (Pbxox1), mRNA
2774	15889	29000	1.23	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zho finger protein (PLZF) gene, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3698	16857		0.76	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4081	17217		0.93	3.2E-01	AL161646.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4614	17653	30641	1.37	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4821	17758	30740	1.35	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4860	17893		6.99	3.2E-01	BF693617.1	EST_HUMAN	602081672F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246503 5'
5386	18588	31560	2.93	3.2E-01	BE173964.1	EST_HUMAN	CM04HT0589-060300-268-10 HT0589 Homo sapiens cDNA
6076	19260	32889	1.08	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:lactate oxidoreductase and flanking genes
6433	19601	32965	0.73	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procolagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6729	19885	33277	0.89	3.2E-01	AV178037.1	EST_HUMAN	AV178037 FHTA Homo sapiens cDNA clone FHTA4BH01 5'
6872	20024		1.17	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8040	21123	34643	0.52	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8365	21446	34969	1.5	3.2E-01	M60266.1	NT	Rat ISO-alpha natriuretic factor gene, complete cds
8461	21542	35072	0.87	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat, map NOS-D12Wax1
8562	21643	35182	15.01	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8565	21646	35187	14.52	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8656	21736		1.24	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8696	21778	36310	0.69	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8698	21778	35311	0.69	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8771	21850	35391	1.14	3.2E-01	AE002015.1	NT	Delnoccocus radiodurans R1 section 152 of 229 of the complete chromosome 1
8871	21950	35485	0.86	3.2E-01	U51026.1	NT	Oryzobagrus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8871	21950	35486	0.86	3.2E-01	U51026.1	NT	Oryzobagrus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9287	22344	35895	0.67	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9278	22354		2.54	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9351	22426	35983	0.61	3.2E-01	AF041828.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9351	22426	35984	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10188	23235	36824	4.33	3.2E-01	U44914.1	NT	Burkholderia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10402	23437	37044	0.62	3.2E-01	BE326230.1	EST_HUMAN	hve9f05.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181568 3'
10518	23453		3.94	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10905	23988	37620	3.05	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Striatagene (cat#936206) Homo sapiens cDNA clone HFBDD221
12289	26083		3.11	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12881	25572		3.26	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12969	25891		2.2	3.2E-01	AF157625.1	NT	Bos taurus insulin 1,4,5-bisphosphate receptor type I mRNA, complete cds
13018	25669		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxydiphosphate deaminase gene, complete cds
13089	26129	31545	1.24	3.2E-01	BE385778.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
							ye010106.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2736	15853	28967	3.39	3.1E-01	R18051.1	EST_HUMAN	gb:1464241 QM PROTEIN (HUMAN);
2782	16001	28985	3.77	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2782	16001	28986	3.77	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2920	16098		1.28	3.1E-01	AW629036.1	EST_HUMAN	h148H08.X1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3242	16416		3.51	3.1E-01	AB029089.1	NT	Mus musculus gene for Ser/Thr kinase KIAMRE, exon 6
4016	17173	30181	0.94	3.1E-01	AJ251698.1	NT	Dactylea cerata mRNA for transcription factor E2F (E2F gene)
5077	18205	31177	0.7	3.1E-01	AE003964.1	NT	Xifolia fastidiosa, section 130 of 229 of the complete genome
5595	18790	31838	8.24	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5717	18910	32205	0.7	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN H1238
5718	18911	32206	0.75	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5729	18922		0.83	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5892	19080	32390	2.65	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6595	19755	33141	1.3	3.1E-01	AV983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6683	19822	33209	0.96	3.1E-01	AI264458.1	EST_HUMAN	q139d01.X1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1874689 3'
6821	19974	33382	0.78	3.1E-01	X71887.1	NT	H. sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6905	20220		0.69	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281099-005-h05 CT0222 Homo sapiens cDNA
7109	25801	31491	2.32	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
							Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
7856	20911	34416	0.7	3.1E-01	4885380	NT	Y94601.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'
8849	21928	35467	0.84	3.1E-01	R45318.1	EST_HUMAN	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10106	23144	36742	0.68	3.1E-01	6679322	NT	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10272	23307	36903	1.04	3.1E-01	BF696399.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10272	23307	36904	1.04	3.1E-01	BF696399.1	EST_HUMAN	q161e11.X1 NCI_CGAP_K143 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:365700
							HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10334	23369	36979	1.68	3.1E-01	A1244001.1	EST_HUMAN	y047h08.s1 Striatagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar
10510	23545		0.98	3.1E-01	T55325.1	EST_HUMAN	to gb:0101036_m02 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11076	24151	37789	1.84	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11474	24533	38203	1.62	3.1E-01	AW074910.1	EST_HUMAN	xa62g09.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2571424 3'
11827	24816	38507	2.08	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11828	24817	38508	1.67	3.1E-01	R55735.1	EST_HUMAN	y89b05.1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:40722 5' similar to contains Alu repetitive element;
12123	25103		1.3	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12418	25298		1.22	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12455	25319		1.73	3.1E-01	AF304162.1	NT	Sitostation vitreum 40S ribosomal protein S11 mRNA, partial cds
12813	25412		3.73	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
13028	26677		3.82	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM6 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α -
13068	26123		1.22	3.1E-01	10946823	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp-pending), mRNA
74	15979	26336	1.65	3.0E-01	6755033	NT	Mus musculus protein kinase C, epsilon (Pkc), mRNA
264	13483	26515	11.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1251	14410	27472	2.35	3.0E-01	AW300400.1	EST_HUMAN	xa63f08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1837	14880	27769	5.77	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
1838	14984	28084	1.2	3.0E-01	X69082.1	NT	A. limnerius putative gene encoding integrase, Mars2 (RIP)
3069	16245		0.8	3.0E-01	AB008677.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3283	16457		1.33	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3968	17123	30129	1.58	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0282-201199-001-g01 ST0262 Homo sapiens cDNA
4082	17237	30243	1.16	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
4636	17772	30752	1.79	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5258	16643	29665	2.33	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-ETC) (GATA-3)
5467	18667	31646	5.1	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5548	18746	31780	0.84	3.0E-01	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5552	18749	31785	1	3.0E-01	AF229247.1	NT	Canis lupus orthopoxvirus hemagglutinin gene, complete cds
5621	18815	31883	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5621	18815	31884	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5658	18852	32135	3.87	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
5970	20108	33624	2.82	3.0E-01	D16313.1	NT	Mouse cyclophilin 15 gene, complete cds
6859	18518	31511	0.76	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/87 kDa laminin-binding protein mRNA, partial cds
7085	20118	33532	1.15	3.0E-01	AF229247.1	NT	Canis lupus orthopoxvirus hemagglutinin gene, complete cds

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7270	20353	33806	0.98	3.0E-01	AL183206.2	NT	Homo sapiens chromosome 21 segment HS21C008
7481	20558	34028	4.3	3.0E-01	10947007	NT	Mus musculus midkolin (Midn-pending), mRNA
7670	20736	34214	1.61	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8111	21193	34713	1.34	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8588	21649		3.1	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3f), mRNA
8658	21738	35279	0.48	3.0E-01	Z70200.1	NT	H. sapiens gene for U5 snRNP-specific 200kD protein
8671	21751	35288	1.23	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 6'
9029	22108	35649	0.69	3.0E-01	AF141876.1	NT	Streptomyces sulfonofaciens isopenicillin N synthase (pcbc) gene, partial cds
9072	22151		0.82	3.0E-01	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9419	22493	36059	1.09	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative entranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9773	22813	36391	0.64	3.0E-01	P76389	SWISSPROT	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9927	22867		0.46	3.0E-01	D90904.1	NT	Synechocystis sp. PCC6803 complete genome, 8/27, 630555-781448
10173	23210	36803	0.84	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4288339 5'
10346	23381	36982	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans Tada (tada), TadaB (tadB), TadaC (tadC), TadaD (tadD), Tade (tade), TadeF (tadF), and TadeG (tadG) genes, complete cds
10346	23381	36993	0.46	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans Tada (tada), TadaB (tadB), TadaC (tadC), TadaD (tadD), Tade (tade), TadeF (tadF), and TadeG (tadG) genes, complete cds
10606	23640	37248	0.6	3.0E-01	AW118111.1	EST_HUMAN	xe03010.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10608	23642	37250	2.51	3.0E-01	AB030231.1	NT	Aspergillus oryzae btpA gene for ER chaperone BIP, complete cds
10629	23663	37271	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10629	23663	37272	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
12067	25048	38755	2.16	3.0E-01	HS1028.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12067	25048	38756	2.16	3.0E-01	HS1028.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12470	25324		1.3	3.0E-01	P94660	SWISSPROT	PONTICULIN PRECURSOR
12731	26062		1.88	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13061	26121		4.48	3.0E-01	6677768	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
1771	14920		0.94	2.9E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and lgt2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1930	15073	28176	0.94	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2080	15220	28340	2.36	2.9E-01	AE000736.1	NT	Aquifex acidicus section 68 of 109 of the complete genome
2322	15454	28555	1.01	2.9E-01	AF222716.1	NT	Chrysothrix synnoides mitochondrion, complete genome
3253	16427	29445	0.96	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3323	16498	28513	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171288-001-r12 CT0328 Homo sapiens cDNA
3323	16498	28514	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171288-001-r12 CT0328 Homo sapiens cDNA
4003	17160	30186	1.12	2.9E-01	AI610836.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Cas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:U15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN)/contains element L1 repetitive element;
4045	17201	30212	0.81	2.9E-01	AI769472.1	EST_HUMAN	w14d10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:G34F6.7 CE15676;
4183	17333	30325	0.81	2.9E-01	AB016428.1	NT	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4195	17345		0.78	2.9E-01	AW002902.1	EST_HUMAN	wf02f10.x1 NCI_CGAP_GC9 Homo sapiens cDNA clone IMAGE:2480395 3'
4608	17745	30724	0.98	2.9E-01	AA284488.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4805	17940		0.73	2.9E-01	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007 repetitive element;
4957	18087	31063	0.59	2.9E-01	AB018029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5222	18344		0.99	2.9E-01	AI670899.1	EST_HUMAN	wa06f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.L2 L1 repetitive element;
5320	18087	31063	0.65	2.9E-01	AB018029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5372	18575		1.59	2.9E-01	R37485.1	EST_HUMAN	y77e12.a1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5511	20137	33555	0.98	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5884	19073	32381	5.27	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5884	19073	32382	5.27	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5897	19085	32397	5.53	2.9E-01		NT	system polypeptides P16, 18, 28, 30 and levanase
6181	19357	32705	1.55	2.9E-01	AA418145.1	EST_HUMAN	Mus musculus Eph receptor A8 (EphA8), mRNA
6411	19580	32941	1.07	2.9E-01	AI797128.1	EST_HUMAN	z067b12.r1 Soares NIHMP1_S1 Homo sapiens cDNA clone IMAGE:7677711 5'
6455	19622	32986	2.22	2.9E-01	U03420.1	EST_HUMAN	we27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.L1 L1 repetitive element;
7001	20137	33555	0.71	2.9E-01	AF321001.1	NT	Bos taurus myosin I mRNA, complete cds
7126	18552	31466	1.4	2.9E-01	AF142329.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7245	20328	33773	3.11	2.9E-01	Q04399	SWISSPROT	Mus musculus Filin protein (Filin) gene, complete cds; and Lgln protein (Lgln) gene, partial cds
7310	20352	33852	1.54	2.9E-01	AF100856.1	NT	POTATIVE MULTICOPPER OXIDASE YDR506C
8104	21186	34705	1.81	2.9E-01	BE540422.1	EST_HUMAN	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds: Bing1 (BING1), tapasin (tapasin), RagDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1, 3-galactosyl tps)
8104	21186	34706	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8104	21186	34706	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8343	21424	34949	0.64	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8343	21424	34950	0.64	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8356	21437		0.75	2.9E-01	BF217743.1	EST_HUMAN	601882670F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4085113 5'
8534	21615		0.53	2.9E-01	AF167456.1	NT	Buchnera achiticola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds
8794	21873	35412	0.82	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9126	22204	35747	1.09	2.9E-01	AF226908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
9233	22311	35863	0.81	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9447	22563	36125	0.98	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9447	22563	36126	0.98	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10405	23440	37047	0.46	2.9E-01	AW294100.1	EST_HUMAN	U1H-B12-ahg-b-02-Q-U1.st NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'
10405	23440	37048	0.46	2.9E-01	AW294100.1	EST_HUMAN	U1H-B12-ahg-b-02-Q-U1.st NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'
11133	24205	37830	1.94	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11433	24404	38159	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11433	24494	38160	1.78	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11881	24869	38566	2.71	2.9E-01	AA833373.1	EST_HUMAN	repetitive element ;
11888	24874	38571	3.12	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
11900	24888	38587	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38588	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12677	25452	32017	1.85	2.9E-01	AW005871.1	EST_HUMAN	wz88105.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER28 repetitive element ;
12774	25516		1.89	2.9E-01	V00202.1	NT	D. melanogaster: part of the 44D cuticle gene cluster encoding cuticle gene I
12777	25519	32001	2.23	2.9E-01	AF082453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
13125	25734	31944	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13125	25734	31945	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13204	25785	31918	1.4	2.9E-01	AF200418.1	NT	Callinectes sapidus cadmium-inducible metallothionein CdMT-1 mRNA, complete cds
582	13774		2.04	2.9E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
587	13778		1.99	2.8E-01	L26145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1107	14272	27331	3.34	2.8E-01	AF168050.1	NT	Glia guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1306	14462	27529	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1308	14482	27530	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1319	14475	27541	1.2	2.8E-01	D86590.1	NT	Human mRNA for serine/threonine protein kinase, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1766	14915	28011	1.87	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0384-120200-065506 CT0384 Homo sapiens cDNA
2069	16210	28326	1.49	2.8E-01	AL047620.1	EST_HUMAN	DKFZp568i2321 J1 588 (synonym: hule1) Homo sapiens cDNA clone DKFZp568i2321
2200	16335	28462	1.51	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28712333 3'
2542	15567	28791	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2542	15567	28792	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2612	15736		2.95	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2730	15948	28958	1.16	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipyltransferase, complete cds
3035	16211		1.37	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
3036	16212	29234	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3036	16212	29235	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3465	16633	29652	1.05	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (477)
4103	17257	30257	1.87	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 88 of 70) of the complete genome
4240	17366		0.6	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4315	17458		2.17	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis NH7 Homo sapiens cDNA clone IMAGE:1040228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
4582	17719	30702	2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4944	18074	31049	0.92	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4950	18080	31056	4.95	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4994	18113	31090	1.52	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brr07 Homo sapiens cDNA clone IMAGE:4180129 5'
5006	18135	31109	3.66	2.8E-01	AI272659.1	EST_HUMAN	q159c11.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR6 repetitive element ;
5318	18473	31404	0.61	2.8E-01	X60787.1	NT	Mouse Kv3.3 gene for potassium channel protein, exon 2
5428	25604	31602	23.61	2.8E-01	AA349897.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5723	18916	32211	2.57	2.8E-01	AB018625.1	NT	Homo sapiens OCTN2 gene, complete cds
5938	19124		0.93	2.8E-01	AW892583.1	EST_HUMAN	GM1-BND024-150200-118-g12 BND024 Homo sapiens cDNA
6042	19225	32548	0.66	2.8E-01	AA765296.1	EST_HUMAN	oa01d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK506-BINDING PROTEIN (HUMAN);
6059	19241		0.84	2.8E-01	AA404576.1	EST_HUMAN	z141f01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6305	26212		0.87	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6347	19517	32874	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6347	19517	32875	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6870	20022	33432	7.84	2.8E-01	BF511215.1	EST_HUMAN	U1-H-B14-act-f-04-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7145	20280	33721	0.64	2.8E-01	U65300.1	NT	Orthogomys heterodius cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7599	20669		1.14	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
8284	21366	34884	1.31	2.8E-01	A1346126.1	EST_HUMAN	q44801.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X068323_cds1
8284	21366	34885	1.31	2.8E-01	A1346126.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8404	21485	35014	2.31	2.8E-01	U51688.1	NT	q44801.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X068323_cds1
8712	21792	35328	0.6	2.8E-01	AA911629.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8789	21888		7.72	2.8E-01	BF347847.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
9666	22628	36189	1.14	2.8E-01	U17251.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
9912	22952		1.16	2.8E-01	L13654.1	NT	602022987F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158525 5'
10092	23130	36733	0.98	2.8E-01	AF132728.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
10092	23130	36734	0.98	2.8E-01	AF132728.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
10152	23189	36786	0.46	2.8E-01	AE001310.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10156	23193	36789	0.7	2.8E-01	AF294393.1	NT	Chlamydia trachomatis section 37 of 87 of the complete genome
10285	23300	36898	3.8	2.8E-01	7706163	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b, nuclear gene for mitochondrial product
10519	23594		1.1	2.8E-01	9626164	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10561	23596	37202	0.5	2.8E-01	BE969727.2	EST_HUMAN	Fujihani sarcoma virus, complete genome
10982	24061	37696	1.88	2.8E-01	BF241062.1	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639765 3'
10982	24061	37698	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11011	24090	37727	3.01	2.8E-01	BF696970.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11119	24191	37823	1.53	2.8E-01	AF051662.1	NT	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
11556	24611		3.58	2.8E-01	BF674023.1	EST_HUMAN	Drosophila heteroneura fruttesa (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11851	24840	38533	1.55	2.8E-01	AJ248285.1	NT	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
11851	24840	38534	1.55	2.8E-01	AJ248286.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12715	25475		12.79	2.8E-01	D83329.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12846	25582	31987	7.91	2.8E-01	BE178699.1	EST_HUMAN	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12875	25582	31998	1.29	2.8E-01	BE900116.1	EST_HUMAN	PM4-HT0608-030400-001-a07 HT0608 Homo sapiens cDNA
13062	26096		1.59	2.8E-01	11433629	NT	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
							Homo sapiens CDC42-binding protein kinase beta (DNMPK-like) (CDC42BPB), mRNA

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489	13683	28717	4.34	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
628	13613	28835	13.64	2.7E-01	AA450061.1	EST_HUMAN	z36b10.s1 Soares_tetral_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1200	14446	27612	2.04	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1650	14803		1.63	2.7E-01	X78815.1	NT	Gambia SR2 gene
1768	14917	28012	3.18	2.7E-01	W56087.1	EST_HUMAN	z322h10.t1 Soares_fetal_heart_Nb4H19W Homo sapiens cDNA clone IMAGE:341443 5'
1817	14966	28058	1.48	2.7E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2204	16057		3.1	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular stomatitis transporter type 2, promoter region and exon 1
2250	15383	28510	0.94	2.7E-01	AI372772.1	EST_HUMAN	EST175678 Infant brain, Bento Soares Homo sapiens cDNA clone UH1801R 5' end
2260	15383	28511	0.94	2.7E-01	AI372772.1	EST_HUMAN	EST175678 Infant brain, Bento Soares Homo sapiens cDNA clone UH1801R 5' end
2440	15568	28895	7.07	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial
2526	15631	28775	4.35	2.7E-01	AI310858.1	EST_HUMAN	te43x11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element
3049	16225		0.99	2.7E-01	BF088284.1	EST_HUMAN	GM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3381	16533	29647	0.66	2.7E-01	8393820	NT	Rattus norvegicus Insulin receptor (Insr), mRNA
4118	17272	30271	1.94	2.7E-01	AI828015.1	EST_HUMAN	wb92et11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4133	17286	30281	0.68	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4133	17286	30282	0.68	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4140	17292	30286	2.39	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5153	18275		4.48	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 G70288 Homo sapiens cDNA
5381	18683	31452	1.88	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
5607	18802		1.31	2.7E-01	AB033171.1	NT	Astraeopora mytilophthalma mitochondrial cytb gene for cytochrome b, partial cds
6472	19639	32993	0.89	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6472	19639	32999	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6745	19801	33293	1.05	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6745	19801	33294	1.05	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6918	20233	33687	1.74	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7197	20662		0.77	2.7E-01	AI540070.1	EST_HUMAN	td08r08.x1 NCL_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2075103 3'
7511	20585	34058	0.92	2.7E-01	Q11078	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0583.3 IN CHROMOSOME X

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7734	20795	34283	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7734	20795	34284	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7835	20919	34425	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7865	20919	34426	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7917	20968	34474	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
7917	20968	34475	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
7976	21026	34540	0.66	2.7E-01	L01081.1	NT	Oryzobolus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8048	21131	34691	0.66	2.7E-01	AA013147.1	EST_HUMAN	zab5b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE360957 3' similar to contains Alu repetitive element
8330	21412	34698	0.56	2.7E-01	AW868503.1	EST_HUMAN	MR1-SN0082-100500-002-d09 SN0082 Homo sapiens cDNA
8380	21461	34984	0.59	2.7E-01	R39257.1	EST_HUMAN	yc91h03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8468	21567	35104	0.83	2.7E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8959	22038	35580	1.4	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9534	22599	36171	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9534	22599	36172	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9537	22602		2.66	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10005	23043	36636	0.8	2.7E-01	D86680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10286	23321	36923	0.9	2.7E-01	AF091848.1	NT	Oryzobolus cuniculus calgranulin C mRNA, partial cds
10323	23358	36868	2.06	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A1c isoform a (NF-A1c) mRNA, complete cds
10455	23490	37099	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10455	23490	37100	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10749	23782		0.51	2.7E-01	AB011678.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
10765	23798	37418	0.88	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10765	23798	37419	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
11050	24127	37761	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11050	24127	37762	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11061	24137	37772	2.58	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12818	25942		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
13034	25681		2.75	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
482	16013	26710	2.8	2.0E-01	P78411	SWISSPROT	IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2

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493	13688		1.94	2.6E-01	D18459.1	NT	Bos taurus mRNA for mb-1, complete cds
1424	14578	27651	1.77	2.6E-01	BE885087.1	EST_HUMAN	801310838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1468	14622	27705	1.09	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1845	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1945	15098	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14889_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2169	15295		10.39	2.6E-01	AW733192.1	EST_HUMAN	Human prealbumin gene, complete cds
2220	15354	28485	1.13	2.6E-01	MF1844.1	NT	Human prealbumin gene, complete cds
2611	16735		11.98	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2960043 5'
3161	16336		1.11	2.6E-01	AW974531.1	EST_HUMAN	EST388635 IMAGE resequences, MAGF Homo sapiens cDNA
3671	16834	28845	0.84	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
							Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3733	16894	29899	1.67	2.6E-01	AF228118.1	NT	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4215	17364	30352	0.79	2.6E-01	AW959510.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4270	17415	30404	10.93	2.6E-01	BE080598.1	EST_HUMAN	Enterococcus faecium strain N97-530 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4476	17616	30597	1.71	2.6E-01	AF175293.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4617	17754	30735	0.89	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4617	17754	30736	0.89	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4970	17805	30784	1.14	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 StrataGene fetal retina 937202 Homo sapiens cDNA clone IMAGE:898477 5'
4770	17905	30887	2.25	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type II chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
							Ophreidia radicata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product y151ed6.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5086	18214	31187	3.63	2.6E-01	H04858.1	EST_HUMAN	am33b11.a1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1488905 3'
5195	18277		0.61	2.6E-01	AA884625.1	EST_HUMAN	Paramecium caudatum gene for PAP, complete cds
5457	18857		1.29	2.6E-01	AB035972.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAax genes, complete cds
5565	18762	31802	0.67	2.6E-01	M96060.1	NT	td18a03.x1 NCI CGAP_C018 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element;
5689	18883		0.84	2.6E-01	A862398.1	EST_HUMAN	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, plm-2 protooncogene homolog plm-2h, and shcl-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds, and unknown g
5895	19083	32394	0.64	2.6E-01	AF207550.1	NT	

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6106	26211		2.57	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6330	19501	32859	1.96	2.6E-01	AI582557.1	EST_HUMAN	is02e12.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6330	19501	32860	1.96	2.6E-01	AI582557.1	EST_HUMAN	is02e12.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6552	19714	33090	0.98	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 617
6807	19961	33364	0.74	2.6E-01	BE792032.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936158 5'
6807	19961	33365	0.74	2.6E-01	BE792032.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936158 5'
7183	20315	33758	1.04	2.6E-01	AI914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7549	20621	34098	0.7	2.6E-01	BE148961.1	EST_HUMAN	CM0-HT0245-031189-085-f04 HT0245 Homo sapiens cDNA
7587	25848		0.96	2.6E-01	AL138077.2	NT	Campylobacter jejuni NCT C11168 complete genome; segment 416
7626	20696		0.78	2.6E-01	AA198149.1	EST_HUMAN	zp92601.f1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:027672 5'
7918	20669	34476	1.73	2.6E-01	R10365.1	EST_HUMAN	y37a03.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8033	21116	34634	1.18	2.6E-01	R02411.1	EST_HUMAN	y682a07.f1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:124212 5'
8088	21170	34685	1.3	2.6E-01	BE14433.1	EST_HUMAN	MR0-HT0196-181199-003-d12 HT0196 Homo sapiens cDNA
8629	21610	35148	2.97	2.6E-01	BF343688.1	EST_HUMAN	602014422F1 NCI CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4150396 5'
8605	21666	35223	1.74	2.6E-01	Q10198	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8892	21971	35506	4.06	2.6E-01	BE830336.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8892	21971	35507	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9667	22629	36200	0.92	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9940	22879		0.5	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	23110	36713	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10072	23110	36714	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10393	23428		0.63	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10727	23760		1.09	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10840	23873		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11815	24804		31.14	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12468	28070		4.14	2.6E-01	BE863491.1	EST_HUMAN	601511032F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12535	25365	32069	3.86	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12922	25507		2.04	2.0E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
13007	25683		1.78	2.0E-01	AE001713.1	NT	Thermodoga maritima section 25 of 136 of the complete genome
13057	25692		2.36	2.0E-01	AF141325.2	NT	Homo sapiens insulin polyphosphate 1-phosphatase (INPP1) gene, complete cds
13098	18735		1.43	2.0E-01	BE272440.1	EST_HUMAN	601128019F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2860043 5'
13107	25722		2.04	2.0E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
13150	25748		2.4	2.0E-01	U30729.1	NT	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds
251	13472	26503	1.87	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
262	13472	26503	1.7	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
265	13484		2.51	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
855	14032	27093	1.23	2.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1085	14251		1.75	2.5E-01	AE002166.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1145	14310	27367	5.45	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1767	14916		4.53	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2479	15608		11.21	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 108 of the complete genome
2563	15688	28814	1.22	2.6E-01	6678216	NT	Mus musculus protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 (Pcm1), mRNA
2565	15690		1.02	2.6E-01	AA251987.1	EST_HUMAN	z51a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2702	15820	28936	1	2.5E-01	X95310.1	NT	B. taurus mRNA for D-aspartate oxidase
3499	16656		3.34	2.5E-01	AW973471.1	EST_HUMAN	EST386404 IMAGE resequences; MAGM Homo sapiens cDNA
3639	16803	29816	7.18	2.6E-01	AL161617.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3650	17108	30105	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4438	17578		0.88	2.5E-01	Q03314	SWISSPROT	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4737	17872	30855	0.7	2.5E-01	AF242431.1	NT	RHIB PROTEIN
4871	18004		1.13	2.5E-01	Q27225	SWISSPROT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naiip6) gene, complete cds; and Naiip3 gene, exons 2-9 and 11-16
4878	18009	30993	3.99	2.6E-01	AF007768.1	NT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4904	18034	31026	2.3	2.5E-01	AE004416.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4926	18058		3.54	2.5E-01	AJ230113.1	NT	Vibrio cholerae chromosome II, section 73 of 63 of the complete chromosome
4954	18084	31090	0.8	2.5E-01	BE889785.1	EST_HUMAN	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
							601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4894	18123	31101	0.61	2.5E-01	U83656.1	NT	Rattus norvegicus NF-KB gene, promoter region
5212	18333	31303	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5212	18333	31304	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5337	18450		1.08	2.5E-01	AA419208.1	EST_HUMAN	z335a06.t1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:755600 5' similar to gb:M88270
5441	18641	31620	12.21	2.5E-01	S83360.1	NT	P59 PROTEIN (HUMAN);
6080	19282	32591	0.6	2.5E-01	AJ006345.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6081	19283		0.81	2.5E-01	AL163207.2	NT	Homo sapiens KVLQ11 gene
6762	19918	33313	0.82	2.5E-01	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C007
7190	20055	33485	0.64	2.5E-01	8394138	NT	Homo sapiens partial steerin-1 gene
7507	20581	34054	0.71	2.5E-01	U13992.1	NT	Rattus norvegicus rabn 3 (RABIN3), mRNA
7536	20609		1.13	2.5E-01	AF134119.1	NT	Feline calicivirus CF/68 RNA helix/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds; and unknown gene
7770	20828	34319	0.62	2.5E-01	AL161508.2	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7814	20869	34366	4.23	2.5E-01	AL163282.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
8028	21111	34630	2.22	2.5E-01	BF108040.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
8039	21122	34642	0.61	2.5E-01	BE960712.1	EST_HUMAN	7157a03.x1 Soares NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8421	21502	35034	1.9	2.5E-01	BF086595.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8591	21672	35210	0.8	2.5E-01	P04492	SWISSPROT	601459238F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3862809 5'
8837	21916	35454	4.07	2.5E-01	HS3238.1	EST_HUMAN	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
9076	22155	35609	1.05	2.5E-01	M88626.1	NT	yq84f07.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
9716	22781	36351	16.86	2.5E-01	U88651.2	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9772	22768	36339	16.85	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9772	22768	36340	2.44	2.5E-01	AF085164.1	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
10303	23338	36943	1.31	2.5E-01	AF085164.1	NT	Hardycore vulgare receptor-like kinase LK10 gene, partial cds
10550	23685	37193	0.51	2.5E-01	AW591997.1	EST_HUMAN	Hardycore vulgare receptor-like kinase LK10 gene, partial cds
10763	23798	37416	1.4	2.5E-01	AW152246.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10767	23800	37422	1.61	2.5E-01	X38491.1	NT	Pocphyra purpurea chloroplast, complete genome
11332	24395	38043	2.98	2.5E-01	D50914.1	NT	xg40c10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
12204	25198	38834	5.16	2.5E-01	AF200528.1	NT	Mouse L1md LINE DNA
12233	26167		6.12	2.5E-01	AL161541.2	NT	Human mRNA for KIAA0124 gene, partial cds
							Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13024	25674		1.22	2.5E-01	AF325363.1	NT	Delia brassica cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial product
567	13759	26783	1.41	2.4E-01	AA8363.10.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
871	14047	27113	4.4	2.4E-01	BF576124.1	EST_HUMAN	802132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271678 6'
1332	14489	27557	16.83	2.4E-01	AJ280880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1332	14489	27568	16.83	2.4E-01	AJ280880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1415	14569	27642	0.97	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1898	15041		26.78	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1940	15092	28193	1.43	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2091	15231	28353	1.64	2.4E-01	A1742958.1	EST_HUMAN	wg76d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:060287 O60287 KIAA0512 PROTEIN.
2206	15340	28487	1.17	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit I gene, complete cds; and unknown genes
2237	15370		1.25	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2336	15467	28602	2.29	2.4E-01	AE000680.1	NT	Aquifex acidicus section 12 of 109 of the complete genome
2602	15726	28845	3.13	2.4E-01	Z36534.1	NT	D. discoideum (Ax3-K) potA gene
2820	15934	29046	2.22	2.4E-01	X71783.1	NT	S. pombe swi6 gene
2846	15950	29069	6.27	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3202	16377		3.03	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofl (gag/pol) genes, complete cds
3217	16391	29402	1.51	2.4E-01	X74206.1	NT	H. sapiens AGT gene, PstI fragment of intron 4
3856	17016	30018	0.97	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4141	17263		0.85	2.4E-01	D28980.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5181	18303	31266	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5181	18303	31287	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5334	18447	31415					Bacillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thiosulfate sulfotransferase, hypothetical 16.1 kDa transcriptional regulator and hypothetical 18.2 kDa>
5335	18448	31416	1.89	2.4E-01	U89914.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5335	18448	31417	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5335	18448	31417	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5578	18773	31818	0.9	2.4E-01	AB25707.1	EST_HUMAN	wc33405.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457120 3'
5578	18773	31819	0.9	2.4E-01	AB25707.1	EST_HUMAN	wc33405.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457120 3'
5602	18787	31847	0.59	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5772	18964	32266	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5772	18964	32287	12.88	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds

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5800	18950	-	0.7	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6010	25815	-	0.97	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (cam2 gene)
6016	19200	32517	2.54	2.4E-01	BF592336.1	EST_HUMAN	715404.x1 NCL CGAP Br10 Homo sapiens cDNA clone IMAGE:338503 3' similar to SW:3FR4 HUMAN Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element
6108	19288	32620	2.47	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6215	19390	32738	2.49	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6289	19443	32792	0.84	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cdaADE11 5'
6516	19681	33051	0.87	2.4E-01	AA398872.1	EST_HUMAN	z170d02.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727683 3'
6665	19824	33212	1.59	2.4E-01	AI698989.1	EST_HUMAN	wc62e11.x1 NCL CGAP Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7498	20573	34046	7.79	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7902	20954	34461	0.69	2.4E-01	AF229644.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8271	21353	34868	0.5	2.4E-01	X97252.1	NT	M.musculus psh gene and promoter
8271	21353	34869	0.5	2.4E-01	X97252.1	NT	M.musculus psh gene and promoter
8392	21473	34899	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8392	21473	35000	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8344	21625	35162	1.29	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8788	21677	35416	1.18	2.4E-01	BF242794.1	EST_HUMAN	60187678F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4106288 5'
9332	22408	35981	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11158 complete genome; segment 4/6
9332	22408	35982	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11158 complete genome; segment 4/6
9763	22701	36287	8.39	2.4E-01	AI693515.1	EST_HUMAN	wd43902.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22.b1 TAR1 repetitive element ;
9905	22845	36530	0.69	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
9905	22845	36531	0.69	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
10954	23689	37297	1.8	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11006	24085	37722	2.15	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11074	24149	37788	1.96	2.4E-01	AF030198.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11447	24508	38174	1.8	2.4E-01	BE286917.1	EST_HUMAN	601176415F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3531843 5'
11447	24508	38175	1.8	2.4E-01	BE286917.1	EST_HUMAN	601176415F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3531843 5'
11478	24537	38277	8.04	2.4E-01	Z11647.1	NT	P. asielica mosaic virus genomic RNA
12169	25127	38827	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 8
12289	25932	-	1.35	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive1-like1 (EIL1) mRNA, complete cds
12360	26258	-	1.62	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12988	25914		1.95	2.4E-01	V01507.1	NT	Gallus gallus gene coding for α -actin
12989	26151		1.37	2.4E-01	BF229976.1	EST_HUMAN	RC3-CT0413-100800-023-b08 CT0413 Homo sapiens cDNA
13072	25701		1.4	2.4E-01	AJ238044.1	NT	Homo sapiens mRNA for bradykinin B1 receptor (BTBR gene)
13102	25718		4.16	2.4E-01	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21C081
400	13597	26633	1.39	2.3E-01	S75698.1	NT	aromatase [Poephila gutturalis-zebra finches, ovary, mRNA, 3189 nt]
654	13840		5.53	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 31 of the complete genome
884	13868	26900	28.31	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 160 of the complete genome
957	14130	27188	3.57	2.3E-01	BE311863.1	EST_HUMAN	601142073F1 NIH_MGC 14 Homo sapiens cDNA clone IMAGE:3505818.5
1634	14796	27872	1.11	2.3E-01	AJ246480.1	NT	Brassica napus elg gene for S-locus glycoprotein, cultivar T2
1681	14813	27898	1.72	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2103	15242		1.78	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type A5-4/FEL gene
2517	15843	28764	1.85	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3531015.5
2717	15835	28945	0.98	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2885	14573	27646	1.5	2.3E-01	AB015033.1	NT	Merhabilia agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain JFO 14957
3028	16204	29227	1.08	2.3E-01	AA601379.1	EST_HUMAN	nc16008.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843.3 similar to contains Alu repetitive element; contains element THR repetitive element;
3153	16328		7.06	2.3E-01	R21732.1	EST_HUMAN	yh21007.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357.3
3456	16823	29644	1.32	2.3E-01	H69836.1	EST_HUMAN	yh7h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283.5
3944	17103	30100	0.98	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rate, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4046	17202		5.15	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4470	17610	30588	0.86	2.3E-01	R82252.1	EST_HUMAN	y1701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017.5
4520	17659		1.91	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4573	17710	30693	1.12	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1727, 1-133859
4611	17748	30728	2.76	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4676	17811	30800	5.65	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5189	18281	31246	0.87	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5223	18345		1.03	2.3E-01	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
5280	18379	31345	0.63	2.3E-01	BF574804.1	EST_HUMAN	602132210F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4271547.5
5419	18620	31596	2.47	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5545	18742	31776	2.03	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCI_CGAP_Oy18 Homo sapiens cDNA clone IMAGE:3476699.3 similar to SW-GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5647	18841	32122	5.25	2.3E-01	X06597.1	NT	C.familialis rom1 gene
5766	18958	32367	0.99	2.3E-01	L39112.1	NT	Vittiforma comeum small subunit ribosomal RNA gene
5870	19060	32367	1.32	2.3E-01	S60371.1	NT	22S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
6062	19244	32559	1.98	2.3E-01	A1708840.1	EST_HUMAN	as27612x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6062	19244	32570	1.98	2.3E-01	A1708840.1	EST_HUMAN	as27612x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
8794	19949	33348	0.66	2.3E-01	AF198089.1	NT	Oryzobolus cuticularis cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
7017	20153	33573	4.63	2.3E-01	A1718148.1	EST_HUMAN	as4212x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
7260	20343	33795	0.88	2.3E-01	8923323	NT	Homo sapiens hypothalamic protein FLJ20345 (FLJ20345), mRNA
7440	20517	33989	0.76	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7573	20648	34123	2.94	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7576	20648	34125	5.37	2.3E-01	AF175389.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7576	20648	34126	5.37	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7784	20840		4.26	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
7789	20845	34338	1.56	2.3E-01	BE888074.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7931	20981		2.8	2.3E-01	N80983.1	EST_HUMAN	zat2608.1 Scars fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:282358 5'
7968	21018	34530	0.71	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC88980), mRNA
7968	21018	34531	0.71	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC88980), mRNA
8035	21118	34637	0.52	2.3E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
8183	21265	34788	1.79	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8690	21770	35300	0.62	2.3E-01	U57999.1	NT	Mus musculus prosaposin (psap/SGP-1) gene, complete cds
8972	22051	35594	0.59	2.3E-01	AW080541.1	EST_HUMAN	xc80606.x1 NCLCGAP_Brn33 Homo sapiens cDNA clone IMAGE:2591554 3'
9089	22168	35715	0.52	2.3E-01	AW084460.1	EST_HUMAN	EST1765333 MAGE resequences, MAGH Homo sapiens cDNA
9341	22417	35970	0.64	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X663388)
9341	22417	35971	0.64	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X663388)
9780	22820	36398	0.5	2.3E-01	8679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA
9830	22970	36559	0.53	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'
9885	23024	36616	0.81	2.3E-01	AW084460.1	EST_HUMAN	EST1765333 MAGE resequences, MAGH Homo sapiens cDNA
10037	23075	36876	1.57	2.3E-01	X62124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))

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10071	23109	38712	0.83	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281299-001-04 DT0036 Homo sapiens cDNA
10138	23176	38773	2.62	2.3E-01	BE173080.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10197	23224	38823	2.48	2.3E-01	AJ283281.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10658	23692	37302	0.94	2.3E-01	AF201828.1	NT	Murine hepatitis virus strain 2, complete genome
10871	23705		5.89	2.3E-01	BF133577.1	EST_HUMAN	601846159R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102082 3'
11465	24524	38195	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11465	24524	38196	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11633	24713	38404	2.43	2.3E-01	AE002187.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
12098	25078		1.36	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADOAGH01 5'
12281	25210		3.07	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2.B-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25284		48.78	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5'
12395	25873		1.23	2.3E-01	AA089819.1	EST_HUMAN	chr1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12464	26086						3x21d07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175
12500	28143	31657	4.08	2.3E-01	AW303623.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;
12553	28376	31562	7.05	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3008889 5'
12612	28411		1.77	2.3E-01	BF063319.1	EST_HUMAN	602144459F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4297719 5'
12708	28470		2.74	2.3E-01	AJ006619.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12712	28411		1.22	2.3E-01	U49845.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
13009	28666		1.84	2.3E-01	AJ006619.1	NT	Rattus norvegicus mRNA for acid gated ion channel
			2.36	2.3E-01	BF475611.1	EST_HUMAN	nac39h12.x1 Lupsk_sclatol_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
							MER33 repetitive element;
92	13327	28355	1.13	2.2E-01	A1052190.1	EST_HUMAN	oz14a10.x1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:1875280 3' similar to
1596	14749	27833	2.74	2.2E-01	AF187850.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
2155	15291	28418	2.19	2.2E-01	M34940.1	NT	Homo sapiens PPAR delta gene, promoter region
2476	15903	28728	7.16	2.2E-01	BF077838.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2654	15777	28890	1.83	2.2E-01	BE618258.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249968 5'
2654	15777	28891	1.83	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866190 5'
2946	16123	29136	4.94	2.2E-01	BE155626.1	EST_HUMAN	601462629F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866190 5'
2946	16123	29137	4.94	2.2E-01	BE155626.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
							PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2987	16163		2.07	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHTT) gene, exon 5
3479	16848		2.35	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62

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3948	17008	30009	0.62	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4211	17360	30349	0.69	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4242	17388		0.6	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4328	17471		1.07	2.2E-01	AF118102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4335	17478	30460	0.62	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K ⁺ channel subunit (Kcnk6) genes, complete cds
4379	17522	30502	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
4379	17522	30503	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
4475	17615	30595	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4475	17615	30596	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4847	18077		1.08	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4952	18082	31058	2.2	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648968 5'
5156	18278		1.57	2.2E-01	L13289.1	NT	Mus musculus Vinculin gene, exon 3
5228	18348	31319	1.34	2.2E-01	BE141035.1	EST_HUMAN	MRQ-HT0067-201089-002-c10 HT0067 Homo sapiens cDNA
5863	19053	32360	1.89	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog 2 (DIAPH2), transcript variant 156, mRNA
5874	19084		3.75	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6122	18301	32640	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6122	18301	32641	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6845	19898	33405	0.77	2.2E-01	AB038490.1	NT	Homo sapiens gene for Fukulin, complete cds
7166	20299	33742	10.63	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
7279	20362	33815	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7279	20362	33816	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7442	20519	33991	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7442	20519	33992	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7655	20723	34199	0.62	2.2E-01	AE000035.2	NT	Human glycophorin B gene, exon 4
7678	20830	34436	0.88	2.2E-01	AF287987.1	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7905	20957	34463	0.71	2.2E-01	AB024559.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
8210	21292		2.45	2.2E-01	AF155143.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8280	21362	34881	2.68	2.2E-01	Z49933.1	NT	Mus musculus mm23-M1 gene, promoter region
8748	21827	35063	0.61	2.2E-01	AJ132918.1	NT	E.coli sepA and sepB genes
9083	22162	35705	0.52	2.2E-01	L23312.1	NT	Pan troglodytes MacP2 gene 3'UTR
							Mouse HD protein mRNA, complete cds

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9083	22162	35706	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9097	22176	35720	4.59	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
9117	22168	35740	0.48	2.2E-01	U09954.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Capd-S) gene, complete cds
9224	22302		2.88	2.2E-01	AW65036.1	EST_HUMAN	PM3-CT0263-241289-008-007 CT0263 Homo sapiens cDNA
9316	22391	35942	1.98	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Dreaphila) (Deaf1), mRNA
9399	22473	36039	1.13	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9489	22546	36109	1.42	2.2E-01	W02988.1	EST_HUMAN	zad408.t1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:291591 5'
9507	22773	36345	15.08	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9552	22817	36187	0.78	2.2E-01	AJ008839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (klp3)
9563	22705	36271	1.05	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9576	22718	36286	4.29	2.2E-01	M69843.1	NT	Brachydanio rerio epandymin beta and gamma chains (Epd) genes, complete cds
9820	22880	36441	0.65	2.2E-01	Q80980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10020	23058	36854	3.84	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (OPsHSP21) mRNA, complete cds;
10159	23196	36792	1.53	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10380	23415	37024	1.11	2.2E-01	9628671	NT	Human herpesvirus 5, complete genome
10540	23575	37182	0.65	2.2E-01	T59472.1	EST_HUMAN	y633408.t1 Stratagene ovary (8937217) Homo sapiens cDNA clone IMAGE:75855 5'
10540	23575	37183	0.65	2.2E-01	T59472.1	EST_HUMAN	y633408.t1 Stratagene ovary (8937217) Homo sapiens cDNA clone IMAGE:75855 5'
10580	23616	37220	0.8	2.2E-01	AF069264.1	NT	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyruvate quinone synthesis A (exaD) genes, complete cds; and pyruvate quinone
10659	23693		0.79	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10707	23740	37344	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J98 section 123 of 132 of the complete genome
10707	23740	37345	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J98 section 123 of 132 of the complete genome
10853	23888	37605	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 11 and AS
11389	24450	38111	1.65	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11707	24704	38396	5.09	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11748	23934	37560	3.7	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12207	25161		1.33	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3650670 5'
12319	26156		1.98	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12407	26286		3.24	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12518	18492	31531	1.88	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141189-021-g04 C10249 Homo sapiens cDNA
12519	25363		1.47	2.2E-01	AW861922.1	EST_HUMAN	h17502.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2972523 3'
13119	26148		3.08	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAH302 5'
993	14165	27228	1.88	2.1E-01	AA66289.1	EST_HUMAN	nm31et1.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
998	14167	27228	0.72	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1148	14312		2.43	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1225	14385	27446	1.45	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1225	14385	27447	1.45	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1540	14692	27771	4.28	2.1E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and lgt2 gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1963	15106	28206	2.19	2.1E-01	AA908824.1	EST_HUMAN	dk73602.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02765
2224	16358	28488	3.55	2.1E-01	BF696073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN); 602063129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2991	16167	29183	2.52	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3533	16698	29709	6.1	2.1E-01	AA639482.1	EST_HUMAN	nc690b10.s1 NCI_CGAP_C69 Homo sapiens cDNA clone IMAGE:1195579 3'
3908	17067		6.81	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4125	17279		0.87	2.1E-01	AE001793.1	NT	Thermotoga maritima section 105 of 136 of the complete genome
4165	17315	30310	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4165	17315	30311	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4495	17635		1.63	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4699	17834	30819	1.82	2.1E-01	AB010273.1	NT	Homo sapiens pshep47 gene, complete cds
4757	17892	30871	0.93	2.1E-01	X93181.1	NT	P. italicum mRNA for small GTPase rab11
5138	18261	31228	0.7	2.1E-01	D13587.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
5418	18618	31692	6.31	2.1E-01	BF672693.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
7027	20163	33585	1.05	2.1E-01	AJ223392.1	NT	Drosophila melanogaster 16S rRNA gene, partial
7038	20091	33508	1.8	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7564	20636	34111	0.77	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7564	20636	34112	0.77	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7576	20647		1.89	2.1E-01	AE000872.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7883	20935	34441	1.54	2.1E-01	AF000946.1	NT	Canis familiaris keratin (KR19) gene, complete cds
7930	20980	34488	1.38	2.1E-01	AF069887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7930	20980	34489	1.38	2.1E-01	AF088887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8283	21345		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b3), mRNA
8700	21780	35313	4.78	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
8897	22076	35615	0.81	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614.5
8997	22076	35616	0.81	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614.5
9159	22237		0.5	2.1E-01	AB022524.1	NT	Homo sapiens APC gene, exon 9
9237	22314	35856	6.7	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YEL025w
9704	22763	36323	0.66	2.1E-01	N42538.1	EST_HUMAN	Y11010.1 Sceres melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270954.5
9704	22763	36324	0.66	2.1E-01	N42538.1	EST_HUMAN	Y11010.1 Sceres melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270954.5
9713	22778	36348	2.72	2.1E-01	X67378.1	NT	A. thaliana mRNA for ATRAP-1b protein
9817	22857	36437	1.02	2.1E-01	AB036528.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10335	23570	37178	1.31	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10569	23604	37209	1.97	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE)
10576	23611	37216	0.72	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831.5
11776	24768		1.34	2.1E-01	AI141875.1	EST_HUMAN	q66008.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691751.3
11882	24850		1.68	2.1E-01	11038647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11879	24867	38565	2.6	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA
12688	25459		1.92	2.1E-01	AF217490.1	NT	Homo sapiens fragile T6D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12694	25646		1.39	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916675.5
13158	26793	31928	1.19	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
205	13428	26460	1.92	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
547	13740		1.97	2.0E-01	7705601	NT	Homo sapiens CGL-18 protein (LOC51008), mRNA
717	13899	26837	1.37	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VH2
833	14011	27067	2.09	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1036	14204	27281	1.83	2.0E-01	D90905.1	NT	Synedochystis sp. PC08803 complete genome, 7127, 781449-920815
1149	14313	27369	2.81	2.0E-01	AL163219.2	NT	Homo sapiens chromosome 21 segment HS21C013
1283	14439	27508	1.19	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1336	14483	27663	1.99	2.0E-01	AW384937.1	EST_HUMAN	PV1-HT0422-281289-002-c06 HT0422 Homo sapiens cDNA
1516	14659	27752	22.4	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1582	14734	27816	2.68	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1588	14740	27821	3.48	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1732	14882	27973	0.98	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14904		2.58	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
1796	14945		3.87	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 87 of 150 of the complete genome
1941	15084	28185	1.46	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2423	15552		1.9	2.0E-01	X82877.1	NT	H. sapiens Nar-D-glucose cotransport regulator gene
2855	16132		0.79	2.0E-01	AF074900.1	NT	Homo sapiens full length insert cDNA YH85A11
3576	16741	29758	0.72	2.0E-01	P46607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3658	16821		0.81	2.0E-01	AW238005.1	EST_HUMAN	xp16502x1 NCLCGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3798	16950	29983	0.86	2.0E-01	P34641	SWISSPROT	MER21 repetitive element:
3802	16963		0.8	2.0E-01	6680797	NT	CED-11 PROTEIN
4688	17823		8.71	2.0E-01	BE828165.1	EST_HUMAN	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA
5152	18274	31243	6.41	2.0E-01	8922080	NT	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5243	18959	29963	0.6	2.0E-01	P34641	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5561	18758	31797	2.55	2.0E-01	X66600.1	NT	CED-11 PROTEIN
5559	19049	32355	2.08	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5963	19149	32484	0.82	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6185	19361	32709	5.99	2.0E-01	U15300.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
6303	19476		0.74	2.0E-01	M75987.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6559	19721	33098	47.65	2.0E-01	X61033.1	NT	Human hepatocyte growth factor gene, exon 1
6659	19818	33206	3.74	2.0E-01	AW360865.1	EST_HUMAN	M. auratus mu class glutathione transferase gene
7445	20522	33995	1.41	2.0E-01	AF250371.1	NT	PM1-CT0247-141089-001-g08 CT0247 Homo sapiens cDNA
7603	20673	34147	0.83	2.0E-01	P84422	SWISSPROT	Mus musculus phosphofructokinase-1 C isozyme (PfkC) gene, exons 3 through 7
8139	21221		6.16	2.0E-01	AF028028.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8395	21476	35003	3.12	2.0E-01	X91151.1	NT	Andes Virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8821	22000		0.48	2.0E-01	BE562247.1	EST_HUMAN	M. musculus ecp2 gene, exon 14
9351	22818	36186	1.17	2.0E-01	U82511.1	NT	607344648F1 NIH MGC 8 Homo sapiens cDNA clone IMAGE:3677704 5'
9590	22845	36215	0.62	2.0E-01	U71122.1	NT	Dichostellum discoloratum random slug cDNA19 protein (rsc19) mRNA, partial cds
9756	22694		5.42	2.0E-01	AE001278.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9947	22886	36579	0.52	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
9947	22886	36580	0.52	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10095	23133		2.24	2.0E-01	AF146692.1	NT	DAUGHTERLESS PROTEIN
							Homo sapiens filamin 2 (FLN2) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23282	36878	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10247	23282	36878	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10371	23408	37016	0.87	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10371	23408	37017	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10419	23484		0.8	2.0E-01	X78388.1	NT	D melanogaster DNA mobile element (hoppe)
10616	23650	37269	0.88	2.0E-01	X97121.1	NT	R. norvegicus mRNA for NTR2 receptor
11079	24154	37791	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11079	24154	37792	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11908	24895	38597	1.33	2.0E-01		NT	Chlorella vulgaris chloroplast, complete genome
11908	24895	38598	1.33	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12666	25443		1.24	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12899	25965		1.64	2.0E-01	AF208837.2	NT	Pinephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12912	25876	31851	1.63	2.0E-01	AF302773.1	NT	Homo sapiens nina1-Lm isoform (nina1) mRNA, complete cds
12952	25652	31956	1.63	2.0E-01	AW975287.1	EST_HUMAN	EST1387405 MAGE resequences, MAGN Homo sapiens cDNA
12977	26636		17.48	2.0E-01	AI023592.1	EST_HUMAN	ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643810 3'
113	13344		4.89	1.9E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
362	13573	26604	5.58	1.9E-01	AF004353.1	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
673	13859	26889	1.54	1.9E-01	U32891.2	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
673	13859	26890	1.54	1.9E-01	U32891.2	NT	Homo sapiens lambda/alpha protein kinase C-interacting protein mRNA, complete cds
680	13866	26897	8.31	1.9E-01	BE070801.1	EST_HUMAN	Homo sapiens lambda/alpha protein kinase C-interacting protein mRNA, complete cds
681	13866	26897	6.7	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-001 BT0502 Homo sapiens cDNA
1010	14181		1.72	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (IL2rg), mRNA
1128	14283	27349	5.63	1.9E-01	AA358813.1	EST_HUMAN	EST 67784 Fetal lung II Homo sapiens cDNA 5' end
1401	14555	27629	2.42	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1466	14620		4.34	1.9E-01	AF194823.1	NT	Plasmodium vivax reticulocyte binding protein-2 (bp-2) gene, complete cds
2466	15584	28711	3.66	1.9E-01	U68066.1	NT	Homo sapiens hypodermal protein FLJ10581 (FLJ10581), mRNA
2989	16165	29181	3.81	1.9E-01	J00922.1	NT	Sigmodon hispidus p53 gene, partial cds
3004	16179		7.53	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3482	16650	29666	4.07	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3569	16734	20750	4.94	1.9E-01	R16467.1	EST_HUMAN	Y42F10.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129547 5'
3907	17066	30065	1.09	1.9E-01	AF284017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4100	17255	30256	3.68	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4193	17343	30336	1.51	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4251	17397		1.31	1.9E-01	AE001912.1	NT	Dattococcus radiodurans R1 section 49 of 229 of the complete chromosome 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4346	17489	30471	0.89	1.9E-01	BE834943.1	EST_HUMAN	MRI-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA
4592	17728	30711	0.8	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5124	18250		1.08	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5721	18914		5.19	1.9E-01	AW130149.1	EST_HUMAN	x22a07.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5761	18953	32266	8.03	1.9E-01	AF127827.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5862	19148	32463	1.08	1.9E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
6008	19181		2.45	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6457	19624	32987	1.03	1.9E-01	AU133116.1	EST_HUMAN	w154h02.x1 NCL_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2394099 3'
6518	19683	33054	1.1	1.9E-01	AW148452.1	EST_HUMAN	x14c08.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7112	18538	31495	1.54	1.9E-01	R43212.1	EST_HUMAN	yg09a12.s1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7138	20273	33712	0.74	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7138	20273	33713	0.74	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7409	20487	33957	0.92	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7638	20707	34186	0.78	1.9E-01	U93698.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
7661	20728	34204	1.38	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (10PP8) gene, complete cds
7708	20773	34258	2.84	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
8174	21256	34778	1.83	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8885	21964	35500	13.56	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1188 protein, partial cds
9146	22225	35768	1.5	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9146	22225	35769	1.5	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10079	23117	36719	0.77	1.9E-01	AA912486.1	EST_HUMAN	cl96g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1637508 3' similar to contains Alu repetitive element
10447	23482	37090	0.81	1.9E-01	BE830353.1	EST_HUMAN	RC5-E10082-060700-022-A02 E10082 Homo sapiens cDNA
10447	23482	37091	0.81	1.9E-01	BE830353.1	EST_HUMAN	RC5-E10082-060700-022-A02 E10082 Homo sapiens cDNA
10880	23665	37593	1.38	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10880	23665	37594	1.38	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
10892	24071	37704	2.18	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12025	25009	38711	2.21	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12047	25028	38735	1.48	1.9E-01	LD7344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
32	13270	26274	1.85	1.8E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds
270	18009	28519	1.47	1.8E-01	AB022090.1	NT	Mus musculus Ccig gene for chaperonin containing TCP-1 gamma subunit, partial cds
381	13589	28625	1.9	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
765	13646	28693	0.78	1.8E-01	AB021480.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1008	14176	27235	1.8	1.8E-01	AI912212.1	EST_HUMAN	wc71f02.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1115	14279	27335	2.14	1.8E-01	AF000580.1	NT	Dicotyledon discoidium plasmid Ddp5, complete genome
1317	14473	27540	0.87	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1533	14686	27765	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1533	14686	27766	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1915	15058		1.91	1.8E-01	AI733708.1	EST_HUMAN	gg22d10.x5 NC1_CGAP_K183 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075936 075936
1965	15108	28208	2.28	1.8E-01	AB051897.1	NT	GAMMA BUTYROBETAINE HYDROXYLASE ;
2756	15873		3.34	1.8E-01	AW935726.1	EST_HUMAN	Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2963	16140		2.3	1.8E-01	AF184589.1	NT	QV3-DT0018-081299-036-p04 DT0018 Homo sapiens cDNA
2968	16144	29163	1.10	1.8E-01	AW182300.1	EST_HUMAN	Jonopodium acule LEAFY protein (LEAFY2) gene, partial cds
3194	16369	28375	1.61	1.8E-01	AW995178.1	EST_HUMAN	x41a03.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2689756 3'
3452	16819	28638	0.77	1.8E-01	BF183582.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3712	16873	28877	0.87	1.8E-01	H03389.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3712	16873	28878	0.87	1.8E-01	H03389.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4483	17593		0.92	1.8E-01	D37954.1	NT	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4678	17813	30801	5.61	1.8E-01	AL161556.2	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4895	18025	31011	2.68	1.8E-01	AB051897.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
5129	18254	31219	0.65	1.8E-01	X79794.1	NT	Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5158	18280	31245	1.79	1.8E-01	AW814270.1	EST_HUMAN	N. tabacum mRNA pNLA-35
5206	18327	31297	2.55	1.8E-01	AF181268.1	NT	MR3-ST0203-151289-112-g08 ST0203 Homo sapiens cDNA
5218	18340	31313	0.89	1.8E-01	AI439981.1	EST_HUMAN	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5291	18409	31370	1.2	1.8E-01	Y08310.1	NT	t57e04.x1 NC1_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5413	18615	31589	0.81	1.8E-01	BE082628.1	EST_HUMAN	RC8-BT0841-300300-011-H03 BT0841 Homo sapiens cDNA
5829	18115	32420	1.19	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6047	19230	32554	0.95	1.8E-01	N28828.1	EST_HUMAN	yc38f08.r1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:284063 5'
6256	19430	32778	0.89	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 8 (Trif8), mRNA
6256	19430	32777	0.89	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6641	19800	33189	1.16	1.8E-01	Q9QY14	SWISSPROT	FORHEAD BOX PROTEIN E3
6688	19846		2.12	1.8E-01	N94853.1	EST_HUMAN	ly62h02.r1 Soares multiple sclerosis 2Nbl-HMSP Homo sapiens cDNA clone IMAGE:278163 5'
7148	20281	33722	1.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wvus, complete cds
7148	20281	33723	1.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wvus, complete cds
7202	20067	33477	0.87	1.8E-01	BE981353.1	EST_HUMAN	601648361R2 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:3932247 3'
7604	20674	34148	0.81	1.8E-01	AF001611.1	NT	Bacillus halodurans genomic DNA, section 5/14
8810	21888	35431	0.58	1.8E-01	AW96618.1	EST_HUMAN	EST378181 MAGE resequencing, MAG1 Homo sapiens cDNA
9543	22608	36176	1.58	1.8E-01	M73288.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9574	22718	36284	1.52	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9692	22741		0.6	1.8E-01	AA463751.1	EST_HUMAN	rh02a05.e1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1
9774	22814	36392	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9774	22814	36393	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9814	22854	36432	1.02	1.8E-01	M28019.1	NT	S.commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9814	22854	36433	1.02	1.8E-01	M28019.1	NT	S.commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9881	23020	36613	0.81	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9986	23026	36617	0.71	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10337	23372		0.67	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10578	23613	37218	1.48	1.8E-01	X63440.1	NT	M.musculus mRNA for P10-protein tyrosine phosphatase
10785	23818	37441	1.21	1.8E-01	AB011171.1	NT	Homo sapiens mRNA for KIAA0599 protein, partial cds
10873	23958	37588	2.02	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10917	24000	37633	5	1.8E-01	U36908.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
10974	20281	33722	3.05	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wvus, complete cds
10974	20281	33723	3.05	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wvus, complete cds
10975	24054	37688	4.41	1.8E-01	AF019107.1	NT	Dityostelium discoideum unknown (DG1041) gene, complete cds
11270	24338	37976	2.06	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11551	24506	38284	1.41	1.8E-01	AW275728.1	EST_HUMAN	xp40ht0.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742983 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11750	23936	37563	8.94	1.8E-01	X57033.1	NT	B. laurus mRNA for potassium channel
12061	25042	38751	3.48	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
12124	25104	38808	1.77	1.8E-01	AJ095094.1	EST_HUMAN	cp2798 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12239	25183		1.79	1.8E-01	10086661	NT	Bovine ephemeral fever virus, complete genome
12306	25224	32103	1.28	1.8E-01	BF346623.1	EST_HUMAN	60201928F1 NCL CGAP Bm87 Homo sapiens cDNA clone IMAGE:4156318 5'
12719	14473	27540	1.18	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12811	25541		3.28	1.8E-01	Q96882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETTI PROTEIN) (PTP PROTEIN)
12942	25620		20.8	1.8E-01	R24494.1	EST_HUMAN	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12988	25643		4.98	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hbk1)
13035	28134	31548	1.7	1.8E-01	9506952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcohe), mRNA
591	13782	26801	6.4	1.7E-01	BE385184.1	EST_HUMAN	601274804F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3915768 5'
828	14006	27063	3.16	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
983	14156		1.78	1.7E-01	P36616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1083	14249	27305	0.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolyhedrovirus, complete genome
1083	14249	27305	0.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolyhedrovirus, complete genome
1880	15006	28113	2.44	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosomes 4, contig fragment No. 69
2038	15179		3.23	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2922	16100	29112	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hepR) gene, complete cds, and YRAL VIBCO gene, partial cds
2922	16100	29113	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hepR) gene, complete cds, and YRAL VIBCO gene, partial cds
2983	16169	29188	1.47	1.7E-01	AA336909.1	EST_HUMAN	EST141651 Endometrial tumor Homo sapiens cDNA 5' end
3061	16237	29257	1.09	1.7E-01	AJ238736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3061	16237	29258	1.09	1.7E-01	AJ238736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3174	16349	29365	1.65	1.7E-01	AF061514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3451	16618	29637	0.81	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3534	16693	29710	1.52	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4049	17203	30215	6.06	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/IRX gene fused to intron 5 of the AF-4/FEL gene
4881	17815		2.49	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4884	18014	30998	0.59	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4861	18090	31066	1.31	1.7E-01	A1247635.1	EST_HUMAN	qf67609.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element;
5231	18363		1.07	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5272	18391	31359	0.72	1.7E-01	BF030010.1	EST_HUMAN	601587268F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827187 5'
5312	18429	31399	0.91	1.7E-01	D37851.1	NT	Rattus norvegicus mRNA for MBP1 (C-myc intron binding protein 1), complete cds
5524	18721	31737	1.88	1.7E-01	AA470686.1	EST_HUMAN	net13a02.s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:981066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5524	18721	31738	1.88	1.7E-01	AA470686.1	EST_HUMAN	net13a02.s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:981066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5710	18603	32198	0.92	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6459	19626	32988	12.64	1.7E-01	H72118.1	EST_HUMAN	ys02g06.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:213658 3'
6517	19682	33052	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6517	19682	33053	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6992	18511	31503	0.75	1.7E-01	BE300286.1	EST_HUMAN	600944087T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
7019	20155		1.94	1.7E-01	AF026562.3	NT	Mesocricetus auratus oviductin precursor (Ovi) gene, complete cds
7140	20275		0.69	1.7E-01	Z82810.1	NT	Homo sapiens HFE gene
7369	20448	33911	1.38	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7448	20625	33998	8.51	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7649	20718	34195	1.21	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7668	25850	34208	0.64	1.7E-01	Q01855	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
8045	21128	34648	1.26	1.7E-01	AF000679.1	NT	Homo sapiens homodentate 1,2-dioxygenase gene, complete cds
8150	21232	34752	0.75	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadC) gene, complete cds
8472	21593	35083	7.36	1.7E-01		NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8472	21593	35084	7.36	1.7E-01		NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8896	21974	35511	0.5	1.7E-01	AW962873.1	EST_HUMAN	RC2.BN0032-120200-01-a10 BN0032 Homo sapiens cDNA
8925	22004	35543	1.93	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9045	22124	35666	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9045	22124	35667	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9198	22276	35814	0.51	1.7E-01	R77002.1	EST_HUMAN	y68g02.11 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:144242 5'
9369	22444	36005	0.53	1.7E-01	BE253142.1	EST_HUMAN	601118672F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184 5'
9369	22444	36006	0.53	1.7E-01	BE253142.1	EST_HUMAN	601118672F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184 5'
9789	22829	36407	9.03	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9899	22939	36524	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9899	22939	36525	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9916	22553	36543	2.08	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9922	23031	36621	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9932	23031	36622	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10013	23051	36645	0.93	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-9), (sp8 gene)
10438	23473		2.77	1.7E-01	AL163284.2	NT	Human sapiens chromosome 21 segment HS21C084
10805	23639	37247	1.56	1.7E-01	11427203	NT	Human sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10807	23641	37249	1.66	1.7E-01	AA627972.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
10919	24002	37636	9.54	1.7E-01	BE390835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613256 5'
11046	24122	37766	2.12	1.7E-01	AA814617.1	EST_HUMAN	643a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1428924 3'
11373	24434	38090	6.81	1.7E-01	7108300	NT	Mus musculus adenomatous polyposis coli binding protein Eb1 (Eb1), mRNA
11373	24434	38091	6.81	1.7E-01	7108300	NT	Mus musculus adenomatous polyposis coli binding protein Eb1 (Eb1), mRNA
11657	24736	38427	1.71	1.7E-01	AA863375.1	EST_HUMAN	645f09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480297 3'
12011	24996		1.5	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12042	25023	38727	1.67	1.7E-01	P56869	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12042	25023	38728	1.67	1.7E-01	P56869	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12142	25117	38825	2	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
12275	26087		1.45	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12567	25920		1.18	1.7E-01	AI824404.1	EST_HUMAN	6d8g05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:U73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12907	25800	31972	7.24	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
128	13356	26388	1.7	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
697	15985	26913	1.16	1.6E-01	R31497.1	EST_HUMAN	Y75F2.T Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1561	14703	27783	4.25	1.6E-01	AF288117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1910	15053		1.27	1.6E-01	AJ235272.1	NT	Rickettsia prowazekii strain Macfarlane, complete genome, segment 3/4
1977	15120	28221	2.14	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2041	15182		1.43	1.6E-01	U10334.1	NT	Grasshopper glabra RNA polymerase II largest subunit mRNA, partial cds
2457	16063	28712	1.09	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2562	16887	28813	2.73	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2857	16134	28149	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2967	16134	28150	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3723	16884	29889	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3723	16884	29890	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3872	17031	30030	0.82	1.6E-01	AE000962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4107	17261		2.8	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome
4144	17266	30288		1.6E-01	AF084496.1	NT	Cribidia fasciculata trypanothione (bnt) gene, complete cds
4448	17588	30569	10.91	1.6E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4578	17715		2.49	1.6E-01	AF196801.1	EST_HUMAN	EST380677 IMAGE sequences, MAGJ Homo sapiens cDNA
4586	17723		4.39	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5060	18188	31162	1.39	1.6E-01	AA088343.1	EST_HUMAN	ZB4H09.s1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:571361 3' similar to TR:E221955
5083	18211	31183	1.8	1.6E-01	AJ006396.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV ;
5083	18211	31184	1.8	1.6E-01	AJ006396.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5345	18459		0.93	1.6E-01	AF045283.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5503	18702	31719	0.81	1.6E-01	L40608.1	NT	Gallus gallus smooth muscle/non-muscle myosin light chain kinase gene, exon 29
							Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5639	18833	31909	2.9	1.6E-01	AW197496.1	EST_HUMAN	XM43701.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:075984 075984
							HYPOTHETICAL 127 6 KD PROTEIN ;
5639	18833	31910	2.9	1.6E-01	AW197496.1	EST_HUMAN	XM43701.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:075984 075984
5651	18845	32126	1.99	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127 6 KD PROTEIN ;
6162	19328	32674	0.73	1.6E-01	BE925803.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebp) gene, complete cds
6558	19720	33096	2.06	1.6E-01	AL101588.2	NT	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6558	19720	33097	2.06	1.6E-01	AL101588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6839	20252	33688	0.79	1.6E-01	AB046786.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6885	20213		0.66	1.6E-01	BF089630.1	EST_HUMAN	Homo sapiens mRNA for KIAA1566 protein, partial cds
7103	18530	31485	4.15	1.6E-01	AW291215.1	EST_HUMAN	602139855F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301004 5'
7451	20528	34001	0.71	1.6E-01	Z49632.1	NT	UI-H-B12-agi-b-06-0-J1.s1 NCL CGAP Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7855	21005	34516	1.63	1.6E-01	AW246369.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR132W
7982	21031	34544	0.84	1.6E-01	6753237	NT	ZB22248 6p/prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822248 5'
7986	21035		1.03	1.6E-01	AU136525.1	EST_HUMAN	Mus musculus Cc-2?>-dependent activator protein for secretion (Cadps), mRNA
8063	21136	34657	1.62	1.6E-01	L48349.1	NT	2822248 6p/prime NIH_MGC 7 Homo sapiens cDNA clone PLACE1004466 5'
8215	21297		0.53	1.6E-01	BE244087.1	EST_HUMAN	Gorilla gorilla androgen receptor gene, partial exon
8310	21392	34916	0.77	1.6E-01	U38243.1	NT	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
							Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mbaA) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8833	21912	35450	1.08	1.8E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2987771 to 3213410
9028	22105	35646	0.77	1.0E-01	R13673.1	EST_HUMAN	yf80h08.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
9133	22212		0.74	1.0E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9171	22249	35792	1.85	1.0E-01	Z49501.1	NT	S cerevisiae chromosome X reading frame ORF YJR001w
9311	22387		0.76	1.0E-01	AF11167.2	NT	Homo sapiens Jan dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9851	22891		1.77	1.0E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-H01 ST0200 Homo sapiens cDNA
9864	22894	36476	1.89	1.0E-01	Z49501.1	NT	S cerevisiae chromosome X reading frame ORF YJR001w
9891	22931		1.16	1.0E-01	BE15564.1	EST_HUMAN	PM2-HT0353-270100-004-H11 HT0353 Homo sapiens cDNA
10826	23859	37482	0.5	1.0E-01	11128016	NT	Homo sapiens nuclear autoantigen (GS2NA), mRNA
10893	23977	37609	2.34	1.0E-01	AW650853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11244	24313	37861	1.34	1.0E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11244	24313	37852	1.34	1.0E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11249	24318	37988	1.62	1.0E-01	BE259849.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11377	24438		3.6	1.0E-01	AF108064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11697	24694	38388	7.53	1.0E-01	6971552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12277	25207	38363	3.89	1.0E-01	AV710585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12697	25402	32043	2	1.0E-01	L14883.1	NT	Rat convertase PCS mRNA, 5' end
12630	25423		1.38	1.0E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-H01_1 LT0074 Homo sapiens cDNA
12733	25893		11.64	1.0E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurine synthase, complete cds
12933	25815		2.71	1.0E-01	AK024466.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
13029	25878		5.04	1.0E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qlu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13054	25880	31964	1.89	1.0E-01	9506522	NT	Rattus norvegicus chondroin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
13080	25894		1.4	1.0E-01	BE267894.1	EST_HUMAN	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'
13189	25782		1.29	1.0E-01	BF672698.1	EST_HUMAN	602192004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283145 5'
258	13477	26508	1.7	1.0E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E08 HT0619 Homo sapiens cDNA
258	13477	26509	1.7	1.0E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E08 HT0619 Homo sapiens cDNA
600	19884		2.5	1.0E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH08 5'
805	13985	27037	1.38	1.0E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21Q084
1116	14281	27337	1.44	1.0E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGS22 myosin heavy chain, 3'UTR
1121	14286	27341	2.7	1.0E-01	AJ281886.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1137	14302		1.85	1.0E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1243	14402	27463	2.37	1.0E-01	AW195516.1	EST_HUMAN	nt38d111.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:266085 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1304	14480	27526	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1304	14480	27527	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1304	14480	27527	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1511	14684	27749	1.38	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1557	16100	28200	0.98	1.5E-01	AW444451.1	EST_HUMAN	UI-H4B13-ekb-b-09-0-UI.st NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733541 3'
2880	18156		0.9	1.5E-01	AW572516.1	EST_HUMAN	wt55a02.x2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_ma1
3100	18276	29290	0.91	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3118	16294	29308	0.62	1.5E-01	O78887	SWISSPROT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3433	16601	28620	5.78	1.5E-01	AA835049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3454	16621	28641	0.73	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3454	16621	28642	0.73	1.5E-01	Z23104.1	NT	L. stagnalis miRNA for G protein-coupled receptor
3851	17011	30011	2.35	1.5E-01	U09984.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3887	17026	30025	0.83	1.5E-01	7108358	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3881	17040	30037	0.77	1.5E-01	M07882.1	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3970	17128	30131	2.45	1.5E-01	AW695983.1	EST_HUMAN	XYNA, Thermotoga bacterium; xyna; 4182 base-pairs
3987	17144	30149	0.68	1.5E-01	AJ003165.1	NT	h1000x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
3987	17144	30150	0.68	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4161	17312	30308	1.16	1.5E-01	AW366659.1	EST_HUMAN	Populus trichocarpa cv. Trichobal ABI3 gene
4210	17359	30348	0.67	1.5E-01	Z12628.1	NT	RC24HT0149-10T099-012-c09 HT0149 Homo sapiens cDNA
4288	17442	30428	9.85	1.5E-01	AL163284.2	NT	B. napus mitochondrion DNA for ORF158
4847	17880	30969	1.54	1.5E-01	BF687655.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4874	16891	29002	2.33	1.5E-01	BF696381.1	EST_HUMAN	602087192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086223 5'
5114	18242	31207	1.5	1.5E-01	AL161550.2	NT	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247637 5'
5370	18573	31441	1.91	1.5E-01	P07995	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5398	18601	31571	1.33	1.5E-01	AF256652.1	NT	THROMBOSPONDIN 1 PRECURSOR
5443	18643		5.95	1.5E-01	P15195	SWISSPROT	Calinin crocodilus MHC class II beta chain (hclibeta) gene, complete cds
5655	18649	32131	4.8	1.5E-01	AW850764.1	EST_HUMAN	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5687	18891	32182	6.66	1.5E-01	U66016.1	NT	IL3-C10219-160200-064-F10 C10219 Homo sapiens cDNA
5697	18891	32183	6.68	1.5E-01	U66016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
6029	19212	32532	0.82	1.5E-01	4509810	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
							Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN9A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6128	18307	32647	1.71	1.5E-01	6763659	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6128	18307	32648	1.71	1.5E-01	6763659	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6188	19344	32690	2.19	1.5E-01	AJ276506.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6324	19496	32852	3.49	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6376	19545		1.08	1.5E-01	4506398	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6474	19641	33002	1.74	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6631	25828	33179	3.68	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6661	19820	33207	4.73	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6672	19831	33220	1.51	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6719	19876	33267	2.35	1.5E-01	Q28492	SWISSPROT	AMELOGENIN
6823	19976	33383	0.86	1.5E-01	AA714760.1	EST_HUMAN	nv30610.s1 NCI_CGAP GC80 Homo sapiens cDNA clone IMAGE:1241671 3'
6862	20005	33414	2.24	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7118	18544	31600	6	1.5E-01	AW970295.1	EST_HUMAN	EST382376 IMAGE resequences, MAGK Homo sapiens cDNA
7158	25840		0.8	1.5E-01	AA811545.1	EST_HUMAN	ob73102.s1 NCI_CGAP GC81 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element
7365	20444		4.73	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7550	20622	34099	1.63	1.5E-01	AI973157.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2491310 3'
7764	20823	34314	0.88	1.5E-01	AF269073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7764	20823	34315	0.88	1.5E-01	AF269073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7775	20832	34322	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-d-05-Q-UJ11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7778	20832	34323	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-d-05-Q-UJ11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7919	20970	34477	0.79	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of <i>lasi1-1</i> (SOL3) gene, complete cds
8248	21330	34846	0.99	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8414	21486	35026	1.1	1.5E-01	AA970317.1	EST_HUMAN	o885g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8507	21568		1.06	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN)
8594	21675		14.14	1.5E-01	C16600.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8628	21708	35245	1.87	1.5E-01	U27535.1	NT	C16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-528H09 5'
8783	21872	35411	2.17	1.5E-01	D84476.1	NT	Pangasinanod gigas growth hormone (GH) mRNA, complete cds
8814	21893		0.79	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9038	22117	35860	3.12	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
							Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9306	2281	35932	2.56	1.5E-01	N74226.1	EST_HUMAN	z59a08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:298868 3' similar to
9394	22499	36033	1.34	1.5E-01	BF585485.1	EST_HUMAN	PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9401	23475		2.52	1.5E-01	AV754819.1	EST_HUMAN	GVO000404 Human Pootasis Differential Display Homo sapiens cDNA
9605	22660		0.84	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9852	21095	34609	6.7	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP300080 5'
							Acipenser transmontanus vitellogenin mRNA, partial cds
10022	23060	36866	0.71	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 6-delta - 4-delta isomerase gene, complete cds
10125	23163	36781	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10125	23163	36782	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10407	23442	37049	2.59	1.5E-01	X98852.1	NT	P. lentusculus mRNA for integrin beta subunit
10495	23530		0.51	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
							wk53h12.x1 NCI CGAP P122 Homo sapiens cDNA clone IMAGE:2419176 3' similar to gb:M27508 BETA
10516	23551	37161	2.36	1.5E-01	AI814048.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
							wk53h12.x1 NCI CGAP P122 Homo sapiens cDNA clone IMAGE:2419176 3' similar to gb:M27508 BETA
10516	23551	37162	2.36	1.5E-01	AI814048.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10568	23633	37242	1.22	1.5E-01	U40632.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds.
10761	23784	37413	1.69	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10761	23784	37414	1.69	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10835	24017	37849	1.87	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10835	24017	37850	1.67	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
11063	24139	37773	4.46	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11063	24139	37774	4.46	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11331	24394	38042	1.38	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-028-D04 CN0024 Homo sapiens cDNA
11925	24911		1.34	1.5E-01	AI193704.1	EST_HUMAN	qe72e01.x1 Soares fetal lung Nbl-HL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to
12232	26953		38.98	1.5E-01	BF700582.1	EST_HUMAN	gb:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12629	26422		1.84	1.5E-01	AF030359.2	NT	602128753FT NIH MGC 56 Homo sapiens cDNA clone IMAGE:4285949 5'
12633	25426		1.23	1.5E-01	AJ238332.1	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12696	25976		6.64	1.5E-01	R83077.1	NT	Mus musculus mRNA for death inducer-obliator-1 (Dio-1)
12749	25498		1.52	1.5E-01	AP001514.1	EST_HUMAN	yp87e04.x1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:164430 5'
12778	26520	32002	1.41	1.5E-01	9695413	NT	Bacillus halodurans genomic DNA, section 8/14
12807	26000		2.59	1.5E-01	AV741272.1	EST_HUMAN	Lymphocystis disease virus 1, complete genome
12932	25896	31657	7.68	1.5E-01	AL139074.2	NT	AV741272 CB Homo sapiens cDNA clone CBDA3D04 5'
							Campylobacter jejuni NCTC11168 complete genome; segment 1/8

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13163	25769	31022	6.61	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium bicarbonate symporter
13227	28138		2.26	1.5E-01	8631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
310	13526		1.23	1.4E-01	AF008603.1	NT	Homo sapiens T cell receptor beta locus, TCRBV856P to TCRBV21S2A2 region
633	14708		3.24	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1288	14444		2.69	1.4E-01	T91864.1	EST_HUMAN	yb54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1787	14936		1.46	1.4E-01	6678960	NT	Mus musculus growth differentiation factor 5 (Griff), mRNA
1780	14939	28032	1.84	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1864	15097		1.27	1.4E-01	AW135741.1	EST_HUMAN	U1H-B11-ect-e-08-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
2042	15183		14.84	1.4E-01	AA720615.1	EST_HUMAN	ly72807.s1 NCL_CGAP_GOB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2544	16689	28793	1.02	1.4E-01	P30706	SWISSPROT	GLYCEOL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2653	15987	28077	3.34	1.4E-01	A1933406.1	EST_HUMAN	wm74607.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
4289	17434	30421	9.45	1.4E-01	A1989094.1	EST_HUMAN	b66602.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4289	17434	30422	9.45	1.4E-01	A1989094.1	EST_HUMAN	b66602.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4352	17465	30476	4.28	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4631	17869		0.7	1.4E-01	AA776287.1	EST_HUMAN	z60b07.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb-X01057_mna1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element
4798	17933	30920	0.79	1.4E-01	5453861	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (durae) (Drosophila)-homolog phosphodiesterase E2 (PDE4A), mRNA
5322	18436	31406	0.62	1.4E-01	AJ005180.1	NT	Lycopodium obscurum genome RAPD band 28
5421	18622	31598	5.21	1.4E-01	T90877.1	EST_HUMAN	yef1c11.s1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:117812 3'
5444	18644	31821	4.33	1.4E-01	AB004568.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5444	18844	31822	4.33	1.4E-01	AB004568.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6427	19565	32981	3.17	1.4E-01	BES26891.1	EST_HUMAN	hr67c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135338 3'
6611	19771	33161	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000789 5'
6611	19771	33162	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000789 5'
6701	19859	33249	3.7	1.4E-01	AW082796.1	EST_HUMAN	z671d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2681761 3'
6716	19873		1.51	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6739	19895	33286	2.48	1.4E-01	BF378533.1	EST_HUMAN	QY1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
7276	20359		0.71	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910.t1761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A0910 5'
7545	20617		1.78	1.4E-01	AW016373.1	EST_HUMAN	w024f12.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2710289 3'
7618	20688		0.73	1.4E-01	AJ762827.1	EST_HUMAN	P49882 CASPASE-4 PRECURSOR ; similar to SW:ICE4_HUMAN

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7621	20691	34187	0.63	1.4E-01	T53770.1	EST_HUMAN	yea0111.2 Stragene placenta (#637225) Homo sapiens cDNA clone IMAGE:68973 5' similar to contains
7789	20855	34345	0.95	1.4E-01	U85845.1	NT	Alu repetitive element
7932	20892	34490	1.02	1.4E-01	A1305192.1	EST_HUMAN	Oryctolagus cuniculus fructose 1,6_bisphosphate aldolase (AldB) gene, complete cds
8162	21244		0.54	1.4E-01	BF310258.1	EST_HUMAN	q19b12.x1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8970	21750		1.32	1.4E-01	AV659047.1	EST_HUMAN	601894760FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124199 5'
8984	22063		0.6	1.4E-01	A1436083.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
9114	22193	35738	4.04	1.4E-01	AA307073.1	EST_HUMAN	ln92b12.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to
9194	22272	35810	0.76	1.4E-01	AW023836.1	EST_HUMAN	TR:002710 002710 GAG POLYPROTEIN ;
9322	22398	35951	1.07	1.4E-01	R62746.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9322	22398	35952	1.07	1.4E-01	R62746.1	EST_HUMAN	d158b03.y1 Morton_Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9388	22463	36027	8.52	1.4E-01	BF310958.1	EST_HUMAN	y110h05.r1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9476	22532	36096	1.72	1.4E-01	W93411.1	EST_HUMAN	y110h05.r1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9547	22612	36180	0.54	1.4E-01	X73293.1	NT	60189465FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9547	22612	36181	0.54	1.4E-01	X73293.1	NT	z194804.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains
9558	22623	36104	1.65	1.4E-01	Y10196.1	NT	element KER repetitive element:
9558	22623	36105	1.65	1.4E-01	Y10196.1	NT	M.vannelli genes rpoH, rpoB and rpoA
9848	21092	34007	1.81	1.4E-01	AF121361.1	NT	M.vannelli genes rpoH, rpoB and rpoA
10009	23047	36641	0.54	1.4E-01	X66092.1	NT	Homo sapiens PHEX gene
10182	23229	36821	0.89	1.4E-01	AF023813.1	NT	Homo sapiens PHEX gene
10283	23328	36831	0.81	1.4E-01	AW021908.1	EST_HUMAN	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase la1 (IAL), and
10293	23328	36832	0.81	1.4E-01	AW021908.1	EST_HUMAN	zinc finger protein (DNZ1) genes, complete cds
10463	23498	37109	0.78	1.4E-01	BF375285.1	EST_HUMAN	C.porfingens ORF for putative membrane transport protein
10463	23498	37110	0.76	1.4E-01	BF375285.1	EST_HUMAN	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein,
10680	23714		0.51	1.4E-01	T84293.1	EST_HUMAN	partial cds
10825	23858	37481	0.7	1.4E-01	Z89117.1	NT	d129h08.y1 Morton_Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10948	24030		1.32	1.4E-01	AA811480.1	EST_HUMAN	d129h08.y1 Morton_Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
11081	24156	37793	2.67	1.4E-01	R53400.1	EST_HUMAN	MP3-ST0218-211299-013-e08 ST0218 Homo sapiens cDNA
11282	24348	37985	1.69	1.4E-01	AW104982.1	EST_HUMAN	MP3-ST0218-211299-013-e08 ST0218 Homo sapiens cDNA
11354	24416	38071	1.58	1.4E-01	T66102.1	EST_HUMAN	MP3-ST0218-211299-013-e08 ST0218 Homo sapiens cDNA
							y47d03.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:111366 5'
							Bacillus subtilis complete genome (section 14 of 21): from 2669461 to 2812870
							ca89a03.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1320364 3'
							y170c05.r1 Soares_breast_2Nb1Bst Homo sapiens cDNA clone IMAGE:154088 5'
							xd73e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'
							y47g10.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120930 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11364	24416	38072	1.58	1.4E-01	T98102.1	EST_HUMAN	yea7g10.17 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'
11358	24418	38075	2.36	1.4E-01	P08848	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11572	24627	38308	1.85	1.4E-01	X68092.1	NT	G perfringens ORF for putative membrane transport protein
11613	20817		1.57	1.4E-01	AW016373.1	EST_HUMAN	UHR-B10-aat-c-08-Q-UJ.st1 NC1_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11757	23943	37570	2.07	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11816	24805		1.51	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
12038	25020	38724	10.18	1.4E-01	AF148793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H6AR (H5ar) gene, complete cds
12560	25382	32038	4.58	1.4E-01	X74773.1	NT	P.salina plasmid gene sacY
12574	25380		3.28	1.4E-01	11888117	NT	Rattus norvegicus deamin (Dea), mRNA
12605	25405		1.71	1.4E-01	BE984935.2	EST_HUMAN	9C1658490R1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3885671 3'
12827	26175		2.83	1.4E-01	BE513802.1	EST_HUMAN	9C1315538F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3634329 5'
12724	25482		7.52	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140W homolog, and glycamide ribonucleotide transferase (GART) genes, complete cds
12742	25483		4.02	1.4E-01	D64004.1	NT	Synchoecysis sp. PCQ8803 complete genome, 23/27 2888767-3002965
12834	25193		3.2	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12928	25612		1.45	1.4E-01	X69192.1	NT	V.plantifolia mRNA for methyltransferase
13084	25977		3.36	1.4E-01	D82883.1	NT	Mus musculus mRNA for prolidase, complete cds
13178	25785		1.68	1.4E-01	AW377898.1	EST_HUMAN	MRO-HT0208-221298-204-c08 H.T0208 Homo sapiens cDNA
332	13548	26576	2.27	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
332	13548	26577	2.27	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
542	13735	26759	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
653	13839	26868	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
653	13839	26867	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
887	14043	27108	1.55	1.3E-01	X53330.1	NT	P.clumerii histone gene cluster for core histones H2A, H2B, H3 and H4
917	14092	27157	1.28	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1052	14218	27274	2.14	1.3E-01	AL117078.1	NT	Bohris cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1151	14315		2.04	1.3E-01	AL115265.1	NT	Bohris cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1242	14401	27482	1.67	1.3E-01	AV712487.1	EST_HUMAN	AV712487 DCA Homo sapiens cDNA clone DCAAFF05 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1475	14628		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1905	15048	28159	1.02	1.3E-01	0680957	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
2014	15164	28259	2.73	1.3E-01	AL117078.1	NT	Bovine chitron strain T4 cDNA library under conditions of nitrogen deprivation
2239	15372		1.09	1.3E-01	AJ243578.1	NT	Rhodopsin pseudomonas acidophilus pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2384	15495		1.39	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2455	15583		3.31	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2653	15776	28899	2.78	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3440	16608	29626	1.21	1.3E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
3539	16704	29715	1.11	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3616	16976	29979	0.85	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3816	16976	29990	0.85	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3822	16982	29985	1.55	1.3E-01	AB032169.1	NT	Homo sapiens DD4 gene for dihydrolipoyl transacylase 4 (AKR 1C4), exon 2
3905	17084	30063	0.86	1.3E-01	6976840	NT	Rattus norvegicus Fibronectin, gamma polypeptide (F99), mRNA
4096	17251		1.08	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4162	18839	28856	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4162	18839	28867	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4257	17402		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4274	17419		3.74	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081289-036-e03 DT0018 Homo sapiens cDNA
4281	17426	30415	1.82	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4302	17445	30431	21.62	1.3E-01	AW273741.1	EST_HUMAN	XI231D.X1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4434	17574		1.19	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4601	17738	30717	0.61	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4656	17792	30776	2.64	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
4748	17883	30865	0.73	1.3E-01	BF878654.1	EST_HUMAN	602164306F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'
5314	18431	31401	0.78	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 99-4001-1168000 nt. position (5/7)
5440	18640	31619	1.01	1.3E-01	AW466988.1	EST_HUMAN	ha07606.x1 NCI_CGAP_K1212 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1 L1 repetitive element
5478	18677	31690	1.83	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-c08 UM0093 Homo sapiens cDNA
5618	18812		0.92	1.3E-01	AF107763.1	NT	Emmericella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5702	18895		0.87	1.3E-01	AF056860.1	NT	Hepatitis C virus 88_CL10 genome polyprotein gene, partial cds
5842	18032	32338	0.72	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6107	19287	32821	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6107	19287	32622	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6612	19772	33163	18.92	1.3E-01	AB031328.1	NT	Schistosoma japonicum gene for Alp41, complete cds
6698	19856	33246	2.28	1.3E-01	X88891.1	NT	C. jacchus intron 4 of visual pigment gene (red allele)
6927	20242		0.74	1.3E-01	W26367.1	EST_HUMAN	2833 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6974	20202	33628	0.7	1.3E-01	BE782926.1	EST_HUMAN	601468557F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866079 5'
6974	20202	33628	0.7	1.3E-01	BE782926.1	EST_HUMAN	601468557F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866079 5'
7155	20289		0.74	1.3E-01	BF528960.1	EST_HUMAN	602044348F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7412	20490		1.97	1.3E-01	H48864.1	EST_HUMAN	Y33302.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
8148	21228		0.79	1.3E-01	BE272939.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990053 5'
8160	21242	34762	1.68	1.3E-01	11423294	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
8182	21274	34797	1.32	1.3E-01	BF680522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298074 3'
8489	21650	35060	0.66	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8540	21621		4.24	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL054c
8580	21681		4.96	1.3E-01	6923918	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8725	21805	35342	1.26	1.3E-01	BF590522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298074 3'
9149	22227	35770	0.57	1.3E-01	R11172.1	EST_HUMAN	Y33911.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP-RL2B RAT P29316 80S RIBOSOMAL PROTEIN ;
9149	22227	35771	0.57	1.3E-01	R11172.1	EST_HUMAN	Y33911.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP-RL2B RAT P29316 80S RIBOSOMAL PROTEIN ;
9420	22494	36060	0.69	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9420	22494	36061	0.69	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9672	22634	36204	4.19	1.3E-01	AF023126.1	NT	Oryzobolus cuniculatus H+K+ATPase alpha 2c subunit mRNA, complete cds
9973	23012		0.73	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10287	23292		1.07	1.3E-01	8353940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
10355	23370	36880	0.95	1.3E-01	AW851699.1	EST_HUMAN	MR2-CT0222-201069-001-001 CT0222 Homo sapiens cDNA
10603	23664	37244	1.08	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10743	23776	37389	0.65	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10797	23830	37464	0.46	1.3E-01	AW247638.1	EST_HUMAN	2820637.3 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
10868	23963		2.31	1.3E-01	BF330999.1	EST_HUMAN	MR4-ET0558-130700-010-108 ET03568 Homo sapiens cDNA
11455	24515		1.34	1.3E-01	BF092708.1	EST_HUMAN	MR4-TN0112-120600-102-008 TN0112 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11529	24585	-	3.2	1.3E-01	6571745	NT	Mus myosin heavy chain 2, muscle (C12), mRNA
11618	24657	38354	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11618	24657	38355	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11895	24883	38581	7.98	1.3E-01	BE279449.1	EST_HUMAN	601188052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12000	24895	-	1.41	1.3E-01	AF012886.1	NT	Thermococcus litoralis trehalase/maltose transporter operon including trehalase/maltose binding protein (malE) and inner membrane proteins MalF (malF) and MalG (malG) genes, complete cds
12023	25007	38708	1.72	1.3E-01	BE619384.1	EST_HUMAN	601473368F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
12052	25033	38739	1.52	1.3E-01	BF683556.1	EST_HUMAN	602139760F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4300863 5'
12399	25279	32080	2.13	1.3E-01	BE618346.1	EST_HUMAN	601482741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12543	25368	-	6.39	1.3E-01	AJ242790.1	NT	Gallus gallus scyl1 gene for lympholactin, exons 1-3
12684	25627	-	1.31	1.3E-01	AB028839.1	NT	Epithelial cell derived cDNA for sALK-6, complete cds
12995	25647	-	1.87	1.3E-01	AW061114.1	EST_HUMAN	wl24409.x1 Soares Dieckgrafe, colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:Q60287 Q60287 KIAA0539 PROTEIN. ;
394	13631	25668	13.87	1.2E-01	A1421744.1	EST_HUMAN	tf39802.x1 NCL CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2086538 3' similar to gb:U05760_mel1 ANNEXIN V (HUMAN);
437	13237	-	1.42	1.2E-01	U86912.1	NT	Dicystostellum discoideum ORF DG1018 gene, partial cds
561	13753	-	3.82	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1408	14562	27636	2.32	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1408	14562	27637	2.32	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1414	14568	-	3.35	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cdA Homo sapiens cDNA clone cDNAJB11 5'
1419	14572	-	0.84	1.2E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1538	14688	-	0.84	1.2E-01	AA897474.1	EST_HUMAN	ai48e09.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 Q16671 ANTIMULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1680	14812	27897	1.1	1.2E-01	Q14834	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-A73)
1682	14834	27919	2.88	1.2E-01	A1285402.1	EST_HUMAN	qf8908.x1 NCL CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1980553 3'
1808	14957	-	25.75	1.2E-01	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
1970	15113	-	1.66	1.2E-01	AW449368.1	EST_HUMAN	UIH-B3-ak-e-10-0-UI.s1 NCL CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734554 3'
2253	15386	28514	1.68	1.2E-01	BF248490.1	EST_HUMAN	601821567F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4046224 5'
2450	15378	-	0.99	1.2E-01	Z21405.1	EST_HUMAN	HSAXAEB21 TEST1, Human adult Testis tissue Homo sapiens cDNA
2556	15779	28893	1.84	1.2E-01	AW996556.1	EST_HUMAN	QV3-BN0046-129-f10 BN0046 Homo sapiens cDNA
2905	16083	29098	1.16	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2967	16143	29162	1.9	1.2E-01	A1720470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05005 60S RIBOSOMAL PROTEIN L30 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3001	16177	29189	3.44	1.2E-01	M16364.1	NT	Human creatine kinase-B mRNA, complete cds
3068	18244	29286	0.91	1.2E-01	XG6882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	16476	29498	2.52	1.2E-01	AW370688.1	EST_HUMAN	QV1-BT0250-261088-021-c05 BT0259 Homo sapiens cDNA
3330	16503		0.74	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
3568	16733		0.66	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3610	16774	29789	1.12	1.2E-01	XG6882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3610	16774	29790	1.12	1.2E-01	XG6882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3694	16733		1.22	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3865	17024		0.95	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053683
4298	17441	30426	2.1	1.2E-01	Z64255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4298	17441	30427	2.1	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4431	17571	30562	0.59	1.2E-01	M15861.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4942	18072		1.94	1.2E-01	X73416.1	NT	W. suavis mitochondria ori
5364	18567	31433	0.89	1.2E-01	AA744369.1	EST_HUMAN	ny83a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282050 3'
5415	18617	31591	0.93	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5426	18628	31601	2.5	1.2E-01	W33035.1	EST_HUMAN	zc08402.r1 Scores: parathyroid tumor_NHHPA Homo sapiens cDNA clone IMAGE:321699 5'
5484	18683	31700	1.65	1.2E-01	Z98286.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5622	18816	31885	1.14	1.2E-01	Z48234.1	NT	M.domestica Borkh. Grammy Smith adh mRNA for alcohol dehydrogenase
6329	19500	32858	1.9	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6377	19546	32903	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6428	19596	32962	2.26	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221089-113-e04 CT0031 Homo sapiens cDNA
6483	19659	33022	1.52	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6681	19723	33101	0.58	1.2E-01	AA747535.1	EST_HUMAN	rx85501.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6785	19940	33338	1.18	1.2E-01	BF347985.1	EST_HUMAN	60203112F1 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4158386 5'
7154	20288	33731	0.64	1.2E-01	H47798.1	EST_HUMAN	yp80f04.r1 Scores: fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:193759 5'
7154	20288	33732	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80f04.r1 Scores: fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:193759 5'
7772	20829	34320	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for Interleukin enhancer binding factor 3 (alternative transcripts drbp76, drbp76 gamma, drbp76 alpha and ILF3)
8076	21168		1.13	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-293000-002-109 BN0137 Homo sapiens cDNA
8148	21231	34751	2.45	1.2E-01	A913753.1	EST_HUMAN	wc8g03.x1 NCI_CGAP_C33 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
8197	21279	34801	0.84	1.2E-01	Q07369	SWISSPROT	Q99735 MICROSMAL GLUTATHIONE S-TRANSFERASE II;
8504	21685	35119	0.83	1.2E-01	A1832881.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CH-B22)
							at71b10.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST-E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8590	21671		10.78	1.2E-01	AW083852.1	EST_HUMAN	xc49d07.x1 NCL_CGAP_E602 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8611	21691		3.76	1.2E-01	AF063772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase 5ln (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8649	21729	36286	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8649	21729	35287	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8800	21879		1.02	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8887	21888		1.44	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 193 of the complete genome
8920	21899		0.77	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9771	22707	36338	1.3	1.2E-01	X17981.1	NT	S.cerevisiae HXT5 gene
10209	23245	36835	0.9	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
11125	24197		2.55	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11320	24383		3.03	1.2E-01	BE962324.2	EST_HUMAN	60165578R1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3846283 3'
11414	24475		1.79	1.2E-01	BF314481.1	EST_HUMAN	601900783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11533	24589	38284	2.78	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNA11 (DNAI1) gene, exon 17
11593	24646	38329	1.72	1.2E-01	R40249.1	EST_HUMAN	Y80c02.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28980 3'
11798	24788		2.47	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12161	25128		2.09	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCF12 3'
12522	25355		4.37	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12614	26126	31544	2	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12732	25486		1.65	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntactin gene, partial cds
12734	13753		18.32	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12863	25574		1.4	1.2E-01	X53981.1	NT	R.horvegicus NF88 gene for 68kDa neurofilament
12968	25629	31981	4.89	1.2E-01	A1299003.1	EST_HUMAN	gn20g05.x1 NCL_CGAP_L15 Homo sapiens cDNA clone IMAGE:1898840 3'
12982	25644		3.46	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12987	26050		6.44	1.2E-01	O96433	SWISSPROT	CYGLIN 1
13031	25678	31060	1.47	1.2E-01	AE0004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13221	25785		1.23	1.2E-01	AF090141.1	NT	Chrysothrix merlingosapitum GOB-1 carboxypeptidase gene, complete cds
578	13770	26792	1.56	1.1E-01	A1661003.1	EST_HUMAN	tt18d08.x1 NCL_CGAP_Birc28 Homo sapiens cDNA clone IMAGE:2187983 3'
630	13815	26838	1.33	1.1E-01	AA566006.1	EST_HUMAN	nm08g11.s1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1056620 3' similar to gb:X06989.na1 HEME OXYGENASE 1 (HUMAN);

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1079	14245	27302	1.61	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1109	14274		1.65	1.1E-01	AL181560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
1186	16031	27405	3.87	1.1E-01	AW972158.1	EST_HUMAN	EST384142 MAGE resequences, MAGI Homo sapiens cDNA
1278	14435	27505	1.88	1.1E-01	D94004.1	NT	Synchocystis sp. PCC6803 complete genome, 23/27, 2889767-3002865
1549	14701	27780	2.75	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2255	15388		1.73	1.1E-01	AJ006701.1	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2388	15519		2.02	1.1E-01	6765215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptrc), mRNA
2603	15959		1.08	1.1E-01	6978673	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2633	16766		1.27	1.1E-01	AW821909.1	EST_HUMAN	RCO-ST0378-210100-032-g04 ST0378 Homo sapiens cDNA
2917	16095	29107	0.89	1.1E-01	S62418.1	NT	Interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 6]
3098	16274	29288	0.81	1.1E-01	F03285.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3422	16591		1.56	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caenatg), mRNA
3508	16676	29685	2.09	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3540	16705	29716	1.47	1.1E-01	X62135.1	NT	G.reinhardtii nuclear gene on linkage group XIX
3580	16746	29763	0.71	1.1E-01	R68948.1	EST_HUMAN	y462g08.s1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element;
3673	16836	29846	0.7	1.1E-01	Y07695.1	NT	A.immerius gene for transposase
3781	16952		0.96	1.1E-01	P67384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3900	16981	29965	1.28	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4228	17374	30359	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4226	17374	30360	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4233	17380						Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
4367	17510		11.45	1.1E-01	AF157088.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4401	17644	30528	0.76	1.1E-01	AW802056.1	EST_HUMAN	IL5-JM0070-020500-068-008 UM0070 Homo sapiens cDNA
4782	17897	30877	0.92	1.1E-01	S44657.1	NT	Tape-1 integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4953	18083	31059	1.23	1.1E-01	Y07695.1	NT	A.immerius gene for transposase
5134	17380		0.75	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
5787	18979		2.59	1.1E-01	AA747216.1	EST_HUMAN	mx76d03.s1 NCLCGAP_Ewt Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5857	19047	32353	1.32	1.1E-01	AF020927.1	NT	0 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5894	19082	32393	0.87	1.1E-01	AL110985.1	NT	Batrachoseps strain T4 cDNA library under conditions of nitrogen deprivation
5927	19113	32426	0.96	1.1E-01	BF339518.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5927	19113	32428	0.96	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5938	19144	32459	1.79	1.1E-01	X88951.1	NT	S. pombe ste8 gene encoding protein kinase
5982	19177	32488	5.15	1.1E-01	M85533.1	NT	Providencia rettgeri penicillin G amidase gene
6150	19329	32671	1.88	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6171	19347	32693	1.37	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6191	19367	32716	7.73	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280989-011-a01 CT0254 Homo sapiens cDNA
6554	19716	33092	0.61	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6562	19724	33102	1.52	1.1E-01	AF035746.1	EST_HUMAN	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6602	19762	33150	0.84	1.1E-01	A1216307.1	EST_HUMAN	qg76008.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841089 3'
6742	19898	33299	3.88	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6843	19996		2.73	1.1E-01	AF032922.1	NT	Homo sapiens syniadn 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6934	20249	33684	2.74	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7183	20058	33488	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7193	20058	33489	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7337	26217		1.01	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7456	25845	34007	0.98	1.1E-01	AP000008.1	NT	P. yarrowii holikoshii OT3 genomic DNA, 1168001-1489000 nt position (617)
7708	20771	34255	7.51	1.1E-01	BF884828.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7708	20771	34256	7.61	1.1E-01	BF884828.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7833	20888	34391	2.16	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
7872	20926		0.64	1.1E-01	Z14088.1	NT	B. subtilis gene encoding hypothetical polypeptide synthase
7873	20927	34433					ak31008.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 5' similar to gb.J03483
8155	21237	34758	3.06	1.1E-01	AA788784.1	EST_HUMAN	CHROMOGGRANIN A PRECURSOR (HUMAN);
8403	21484	35012	1.55	1.1E-01	U87492.1	NT	Methanococcus jannaschii section 34 of 150 of the complete genome
8403	21484	35013	1.55	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382
8449	21530	35059	1.26	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382
8489	21570		0.94	1.1E-01	X91233.1	NT	H. sapiens L15 gene
8548	21627	35165	2.31	1.1E-01	AW817918.1	EST_HUMAN	PM1-S10270-080200-001-f09 ST0270 Homo sapiens cDNA
					AL134349.1	EST_HUMAN	DKFZ0547P184_f1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZ0547P194 5'
							Pedococcus acidilactici H plasmid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC and papD genes, complete cds
9018	22097	35637	5.67	1.1E-01	U02482.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9113	22192	35737	1.04	1.1E-01	AB07474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
9210	22288	35830	0.5	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
9243	22320	35863	2.25	1.1E-01	AA192183.1	EST_HUMAN	z983b12.11 Straglene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9243	22320	35864	2.25	1.1E-01	AA192183.1	EST_HUMAN	z983b12.11 Straglene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9335	22411	35984	0.71	1.1E-01	Y12727.1	NT	P. furiosus partial dph5 gene and argF gene
9368	22441	36001	2.78	1.1E-01	U72675.1	EST_HUMAN	y419h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9392	22467		0.83	1.1E-01	BE893260.1	EST_HUMAN	601439872F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9622	22677		0.99	1.1E-01	BE142305.1	EST_HUMAN	CM3-HT0142-271086-026-g11 HT0142 Homo sapiens cDNA
9696	22745		2.33	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10114	23162		0.77	1.1E-01	AL181643.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10410	23445		1.23	1.1E-01	R80590.1	EST_HUMAN	y986d00.e1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147084 3'
10544	23579	37188	1.29	1.1E-01	U60529.1	NT	Ceratit capillata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10914	23697	37631	1.38	1.1E-01	AF245277.1	NT	Dicotyledon discoderm xhresin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
11044	16274	29288	1.78	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized Infant brain cDNA Homo sapiens cDNA clone c-1r02 3'
11162	24233		2.47	1.1E-01	AF169032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
11300	24396	38007	3.11	1.1E-01	R23708.1	EST_HUMAN	y435f12.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131769 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11483	24542	38212	2.6	1.1E-01	Z11810.1	NT	Z.mobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11483	24542	38213	2.6	1.1E-01	Z11810.1	NT	Z.mobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11510	24568	38245	1.69	1.1E-01	BE90297.1	EST_HUMAN	601676924F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959698 5'
11586	24639	38319	3.21	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11971	24968		1.33	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12378	25289		3.78	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-403 NT0112 Homo sapiens cDNA
12649	25910		3.18	1.1E-01	BE974558.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
13136	25736	31947	1.98	1.1E-01	BF239753.1	EST_HUMAN	601806350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1228	14388		1.51	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1301	14457	27823	2.18	1.0E-01	AI985499.1	EST_HUMAN	w98d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.8
1423	14577	27850	2.3	1.0E-01	AL161504.2	NT	MER7 repetitive element;
2558	15883	28808	1.01	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3813	16973	29978	1.11	1.0E-01	BF239818.1	EST_HUMAN	UI-H-813-alc-d-07-0-UI.s1 NCI_CGAP Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
4064	17220	30228	2.6	1.0E-01	BF368703.1	EST_HUMAN	601806489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4527	17665	30651	1.44	1.0E-01	AE002265.2	NT	Chlamydia pneumoniae AR39, section 91 of 94 of the complete genome
4677	17812		0.78	1.0E-01	AI792349.1	EST_HUMAN	h32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4834	17867	30955	2.17	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5039	18167	31143	2.17	1.0E-01	AW952344.1	EST_HUMAN	EST304414 IMAGE resequences, MAGB Homo sapiens cDNA
5261	18380	31346	0.61	1.0E-01	BE389100.1	EST_HUMAN	601286969F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813552 5'
5436	18636		9.49	1.0E-01	W88490.1	EST_HUMAN	z62h04.s1 Scores fetal_liver_spleen_infls_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5534	18731		0.87	1.0E-01	X54015.1	NT	X.campestris genes for sensor and regulator protein
6001	18186		1.08	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00055 protein, partial cds
6148	19325	32670	13.08	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6465	19632	32983	0.9	1.0E-01	AA481878.1	EST_HUMAN	z4410.s1 Scores ovary tumor NbHOT1 Homo sapiens cDNA clone IMAGE:756258 3' similar to contains
6479	19646	33008	0.72	1.0E-01	AA406039.1	EST_HUMAN	z67c12.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:743082 3'
7164	20297		1.87	1.0E-01	R23821.1	EST_HUMAN	y34h06.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:131676 5' similar to contains Alu repetitive element;
7914	20965		2.39	1.0E-01	Y12488.1	NT	M.musculus wtn gene
8118	21200	34721	0.89	1.0E-01	AA861091.1	EST_HUMAN	ak22901.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8141	21223	34741	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8141	21223	34742	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8689	21769		0.86	1.0E-01	AW189797.1	EST_HUMAN	x09b01.x1 NCL OGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S
9367	22462	36026	1.12	1.0E-01	AF102855.2	EST_HUMAN	RIE50MAL PROTEIN S4 (HUMAN) contains TAR1.3 TAR1 repetitive element;
9695	22744	36314	0.87	1.0E-01	R44983.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synanon mRNA, complete cds
9707	22756		1.9	1.0E-01	M76729.1	NT	y53h04.s1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34549 3'
9750	22888		3.15	1.0E-01	AE001501.1	NT	Human pro-alpha-1(V) collagen mRNA, complete cds
9764	22761	36331	0.55	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
10028	23064	36661	1.88	1.0E-01	BF240154.1	EST_HUMAN	zc66010.s1 Scores fetal_heart_NBHHT9W Homo sapiens cDNA clone IMAGE:327282 3'
10139	23177	36774	8.92	1.0E-01	AB046799.1	NT	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10139	23177	36775	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10347	23382		1.06	1.0E-01	AW997425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10351	23386	36995	0.62	1.0E-01	T51952.1	EST_HUMAN	EST369915 IMAGE resequences, IMAGE Homo sapiens cDNA
10537	23572	37179	1.27	1.0E-01	BE762750.1	EST_HUMAN	y629a08.s1 Stragene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10894	23978		1.77	1.0E-01	AU159127.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3639096 5'
							AU169127 THYRO1 Homo sapiens cDNA clone THYRO100895 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11286	24352	37991	2.17	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11286	24352	37992	2.17	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11885	24684	38874	3.84	1.0E-01	BE780543.1	EST_HUMAN	601682558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938734 5'
11814	24803		1.75	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain-RIMD 0508952
12364	25633		1.73	1.0E-01	BE537119.1	EST_HUMAN	601055554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12609	25408		1.73	1.0E-01	7662168	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12939	26119		3.11	1.0E-01	U52691.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP-1) mRNA, complete cds
12973	25633		1.8	1.0E-01	BE537119.1	EST_HUMAN	601055554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13045	28085		25.82	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13117	25729		6.58	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
13219	26106		1.45	1.0E-01	AE002138.1	NT	Ureaplasma urealyticum section 39 of 59 of the complete genome
2639	15953	28060	0.96	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1) mRNA, complete cds
2847	15961	28070	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2847	15961	28071	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3340	18513	28528	1.31	9.9E-02	AF096810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
7110	18536	31492	8.96	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
8099	21181	34699	0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.xt NC1_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2598528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
8099	21181		0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.xt NC1_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2598528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
9457	22573	36139	1.35	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.xt NC1_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2598528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
12132	25112	38816	3.07	9.9E-02	D86980.1	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
577	13769		2.18	9.8E-02	X66338.1	NT	O saliva RAmYc gene for alpha-amylase
3214	16388	29398	3.66	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4339	17482	30463	9.93	9.8E-02	AF257328.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4339	17482	30464	9.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7651	20719		0.98	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9454	22570		1.16	9.8E-02	U61943.1	NT	Human laminin B1 chain gene, exon 28
11747	29833	37559	1.73	9.8E-02	BF037421.1	EST_HUMAN	601460783F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3864287 5'
12332	25240		1.29	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1381	14536	27611	1.92	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1617	14769		1.01	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2035	15466	28601	2.56	9.7E-02	BE168680.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
4091	17240		4.05	9.7E-02	Q98796	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5461	18861	31639	0.59	9.7E-02	AF069189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5461	18861	31640	0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
8138	19316	32857	1.39	9.7E-02	AW054476.1	EST_HUMAN	EST366548 MAGC resequences, MAGC Homo sapiens cDNA
7450	20527	34000	3.05	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21), from 299771 to 3213410
8171	21253	34774	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.e1 Walzmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8171	21253	34775	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.e1 Walzmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9050	22129	35673	1.49	9.7E-02	AI953984.1	EST_HUMAN	wk78b06.x1 NCL CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2649747 3' similar to gbX52851_ma1
11472	24531		1.72	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2073	15213	28330	1.33	9.6E-02	AI080721.1	EST_HUMAN	Mus musculus ligatin (Lgtn) mRNA, partial cds
2073	15213	28331	1.33	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NHHMPU_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4464	17604	30582	6.67	9.6E-02	Z32686.2	NT	oz47d11.x1 Soares_NHHMPU_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
5117	18244	31209	0.95	9.6E-02	AW066230.1	EST_HUMAN	Protein fibrinolytic fibrinogen, strain H14320
6231	19406		2.75	9.6E-02	BE010039.1	EST_HUMAN	EST378303 MAGC resequences, MAGC Homo sapiens cDNA
8017	21068		0.78	9.6E-02	6678753	NT	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8571	21652		0.65	9.6E-02	AU137084.1	EST_HUMAN	Mus musculus lymphocyte antigen 78 (LY78), mRNA
9744	22808	36386	1.49	9.6E-02	AV087898.1	EST_HUMAN	AU137084 PLACET Homo sapiens cDNA clone PLACE1006740 5'
10076	23114		1.34	9.6E-02	BE894895.1	EST_HUMAN	AV087898 GKCH Homo sapiens cDNA clone GKCAH02 5'
10245	23280	36876	1.04	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916363 5'
10245	23280	36877	1.04	9.6E-02	BF677270.1	EST_HUMAN	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10325	23360	36970	0.62	9.6E-02	AB013985.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10354	23389	36988	1.56	9.6E-02	AB013985.1	NT	602086786F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10354	23389	36999	1.58	9.6E-02	AB013985.1	NT	Antitritin majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10465	23500	37113	3.43	9.6E-02	P08174	SWISSPROT	Antitritin majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10961	24060	37694	6.27	9.6E-02	Z79702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
12019	25003	38704	2.8	9.6E-02	AA626755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 102/182
13015	25668		1.7	9.6E-02	H14399.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
							ym19h03.e1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13143	25743	31949	1.41	9.0E-02	AJ295624.1	NT	Gallus gallus ALPHA 10 nACHR gene for alpha 10 subunit of nicotinic acetylcholine receptor, exons 1-5
4217	17366	30355	2.16	9.5E-02	AW92396.1	EST_HUMAN	CM2-EN0023-050200-087-412 EN0023 Homo sapiens cDNA
5782	18974	32280	0.88	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7455	20532	34006	4.84	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7741	20802	34292	7.77	9.5E-02	AL161638.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7876	18974	32280	0.81	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8064	21146	34686	2.85	9.5E-02	BF036891.1	EST_HUMAN	601453642F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3857243 5'
8084	21146	34687	2.85	9.5E-02	BF036891.1	EST_HUMAN	601453642F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37634	4.09	9.5E-02	BF036891.1	EST_HUMAN	601453642F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37635	4.09	9.5E-02	BF036891.1	EST_HUMAN	601453642F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3857243 5'
12104	26084		1.82	9.5E-02	7657416	NT	Mus musculus odd Oz1en-m homolog 3 (Drosophila) (Odz3), mRNA
13097	25715		2.81	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1880	15024	28130	3.95	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4281917 5'
3985	17142	30147	4.64	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
6447	19614	32978	0.95	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101e) mRNA, complete cds
7769	20827	34318	0.68	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and lp35 gene, partial cds
8799	21878		2.5	9.4E-02	Z48863.1	NT	Acinetobacter sp. oysD, cobQ, cobP, lyeS, rubA, rubB, estB, oxyR, ppk, mlgA, ORF2 and ORF3 genes
11174	20827	34318	1.9	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and lp35 gene, partial cds
12214	26011		7.72	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13198	25780	31936	4.84	9.4E-02	U27699.1	NT	Human pepsinogen-1 (Pepsinogen-1) mRNA, complete cds
3054	16230		2.37	9.3E-02	4809280	NT	Homo sapiens BA11-associated protein 3 (BA1AP3) mRNA
3084	16270		8.03	9.3E-02	6012525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3329	16502	28521	2.17	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4288289 5'
4268	17413	30400	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607853 5'
4288	17413	30401	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607853 5'
4857	17890		1.82	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone IMAGE:3607853 5'
5779	18971		0.67	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 11/4
8442	21523	35052	0.56	9.3E-02	AW566007.1	EST_HUMAN	EST69 Human Fetal Brain MAT-CH-MAKER cDNA Library Homo sapiens cDNA
9324	22400		0.5	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9911	22961	36537	2.3	9.3E-02	BE062631.2	EST_HUMAN	601655988F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3855981 3'
10394	23429	37036	3.8	9.3E-02	Q16034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10394	23429	37036	3.6	9.3E-02	Q16034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10526	25561		3.96	9.3E-02	AW206117.1	EST_HUMAN	UI-H-B11-ark-h-05-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12485	25533		2.08	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12905	25964		22.03	9.3E-02	AW468950.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
13139	28010		2.87	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; BING1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
238	13460	26486	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26487	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26488	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2302	15434		3.08	9.2E-02	R54186.1	EST_HUMAN	yg88d7.1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:41618 5'
3247	16421	26437	3.7	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3379	16551	26564	1.01	9.2E-02	AA634354.1	EST_HUMAN	nt79e01.s1 NCL_CGAP_C33 Homo sapiens cDNA clone IMAGE:926136 3'
3676	16839		1.14	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4353	17495		1.05	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4425	17565		0.88	9.2E-02	BE29722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980176 5'
4760	17895	30876	3.44	9.2E-02	X96402.1	NT	G.gallus Mla-Ck gene
8198	21280	34802	1.82	9.2E-02	T48920.1	EST_HUMAN	ya89cd9.11 Stralagene placenta (#637225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to
8370	21451	34974	2.18	9.2E-02	X65256.1	NT	gb:X66009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
13120	26201		1.2	9.2E-02	11466872	NT	H.wulgaris xylose isomerase gene
436	13236	26237	2.23	9.1E-02	X77665.1	NT	Podospira anserina mitochondrion, complete genome
3760	16921		0.97	9.1E-02	AW372569.1	EST_HUMAN	O. curvicaulis K12 keratin gene
4607	17744	30723	1.78	9.1E-02	AL161554.2	NT	PM2-BT0349-161289-001-402 B10349 Homo sapiens cDNA
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5948	19036	32345	1.23	9.1E-02	AF129766.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7459	26218		0.61	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7546	20618	34094	12.21	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7852	20907	34411	0.95	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7887	20939	34445	1.02	9.1E-02	U38073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
9124	22203	35746	0.96	9.1E-02	Y14376.1	NT	Homo sapiens gamma adducin gene, exon 9
10642	23678		1.46	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stralagene Homo sapiens cDNA clone FB19F10 3'end
10674	23708	37316	1.02	9.1E-02	S74059.1	NT	Tg616-Cyl actin (Tritpneustes gratilla=sea urchins, embryos, Genomic, 6275 nt)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10703	23736	37341	0.8	9.1E-02	Y11187.1	NT	A. italiana RH1, TC1, G14587-6, G14587-8, and PRL1 genes
11441	24602	38170	2.13	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor mRNA, complete cds
12151	26121		7.04	9.1E-02	9633494	NT	Bacteriophage M1, complete genome
12393	26124		1.42	9.1E-02	AA179901.1	EST_HUMAN	2038h12.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to
12473	26326		1.32	9.1E-02	AF032695.1	NT	SW-TRT3_HUMAN P48378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12966	26954		13.49	9.1E-02	AJ291380.1	NT	Rattus norvegicus cell cycle protein p55CDG gene, complete cds
13230	26789		1.27	9.1E-02	AF226888.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
							Bombyx mori fibrin heavy chain Fib-H (fib-H) gene, complete cds
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
763	13944	26990	6.89	9.0E-02	P15328	SWISSPROT	hV39g10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
1664	14816	27899	7.33	9.0E-02	BE220482.1	EST_HUMAN	IL6-UM0067-240300-050-H06 UM0067 Homo sapiens cDNA
2454	15552	28710	1.18	9.0E-02	AW801384.1	EST_HUMAN	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2864	15976	29088	4.99	9.0E-02	AF138622.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2864	15978	29089	4.99	9.0E-02	AF138622.1	NT	Dichytalium discoidum spore coat structural protein SP65 (cotE) gene, complete cds
3417	16586	29603	1.11	9.0E-02	AF279135.1	NT	corticosteroid-binding globulin [Salinifil sciurus=squirrel monkeys, liver, mRNA, 1474 nt]
4414	17555	30541	0.8	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Salinifil sciurus=squirrel monkeys, liver, mRNA, 1474 nt]
4414	17555	30542	0.6	9.0E-02	S68757.1	NT	Plasmodium falciparum P-type ATPase 3 gene
4790	17925	30913	2.03	9.0E-02	X65740.2	NT	z68a12.r1 Soerea_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to P1F3S62171 S62171 email G protein - human ;
6118	19298	32634	7.2	9.0E-02	W96037.1	EST_HUMAN	Th63d03.x1 NCI CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element;
6880	20012		0.93	9.0E-02	BF062851.1	EST_HUMAN	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), EscD (escD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Trp (trp), OrfU (orfU), >
12819	25546		1.82	9.0E-02	AF022236.1	NT	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1469	14623	27708	1.25	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1469	14623	27707	1.25	8.9E-02	BF701593.1	EST_HUMAN	PMO-HT0339-251169-003-d01 HT0339 Homo sapiens cDNA
2460	15587	28714	1.64	8.9E-02	BE153572.1	EST_HUMAN	Attrichium angustatum AttranFid2 protein (AttranFid2) gene, partial cds
4316	17459		1.69	8.9E-02	AF286055.1	NT	UI-H-B13-alc-108-QJ1 at NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
5972	19158	32474	2.7	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-108-QJ1 at NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
5972	19158	32475	2.7	8.9E-02	AW452122.1	EST_HUMAN	Homo sapiens similar to endoglycan (H, sepiens) (L-OC83107), mRNA
5987	19172	32494	3.34	8.9E-02	11433478	NT	

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7343	20423	33886	1.6	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
7731	20763		1.77	8.9E-02	Z79021.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA20F8
8240	21322	34839	1.19	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (NNOS)
8323	21405	34932	0.76	8.9E-02	BF701686.1	EST_HUMAN	(CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8323	21405	34933	0.76	8.9E-02	BF701685.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8797	21876	36416	5.85	8.9E-02	AA309319.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
9819	22859	36439	0.84	8.9E-02	AI285627.1	EST_HUMAN	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9819	22859	36440	0.84	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
9834	22873	36565	0.63	8.9E-02	AA339358.1	EST_HUMAN	MER10 repetitive element ;
12213	25062		1.8	8.9E-02	P19524	SWISSPROT	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
12366	25262		3.82	8.9E-02	BF986918.1	EST_HUMAN	MER10 repetitive element ;
12537	25366		2.75	8.9E-02	U28895.1	NT	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
12594	25393		2	8.9E-02	U40463.1	NT	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
12827	26198		1.16	8.9E-02	AE001814.1	NT	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
12880	26133		1.54	8.9E-02	Q27474	SWISSPROT	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
1404	14558	27632	0.96	8.8E-02	Q27474	SWISSPROT	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
4012	17169	30177	1.07	8.8E-02	AA299128.1	EST_HUMAN	EST1180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
4145	17297		6.23	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII-130)
4418	17559		0.75	8.8E-02	4580423	NT	(TAFII130)
7716	20780		0.71	8.8E-02	D17620.1	NT	Homo sapiens paired box gene 6 (antitridia, keratitis) (PAX6), isoform b, mRNA
9188	22266	35807	2.07	8.8E-02	AA151872.1	EST_HUMAN	Homo sapiens paired box gene 6 (antitridia, keratitis) (PAX6), isoform b, mRNA
11380	24441	38089	2.79	8.8E-02	BE284455.1	EST_HUMAN	Sheep mRNA for angiotensinogen, complete cds
11380	24441	38100	2.79	8.8E-02	BE284455.1	EST_HUMAN	z199a05.s1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11541	24597	38273	5.25	8.8E-02	AL040129.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
12443	25314	32090	1.19	8.8E-02	Z71561.1	NT	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
3785	16946	29853	4.17	8.7E-02	U82695.2	NT	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
							DKFZp434D1313.1 434 (synonym: hta53) Homo sapiens cDNA clone DKFZp434D1313 5'
							S. cerevisiae chromosome XIV reading frame ORF YNL285w
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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3785	16946	29954	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4829	17992	30050	1.4	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5211	18332		1.07	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5429	18829	31605	5.49	8.7E-02	AA286875.1	EST_HUMAN	ze55g08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5429	18829	31606	5.49	8.7E-02	AA286875.1	EST_HUMAN	ze55g08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6884	20212	33842	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6884	20212	33843	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7188	20053	33463	0.57	8.7E-02	AF281942.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
8046	21129		0.56	8.7E-02	AA284532.1	EST_HUMAN	z220603.s1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:713692 3'
8713	21793	35328	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8713	21793	35330	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
10851	24033		2.01	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11591	24644	38326	1.48	8.7E-02	AJ007763.1	NT	Glucobacter oxydans (RNA) 1le and 5RNA-Ala genes
12431	25306		2.2	8.7E-02	X17118.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12848	25432		2.85	8.7E-02	6878057	NT	Mus musculus nidogen 2 (Nid2), mRNA
13033	26880		2.05	8.7E-02	X85282.1	NT	Gallus gallus mRNA for vigilin
1281	14437	27506	7.73	8.6E-02	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 22
2317	15448	28581	2.2	8.6E-02	BE408667.1	EST_HUMAN	601304010F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688643 5'
3257	16431	29448	2.35	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3734	16895		3.69	8.6E-02	AF163362.1	NT	Dictyostelium discoideum adenyl cyclase (acrA) gene, complete cds
3880	17039		0.6	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnp) and prion-like protein (Prnd) genes, complete cds
4609	17746	30725	0.66	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galeolin-3 gene, untranslated exon and 5' flanking region
5330	18443		1.02	8.6E-02	AB011163.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
6219	19394	32743	4.74	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6504	19570	33035	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6504	10670	33036	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7755	20814	34306	0.89	8.6E-02	P14916	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8115	21197	34716	1.09	8.6E-02	5730068	NT	Homo sapiens Srt2-related GTP activator protein (SRCAP) mRNA
8115	21197	34717	1.09	8.6E-02	5730068	NT	Homo sapiens Srt2-related GTP activator protein (SRCAP) mRNA
8261	21343	34860	0.56	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8324	21406		0.76	8.0E-02	U60168.1	NT	Dictyostellium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9938	22977	36598	1.24	8.0E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9975	23014		1.4	8.0E-02	AF068253.1	EST_HUMAN	h120c08.x1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2972846 3'
10356	23391	37001	1.07	8.0E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11188	24257	37892	1.82	8.0E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11188	24257	37893	1.82	8.0E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11527	24583	38259	3.02	8.0E-02	BF303506.1	EST_HUMAN	G01893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11527	24583	38260	3.02	8.0E-02	BF303506.1	EST_HUMAN	G01893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11724	23910	37534	7.87	8.0E-02	AE001079.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11876	24863	38559	2.29	8.0E-02	AF283660.1	NT	Bacillus stearothermophilus BarFI methylase (FIM) and BarFI restriction endonuclease (FIR) genes, complete cds
2470	15597	28722	2.59	8.0E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5292	18410		0.68	8.0E-02	N76915.1	EST_HUMAN	y448108.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:245923 5'
5786	18978	32283	0.73	8.0E-02	AA985491.1	EST_HUMAN	cc83567.s1 NCI_CGAP_Kd6 Homo sapiens cDNA clone IMAGE:1692917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5828	18016		1.99	8.0E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6136	19314	32653	6.61	8.0E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8805	21884	35424	1.98	8.0E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
10041	23079	36680	3.27	8.0E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10041	23079	36681	3.27	8.0E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10572	23607	37212	0.64	8.0E-02	X76731.1	NT	V. ammodytes gene for ammodytoxin C
10702	23735	37340	0.82	8.0E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11424	24485		8.03	8.0E-02	AF165510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11446	24507	38173	3.82	8.0E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12873	25986		2.76	8.0E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
13070	25700		2.44	8.0E-02	AA362834.1	EST_HUMAN	ESTT2736 Ovary II Homo sapiens cDNA 5' end
2732	16070	28961	4.05	8.0E-02	W69330.1	EST_HUMAN	z444e11.r1 Soares fetal heart_NHHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5427	18027	31603	9.84	8.0E-02	BE267163.1	EST_HUMAN	G0189436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:353493 5'
6828	19881	33388	1.46	8.0E-02	AK024468.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8218	21300	34821	6.95	8.0E-02	BE095074.1	EST_HUMAN	CM3-BT0760-260400-162-d05 BT0760 Homo sapiens cDNA
8043	22122	35664	1.15	8.0E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10571	23606	37211	1.84	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPUR87 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
10631	23665		0.48	8.4E-02	AV730882.1	EST_HUMAN	O88312 G08-4 ;
12351	26254	32114	1.87	8.4E-02	R78408.1	EST_HUMAN	AV730882 HTF Homo sapiens cDNA clone HTFBM/G04 5'
3382	18845	29853	7.77	8.3E-02	P75334	SWISSPROT	V83h12.11 Soares placenta N12HP Homo sapiens cDNA clone IMAGE:145895 5'
3709	18870	29873	0.75	8.3E-02	AI436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3709	18870	29874	0.75	8.3E-02	AI436797.1	EST_HUMAN	ih82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4417	17558		0.68	8.3E-02	IM54964.1	NT	ih82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6389	19558	32917	0.74	8.3E-02	AI942638.1	EST_HUMAN	C.hummi A2b region open reading frame, complete cds
6496	19662	33025	2.87	8.3E-02	AF052883.1	NT	wo79f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
8169	21251	34771	3.08	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8202	21284		1.06	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drip2) mRNA, complete cds
8495	21576		1.31	8.3E-02	AA987873.1	EST_HUMAN	cg88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.L1 L1 L1
							repetitive element ;
							cg81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
9738	22803	36377	1.09	8.3E-02	AW593503.1	EST_HUMAN	la05h10.x1 Human Pancreatic islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
9751	22899		2.02	8.3E-02	AL161595.2	NT	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE ;
10548	23584		0.72	8.3E-02	AF020409.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
12448	25128		1.81	8.3E-02	BE958458.1	EST_HUMAN	Dicotyledon discoidium Doca (dcca) mRNA, complete cds
1410	14554		9.13	8.2E-02	Y08170.2	NT	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928863 5'
1525	14678	27759	2.03	8.2E-02	AF167077.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
3141	16317		1.97	8.2E-02	AL163206.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3804	17063		1.35	8.2E-02	AL161498.2	NT	Homo sapiens chromosome 21 segment HS21C006
4114	17258	30268	0.99	8.2E-02	AL163206.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4399	17542	30523	6.58	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4399	17542	30524	6.58	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4399	17542	30525	6.58	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5192	18314	31282	3.43	8.2E-02	U76009.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5480	18650	31629	1.49	8.2E-02	BE897030.1	EST_HUMAN	Mus musculus zinc transporter (Znt-3) gene, complete cds
7165	20298	33741	3.16	8.2E-02	AF309555.1	EST_HUMAN	601439676F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7910	20962		0.59	8.2E-02	AF743341.1	EST_HUMAN	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8905	21984		0.69	8.2E-02	U23937.1	NT	AV743341 CB Homo sapiens cDNA clone CELANF07 5'
8971	22050	35593	3.24	8.2E-02	AW875128.1	EST_HUMAN	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9799	22839	36415	4.89	8.2E-02	X04197.1	NT	RC2-PT0004-031289-011-405 PT0004 Homo sapiens cDNA
							Beet necrotic yellow vein virus RNA-2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9965	23004	36599	2.27	8.2E-02	BE254318.1	EST_HUMAN	601116055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355698 5'
12454	25318	32094	3.93	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12686	25458	32021	1.43	8.2E-02	AW862185.1	EST_HUMAN	QV4-CT0361-021299-040-b01 CT0361 Homo sapiens cDNA
12609	25875		2.58	8.2E-02	AF275386.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 6 through 28, and complete cds, alternatively spliced
1524	14677	27758	0.96	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
5873	19063	32371	1.03	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6509	19674	33043	0.89	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7347	20427		0.83	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7756	20815		0.99	8.1E-02	AI692681.1	EST_HUMAN	wd86f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338603 3'
8535	21616	35151	0.86	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8535	21619	35152	0.59	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
10116	23154		1.83	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
10685	23719		0.7	8.1E-02	AW269778.1	EST_HUMAN	xy45b11.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2816061 3'
10868	23891	37511	0.47	8.1E-02	AW450487.1	EST_HUMAN	UI-H-B13-eko-g-01-0-UI.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
10858	23891	37512	0.47	8.1E-02	AW450487.1	EST_HUMAN	UI-H-B13-eko-g-01-0-UI.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
11790	24780	38477	1.99	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	16003	26246	7.61	8.0E-02	AW954863.1	EST_HUMAN	EST368723 IMAGE resequences, MAGC Homo sapiens cDNA
959	14132	27191	0.85	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1733	16046	27074	11.83	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1733	16046	27975	11.83	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1952	15095	28196	4.4	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2447	15575	28704	0.93	8.0E-02	D80915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2447	15575	28705	0.89	8.0E-02	D80915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2541	15666		3.21	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2881	14280	27336	1.55	8.0E-02	M23449.1	NT	Dicystosallum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2965	16141	29159	1.05	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3919	17078	30075	0.83	8.0E-02	AW986118.1	EST_HUMAN	EST378181 IMAGE resequences, MAGI Homo sapiens cDNA
4182	17332		0.74	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4935	18085		6.87	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
5038	18186	31142	0.82	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene.s
6012	19186	32513	3.59	8.0E-02	AF275948.1	NT	complete cds, and small nuclear RNAs (uRNAs)
							Homo sapiens ABCA1 (ABCA1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7330	19166	32513	1.61	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8319	21401	34926	2.41	8.0E-02	AL114993.1	NT	Bdysis chirens strain T4 cDNA library under conditions of nitrogen deprivation
9589	22644	36213	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9589	22644	36214	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10361	23366		0.49	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11032	24111	37747	2.84	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helixase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12127	25107	38811	1.63	8.0E-02	4507608	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9) mRNA
12488	25337	32061	3.54	8.0E-02	AJ005376.1	NT	Drosophila arena hunchback region
13134	17332		1.85	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2243	16376	28504	3.37	7.9E-02	BE250008.1	EST_HUMAN	60094319T1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
3043	16219	28240	12.53	7.9E-02	AI562029.1	EST_HUMAN	ar8ec08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3953	17111	30110	4.47	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
3953	17111	30111	4.47	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4932	18062		1.16	7.9E-02	AB008018.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6836	19989		1.14	7.9E-02	BF366016.1	EST_HUMAN	RC3-GN0042-310800-024-411 GN0042 Homo sapiens cDNA
8221	21303	34824	3.1	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
10234	23269	36839	5.6	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NC1_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
10234	23269	36860	5.6	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NC1_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
13008	25564		1.27	7.9E-02	AI761638.1	EST_HUMAN	wg08h01.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
1237	14396	27457	1.49	7.8E-02	AI793276.1	EST_HUMAN	oo59d02.v5 NC1_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
1237	14396	27458	1.49	7.8E-02	AI793276.1	EST_HUMAN	oo59d02.v5 NC1_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
4915	18045	31035	0.6	7.8E-02	BE836331.1	EST_HUMAN	repetitive element
5198	17003		2.97	7.8E-02	BE260048.1	EST_HUMAN	oo59d02.v5 NC1_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
7223	20087	33504	1.1	7.8E-02	U82986.2	NT	PM3-FN0058-140700-005-f09 FN0058 Homo sapiens cDNA
							800943035F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7223	20087	33505	1.1	7.8E-02	U82696.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8985	22084	35604	0.83	7.8E-02	BE697847.1	EST_HUMAN	601440.439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
9081	22160	35702	0.89	7.8E-02	X78344.1	NT	<i>S. cerevisiae</i> CAT8 gene
9253	22330	35877	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9253	22330	35878	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9561	22703	36269	0.9	7.8E-02	AA469354.1	EST_HUMAN	nc88006.t1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:771731
10006	23044	36837	0.55	7.8E-02	Z89124.1	NT	<i>Bacillus subtilis</i> complete genome (section 21 of 21); from 3989281 to 4214814
10001	23085	37616	2.19	7.8E-02	U32323.1	NT	Human Interleukin-11 receptor alpha chain gene, complete cds
12910	28602	31973	1.35	7.8E-02	U72847.1	NT	Homo sapiens envoplakin (EVPK) gene, exons 15 through 18
1431	16038	27659	1.22	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3677	16840		2.01	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
8093	21175	34690	5.38	7.7E-02	AA402949.1	EST_HUMAN	TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN .
10040	23078	36679	4.88	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10336	23371	36981	0.84	7.7E-02	AI318662.1	EST_HUMAN	ta80h08.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S
10336	23371	36982	0.84	7.7E-02	AI318662.1	EST_HUMAN	ta80h08.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S
11262	24331	37872	3.98	7.7E-02	11422757	NT	RIBOSOMAL PROTEIN L38 (HUMAN);
3474	16641	20660	3.1	7.6E-02	BE614432.1	EST_HUMAN	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3494	16661	29673	0.98	7.6E-02	AA288447.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3649	16812	29825	0.96	7.6E-02	AJ400877.1	NT	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
6222	16397	32746	0.69	7.6E-02	AI061276.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6486	19663	33015	1.14	7.6E-02	BE378328.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
9570	22712	36280	1.11	7.6E-02	AJ131016.1	NT	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
10101	23139		0.99	7.6E-02	AL139078.2	NT	Homo sapiens SCL gene locus
10424	23459	37064	0.5	7.6E-02	BE708002.1	EST_HUMAN	<i>Campylobacter jejuni</i> NCTC11168 complete genome; segment 5/6
10557	23592		1.04	7.6E-02	BE969338.2	EST_HUMAN	RC1-HT0545-020800-017-306 HT0545 Homo sapiens cDNA
10815	23848	37489	0.97	7.6E-02	X92658.1	NT	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
							<i>L. esculentum</i> mRNA for trice phosphate translocator

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10815	23848	37470	0.97	7.8E-02	X62886.1	NT	L esculentum mRNA for those phosphate translocator
11974	24959	38661	1.93	7.8E-02	AW1886445.1	EST_HUMAN	QV3-BN0048-150400-161-c04 BN0046 Homo sapiens cDNA
807	13887	27039	1.65	7.5E-02		NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC9A9), mRNA
807	13887	27040	1.95	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC9A9), mRNA
1071	15114	28214	0.99	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630	17766	30748	0.74	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5974	19159	32477	1.45	7.5E-02	AI648714.1	EST_HUMAN	wq24r09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8533	21614	35150	1.28	7.5E-02	AI864367.1	EST_HUMAN	w13r02.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:U14328 ALPHA
8705	21785	35318	1.36	7.5E-02	AU116913.1	EST_HUMAN	ENOLASE (HUMAN);
10238	23273		0.49	7.5E-02	BF221730.1	EST_HUMAN	7c61c05.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone HEMBA1000264 5'
10711	23744	37350	0.73	7.5E-02	BF206809.1	EST_HUMAN	MER27 repetitive element;
10816	23849	37471	0.82	7.5E-02	X79460.1	NT	601970205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
490	13684	20718	1.41	7.4E-02	AW838547.1	EST_HUMAN	C.fimi DSM 20113 T6S cDNA
1489	14642		1.21	7.4E-02	AF030027.1	NT	RC5-LT0084-260100-011-H09 LT0054 Homo sapiens cDNA
2848	15771		0.96	7.4E-02	6755069	NT	Equine herpesvirus 4 strain NS80567, complete genome
3583	16846	29854	1.21	7.4E-02	AI807885.1	EST_HUMAN	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
4926	17959	30946	1.19	7.4E-02	L78810.1	NT	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4914	18044	31034	2.65	7.4E-02		NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
5056	18184	31159	4.42	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
6624	19784		1.69	7.4E-02	R17477.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
6717	19875	33266	0.66	7.4E-02	AF030422.1	NT	yg14g06.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
7636	20705	34184	0.84	7.4E-02	AA605132.1	EST_HUMAN	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
8085	21167	34683	1.11	7.4E-02	BE880112.1	EST_HUMAN	no71d02.61 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
8898	21779	35312	1.26	7.4E-02	U56089.1	NT	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
9367	22442	36002	1.08	7.4E-02	AW629805.1	EST_HUMAN	Human perlecan tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9367	22442	36003	1.08	7.4E-02	AW629805.1	EST_HUMAN	hh67df1.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9639	21082	34593	0.58	7.4E-02	AI672939.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2;
9639	21082	34594	0.58	7.4E-02	AI672939.1	EST_HUMAN	hh67df1.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
							O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2;
							we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
							we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10019	23057	36653	1	7.4E-02	U62203.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10148	23184	36780	0.49	7.4E-02	BF512878.1	EST_HUMAN	UI-H-BW1-amg-g-06-Q-UJ.s1 NCJ_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
11266	24335	37975	1.46	7.4E-02	AA059187.1	EST_HUMAN	Zf64e01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
11914	24901	38604	1.42	7.4E-02	AI125063.1	EST_HUMAN	ao11007.s1 Barstead aorta HPLRB3 Homo sapiens cDNA clone IMAGE:1726285 3' similar to gb:M86492
12409	26288		1.22	7.4E-02	11625893	NT	GLIA MATURATION FACTOR BETA (HUMAN);
12692	26101		3.74	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12870	26580	31985	2.61	7.4E-02	BF035099.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
12882	25595	31988	1.44	7.4E-02	AJ223459.2	NT	601453813F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3857738 5'
481	13878	28708	1.15	7.3E-02	BE984981.2	EST_HUMAN	Aspergillus nidulans prnD, prnX, prnA genes
481	13678	26709	1.15	7.3E-02	BE984981.2	EST_HUMAN	601658738R1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3886209 3'
702	13885	26917	2.65	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3886209 3'
1510	16040	27748	3.26	7.3E-02	AW900281.1	EST_HUMAN	Thermoboga maritima section 101 of 136 of the complete genome
1893	16050		15.79	7.3E-02	AL163302.2	EST_HUMAN	CM0-NN1004-130300-284-gb8 NN1004 Homo sapiens cDNA
5112	18240		1.02	7.3E-02	U12283.1	NT	Homo sapiens chromosome 21 segment HS21C102
6682	19744	33126	1.46	7.3E-02	AA779977.1	EST_HUMAN	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
7633	20702	34180	2.37	7.3E-02	P05143	SWISSPROT	Z24402.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7633	20702	34181	2.37	7.3E-02	P05143	SWISSPROT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7981	21030		0.59	7.3E-02	BF916087.1	EST_HUMAN	PROLINE-RICH PROTEIN MP-3
8361	21442		1.36	7.3E-02	7682107	NT	PROLINE-RICH PROTEIN MP-3
8598	21677	36214	0.5	7.3E-02	Y10887.2	NT	60186047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125615 5'
9411	22465		1.17	7.3E-02	AB011090.1	NT	Homo sapiens KIAA0424, protein (KIAA0424), mRNA
11492	19744	33126	1.78	7.3E-02	AA779977.1	EST_HUMAN	Mus musculus cdh5 gene, exon 1, partial
122	13352	26382	0.6	7.2E-02	AE000882.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
122	13352	26383	0.6	7.2E-02	AE000882.1	NT	Z24402.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
1505	14658	27739	2.6	7.2E-02	AL163301.2	NT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
1505	14658	27740	2.6	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 149) of the complete genome
2814	18738		3.34	7.2E-02	U14794.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 149) of the complete genome
3991	17148	30154	0.63	7.2E-02	AW298322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
						NT	Homo sapiens chromosome 21 segment HS21C101
						NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
						EST_HUMAN	UI-H-BW0-ajl-a-05-Q-UJ.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732049 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4465	17605	30583	3.07	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5402	18004	31576	2.73	7.2E-02	U67831.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5403	18605	31577	8.78	7.2E-02	P11120	SWISSPROT	CALMODULIN
6244	19418		1.11	7.2E-02	BF217598.1	EST_HUMAN	601883909F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086224 5'
7318	20400	33863	1.32	7.2E-02	BF216088.1	EST_HUMAN	601883958F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085710 5'
7335	20416	33878	0.7	7.2E-02	AF221128.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7359	20438		1.53	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8382	21463	34987	0.6	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8382	21463	34988	0.6	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9264	22341		0.57	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9775	22815		0.51	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9811	22851	36430	2.19	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUG01 5'
9861	23000	36596	4.88	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10118	23156	36754	0.96	7.2E-02	BF126399.1	EST_HUMAN	601763923F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
10206	23242	36833	2.34	7.2E-02	AW873187.1	EST_HUMAN	hq24f11.x1 NCL_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340
10395	23430	37037	0.8	7.2E-02	AA768204.1	EST_HUMAN	ca82c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10560	23595	37201	2.15	7.2E-02	U82595.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10692	23725	37331	5.57	7.2E-02	BE565003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885951 5'
10716	23749		3.47	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451650 5'
10837	23870	37492	0.55	7.2E-02	AA706897.1	EST_HUMAN	228103.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451647 3'
11153	24224	37853	4.14	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mst1 (Mst1) gene, complete cds
12316	25230	32104	2.12	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12350	25253		3.83	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D6 3'
12411	25290		2.05	7.2E-02	AA584465.1	EST_HUMAN	nc05h08.s1 NCL_CGAP_Pho1 Homo sapiens cDNA clone IMAGE:1099859 3'
12474	25327		4.23	7.2E-02	U82628.1	NT	Homo sapiens alaxia telangiectasia (ATM) gene, complete cds
12488	25337		7.37	7.2E-02	AW000682.1	EST_HUMAN	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
13048	25687		1.63	7.2E-02	AA401779.1	EST_HUMAN	zif57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728464 5'
1953	15088	28197	2.05	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (Dg) proviral structural capsid protein (gag) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2388	15497	28623	6.8	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
8091	21173	34697	1.03	7.1E-02	AI125264.1	EST_HUMAN	cd82a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
10866	23898	37521	0.53	7.1E-02	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C049
12193	25150		6.46	7.1E-02	BE304784.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
541	13734	26768	1.4	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1529	14682		1.28	7.0E-02	X96577.1	NT	Marattia Mitut-1 gene
1801	14960	28044	1.18	7.0E-02	AA056343.1	EST_HUMAN	z166f04.s1 Striatogene colon (#837204) Homo sapiens cDNA clone IMAGE:509599 3'
3095	18271	29266	2.02	7.0E-02	AW138152.1	EST_HUMAN	UJ-HB11-acy-c-07-0-UJ.st NCI_CGAP_Sub83 Homo sapiens cDNA clone IMAGE:2716020 3'
4004	17161	30187	0.65	7.0E-02	AA815438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376678 3' similar to gb:K03002 60S
4155	17307	30301	1.19	7.0E-02	BE070284.1	EST_HUMAN	QV4-BT0407-260100-090-a10 BT0407 Homo sapiens cDNA
4258	17403		1.14	7.0E-02	AW792962.1	EST_HUMAN	CM0-UM0001-060300-270-a12 UM0001 Homo sapiens cDNA
4330	17473	30468	1.19	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5045	18173	31150	7.97	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4050071 5'
5493	18692		0.92	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7560	20632	34107	0.9	7.0E-02	AV889285.1	EST_HUMAN	AV889285 GKC Homo sapiens cDNA clone GKCCAE08 5'
7762	20838	34331	0.68	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial acanthin, XL spliced variant (acz gene)
8299	22375	35926	1.24	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
9797	22837	36415	1.31	7.0E-02	K02901.1	NT	Rat Ig gamma epsilon chain gene C-region, 3' end
10158	23195	36791	0.88	7.0E-02	U27268.1	NT	Human myosin binding protein H (MYBP-H) gene, complete cds
11654	24733	38424	2.6	7.0E-02	AA724285.1	EST_HUMAN	ah88a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
13022	25673	31958	1.2	7.0E-02	11421638	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
527	13720	26744	7.08	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
527	13720	26745	7.08	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1364	14318		1.58	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3893	17052	30051	1.34	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of G2-selective protein signaling (ZGAP1) mRNA, and translated products
3893	17052	30052	1.34	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5302	18419	31989	4.11	6.9E-02	Z70163.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5316	18433	31403	0.83	6.9E-02	M34956.1	NT	H-sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA24f7
7793	20849		0.87	6.9E-02	AF164967.1	NT	M. hyarhitis 115 kDa protein (p115) gene, complete cds
8242	21324		1.14	6.9E-02	U12022.1	NT	Canine distemper virus strain A7517, complete genome
8750	21829	35368	1.01	6.9E-02	BE587435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
							601340561F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8750	21829	35367	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH MGC 53 Homo sapiens cDNA clone IMAGE:3663030 5'
9320	22396	35949	0.67	6.9E-02	U22967.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11374	24435	38092	1.46	6.9E-02	S81752.1	NT	DPH2L=candidate tumor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
11374	24435	38093	1.46	6.9E-02	S81752.1	NT	DPH2L=candidate tumor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
12346	25257		10.94	6.9E-02	X74316.1	NT	X.laavis XPD2 mRNA for fork head protein
12524	25357		1.56	6.9E-02	P44821	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFQ HOMOLOG
12770	25513		3.37	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1932	15075	28177	1.18	6.8E-02	AA466759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1932	15075	28178	1.18	6.8E-02	AA466759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1956	15099	28189	3.85	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4576	17810		0.64	6.8E-02	BE141078.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
6768	19914		0.65	6.8E-02	P20792	SWISSPROT	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
7040	20083		0.99	6.8E-02	BE061890.1	EST_HUMAN	MR0-HT0069-071099-001-c03 HT0069 Homo sapiens cDNA
7432	20509	33981	8.22	6.8E-02	AL163268.2	NT	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA
7661	20915	34420	0.6	6.8E-02	U16856.1	NT	Homo sapiens chromosome 21 segment HS21C068
8483	21564	35099	6.03	6.8E-02	AJ248287.1	NT	Dicystellum discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8483	21564	35100	6.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
12141	28155		1.47	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome, segment 5/6
12276	25206		1.64	6.8E-02	AA758014.1	EST_HUMAN	FB4A8 Fetal brain, Stragene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12506	25599		1.34	6.8E-02	AW875839.1	EST_HUMAN	ah6705.s1 Soares testis, NHT Homo sapiens cDNA clone 1320705 3'
12972	25632		2.3	6.8E-02	9910585	NT	EST387948 IMAGE resequences, MAGN Homo sapiens cDNA
13203	26091	31660	1.24	6.8E-02	6978895	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1558	14711		2.71	6.7E-02	AF115538.1	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1842	15095	28186	2.17	6.7E-02	AJ220285.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OmyTAP1 3' allele, complete cds
3811	16971	29973	4.48	6.7E-02	P17278	SWISSPROT	gg79e04.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1841408 3'
4065	17221	30229	0.74	6.7E-02	U63783.1	NT	HOMEOBOX PROTEIN HOXD4 (HOXA)
4065	17221	30230	0.74	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
7969	21019	34532	0.66	6.7E-02	W57759.1	EST_HUMAN	Cyprinus carpio Rap1b mRNA, complete cds
8034	21117	34635	0.74	6.7E-02	X62695.1	NT	zd20g11.s1 Soares fetal heart, NBHH19W Homo sapiens cDNA clone IMAGE:341282 3' similar to contains AU repetitive element; contains element L1 repetitive element ; H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8034	21117	34636	0.74	6.7E-02	X82895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8633	21713	35260	0.73	6.7E-02	AW082888.1	EST_HUMAN	xb61c11.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2680788 3'
9800	22840	36417	0.59	6.7E-02	AW137359.1	EST_HUMAN	UIH-BI1-act-g-01-0-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9800	22840	36418	0.59	6.7E-02	AW137359.1	EST_HUMAN	UIH-BI1-act-g-01-0-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1379	14534	27608	0.98	6.0E-02	A1735509.1	EST_HUMAN	at12e08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2384920 3' similar to SW/LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.;
2252	15385	28513	3.73	6.0E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3552	16717	29731	12.38	6.0E-02	R64306.1	EST_HUMAN	Y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3667	16732	29748	3.11	6.0E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3667	16732	29749	3.11	6.0E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4191	17341	30334	1.61	6.0E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5093	18221	31181	12.07	6.0E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5093	18221	31182	12.07	6.0E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5130	18255	31220	0.64	6.0E-02	AA393244.1	EST_HUMAN	ZT74a07.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5130	18255	31221	0.64	6.0E-02	AA393244.1	EST_HUMAN	ZT74a07.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6714	19872	33264	3.92	6.0E-02	X06411.1	NT	P.vulgaris mRNA for chalcone synthase
6749	19905	33298	0.82	6.0E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6749	19905	33299	0.82	6.0E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6837	19905	33299	0.88	6.0E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6937	19905	33299	0.88	6.0E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
8133	21215	34736	1.51	6.0E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8669	21749	35287	0.77	6.0E-02	AF006055.1	NT	Dicotyledon discoidium darlin (darA) gene, complete cds
8979	22068		0.53	6.0E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
9121	22200	35741	1.28	6.0E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9121	22200	35742	1.28	6.0E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10157	23184	36790	0.54	6.0E-02	AI458752.1	EST_HUMAN	igf1g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
10292	23327	36930	1.5	6.0E-02	Y07848.1	NT	Homo sapiens EWS, ger22, rrp22 and bam22 genes
10327	23362		0.65	6.0E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10710	23743	37349	0.49	6.0E-02	BF694059.1	EST_HUMAN	S02080608F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245336 5'
11205	24274	37911	4.95	6.0E-02	BF374248.1	EST_HUMAN	MR1-SN0084-010600-008-a12 SN0084 Homo sapiens cDNA
12761	25505		4.84	6.0E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
13124	25733		1.26	6.0E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
595	13785	28805	1.57	6.5E-02	BF027638.1	EST_HUMAN	601671048F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1011	14183	27245	1.3	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1422	14576	27649	3.38	6.5E-02	U47624.1	NT	Xeropus laevis alpha(E)-catenin mRNA, complete cds
1773	14922	28016	2.04	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 86 of 109 of the complete genome
5676	18870	32156	2.07	6.5E-02	AA443991.1	EST_HUMAN	zx49h12.s1 Soares ovary tumor NHPOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M28038
6673	19832	33221	0.73	6.5E-02	BF665340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7113	18539	31496	1.02	6.5E-02	U22861.1	NT	602116887F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4276029 5'
10147	23185	36781	0.57	6.5E-02	BE963200.2	EST_HUMAN	Azobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
10147	23186	36782	0.57	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10683	23717	37323	0.81	6.5E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10875	23960	37589	4.45	6.5E-02	AA195648.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
12163	25129	26363	3.78	6.5E-02	M21496.1	NT	ar32g06.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666144 3'
12633	26363		3.67	6.5E-02	AF102893.1	NT	Rabbit microsomal epoxide hydrolase
589	13780	26799	1.49	6.4E-02	X94549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
1770	14919	28013	0.99	6.4E-02	AE001777.1	NT	A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene
1770	14919	28014	0.99	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
							Thermotoga maritima section 89 of 136 of the complete genome
5566	18763	31803	1.11	6.4E-02	AI191956.1	EST_HUMAN	qcd7b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.63
6239	19413	32761	2.64	6.4E-02	AF052733.1	NT	LTR8 repetitive element
6239	19413	32762	2.64	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6532	19886	33069	1.23	6.4E-02	AF052733.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6957	20270	33708	4.11	6.4E-02	BE974448.1	EST_HUMAN	we73g12.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
8531	21612		2.47	6.4E-02	6753323	NT	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3960503 3'
8865	21944	35478	4.17	6.4E-02	AA093305.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cot6a), mRNA
9327	22403	35955	0.98	6.4E-02	AF160195.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9785	22825		0.61	6.4E-02	BE834083.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAJA10
9918	22958	36545	1.87	6.4E-02	AB011126.1	NT	RC1-OT0083-150600-014-806 OT0083 Homo sapiens cDNA
10468	23503	37116	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10468	23503	37117	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12008	24993	38697	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12008	24893	38608	1.85	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12427	28048		2.7	6.4E-02	AF107890.1	NT	Homo sapiens nudh 5B (NUC5B) gene, partial cds
12479	25331	32036	2.61	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1793	14942	28035	2.51	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III region Hec70t gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3892	18854		2.29	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6264	19438	32785	1.12	6.3E-02	BF210738.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7391	20469		1.84	6.3E-02	X67869.1	NT	H.sapiens gene encoding La autoantigen
9491	22548	36111	0.99	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominia gene, exons 1-3
10218	23264	38843	3.52	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10478	23513		1.31	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GK0 Homo sapiens cDNA clone GKCAHE01 5'
10954	19438	32785	2.36	6.3E-02	BF210738.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
2549	15674	28707	1.04	6.2E-02	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4365	17508	30489	4.22	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4458	17598		1.03	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4705	17540		5.66	6.2E-02	Q82191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6935	20250	33685	0.78	6.2E-02	D46530.1	NT	Spirulina platensis DNA for acetylase cyclase, complete cds
7805	20861	34354	0.86	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8016	21067		0.58	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9148	26225		0.82	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9544	22609	38177	0.47	6.2E-02	AA778450.1	EST_HUMAN	af20a06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9881	22730	36300	1.19	6.2E-02	6677898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdrf2) mRNA
11415	24476	38140	1.42	6.2E-02	AF217460.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11629	24709	38401	1.54	6.2E-02	AJ242735.1	NT	Melanizium antisoplae mRNA for Chymotrypsin (Chyt) gene
12263	26191		3.63	6.2E-02	AE000750.1	NT	Aquifex seductus section 82 of 108 of the complete genome
12617	25415		1.24	6.2E-02	BE763085.1	EST_HUMAN	601883773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
12703	25467	32024	3.61	6.2E-02	BF112039.1	EST_HUMAN	787008.x1 Soares_NSF_F8_9w OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y4S8 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1]
266	13485	26516	3.63	6.1E-02	D18471.1	NT	Human mRNA, Xq terminal portion
4099	17254		2.85	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKG1) gene, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	19414		1.57	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8458	21539	35068	3.65	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8861	21940	35474	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651088R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8861	21940	35475	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651088R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10867	24048	37881	3.9	6.1E-02	BE179543.1	EST_HUMAN	U3-H10818-110500-138-C06 HT0818 Homo sapiens cDNA
12134	25114	38818	1.66	6.1E-02	AB025333.1	NT	Epiplatys burgeri mRNA for RNA polymerase III largest subunit, partial cds
12218	26033		30.03	6.1E-02	X70869.1	NT	S. japonicum mRNA for serine-enkephalin
12836	25957		1.58	6.1E-02	AI886911.1	EST_HUMAN	U259107.x1 NCI_CGAP_OV35 Homo sapiens cDNA clone IMAGE:2292901 3'
12993	25645		6.43	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1291	14447	27513	1.58	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2740	15937	28069	1.17	6.0E-02	AW968848.1	EST_HUMAN	EST380924 IMAGE resequencing, MAG.J Homo sapiens cDNA
2832	15946		1.43	6.0E-02	AB031289.1	NT	Mesocricetus corollae mitochondrial DNA, NADH dehydrogenase subunit 4, rRNA-Gln, rRNA-Phe, rRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
3002	13335	26362	1.53	6.0E-02	AA188730.1	EST_HUMAN	2p78c04.r1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:626310 5'
3002	13335	26363	1.53	6.0E-02	AA188730.1	EST_HUMAN	2p78c04.r1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:626310 5'
3301	15475	29496	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3301	16475	29497	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3725	16886		0.76	6.0E-02	BE984443.2	EST_HUMAN	601658160R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5514	18712		1.01	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0263-011199-013-b04 BT0263 Homo sapiens cDNA
6345	19515	32872	1	6.0E-02	AI607537.1	EST_HUMAN	wf48h06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356873 3' similar to contains L1.11 L1 L1 repetitive element
7127	18553	31467	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
7127	18553	31468	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
7338	20418	33880	2.37	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4049226 5'
7857	20912	34417	1.78	6.0E-02	AI204275.1	EST_HUMAN	qf68h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754169 3'
8617	21897		0.46	6.0E-02	11468495	NT	Racibonoma americana mitochondrion, complete genome
9472	22529	36092	1.29	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
9472	22529	36093	1.29	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
9606	22661	36233	2	6.0E-02	AI245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9606	22661	36234	2	6.0E-02	AI245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
10109	23147	36746	0.72	6.0E-02	AA309767.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10109	23147	36747	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180664 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11618	24669		1.42	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565168 5' similar to gb: X69181 60S RIBOSOMAL PROTEIN L31 (HUMAN); wf62h03.x1 Soares_NFL_T_CGC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
12921	25606		5.12	6.0E-02	AI809273.1	EST_HUMAN	OB0288 KIAA0051 PROTEIN
239	13481	28489	5.86	5.8E-02	AW934710.1	EST_HUMAN	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
3048	16224	29246	2.77	5.9E-02	AF190269.1	NT	Duck parvovirus strain 90-2193 capsid protein (VP3) gene, partial cds
4864	17997		0.77	6.9E-02	AF186111.1	NT	Mus musculus trochus related homeobox 5 (Drosophila) (trx5), mRNA
8817	21896	35435	2	5.9E-02	9055249	NT	60187606F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4105994 5'
9650	21093		0.97	5.9E-02	BF242748.1	EST_HUMAN	Mus musculus follistatin-like (Fst), mRNA
11025	24104		7.39	5.9E-02	6879870	NT	602076548F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243834 5'
11835	24824		1.36	5.9E-02	BF572539.1	EST_HUMAN	Gallus gallus HKC9 telomere junction
11850	24839		1.37	5.9E-02	AJ240733.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
956	14129		8	5.8E-02	D90110.1	NT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
1693	14845	27929	0.97	5.8E-02	Q61768	SWISSPROT	Thermotoga maritima section 87 of 136 of the complete genome
3753	16914	29917	1.68	5.8E-02	AE001775.1	NT	wz24602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4474	17614	30593	6.79	5.8E-02	AW051927.1	EST_HUMAN	wz24602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4474	17614	30594	6.79	5.8E-02	AW051927.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_TNFRSF11B_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); qh56f01.x1 Soares_fetal_liver_spleen_TNFRSF11B_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4669	17804	30792	4.64	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_TNFRSF11B_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4669	17804	30793	4.64	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_TNFRSF11B_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4698	17831		2.1	5.8E-02	AF086284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7855	20910	34414	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7855	20910	34415	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8866	21945	35479	0.81	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12365	25261		1.65	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12681	26180		4.65	5.8E-02	AA604269.1	EST_HUMAN	no76e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112884 3'
3123	16299	29312	1.14	5.7E-02	AI081644.1	EST_HUMAN	pi83h05.s1 NCI_CGAP_BR2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3139	16316	29328	1.09	5.7E-02	AF119117.1	NT	CS086111
3902	17061	30060	2.3	5.7E-02	AW686791.1	EST_HUMAN	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
4807	17941		0.95	5.7E-02	M95099.1	NT	EST178865 MAGE resequences, MAGE Homo sapiens cDNA Bos taurus lysoczyme gene (cow 3), complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6000	19185		0.67	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7630	20699	34175	0.88	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7630	20699	34178	0.68	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7710	20775	34260	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7710	20775	34261	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8349	21430	34954	1.45	5.7E-02	AJ286900.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
10055	23093	36695	0.82	5.7E-02	6681260	NT	Mus musculus ec2 oncogene (Ect2), mRNA
11464	24523	38183	3.14	5.7E-02	AJ752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11464	24523	38184	3.14	5.7E-02	AJ752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11030	24710		1.68	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12586	25969		19.03	5.7E-02	D50320.1	NT	Pig DNA for SPAT-2, complete cds
12789	25512		2.17	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
12853	26042		3.04	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
13012	26165		5.21	5.7E-02	AF281280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
13171	25759	31929	1.18	5.7E-02	R48513.1	EST_HUMAN	Y64d10.x1 Soares breast 2Nbl-Bst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element;
1556	14709	27789	1.1	5.6E-02	AF084455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (pL16) gene, intron; chloroplast gene for chloroplast product
2362	15493		1.95	5.6E-02	BE904308.1	EST_HUMAN	601494576F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3866310 5'
4763	17898	30878	1.37	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4818	17951	30935	1.31	5.6E-02	AA230599.1	EST_HUMAN	za45cd01.st NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6799	19954	33354	5.87	5.6E-02	AW172708.1	EST_HUMAN	X02c10.x1 NCL_CGAP_U02 Homo sapiens cDNA clone IMAGE:2859050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN ;
7031	20167	33589	1.02	5.6E-02	AA865182.1	EST_HUMAN	cd47112.st NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7301	20393	33842	3.3	6.6E-02	BE080001.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
8010	21080	34572	1.32	5.6E-02	AI183563.1	EST_HUMAN	cd64g11.x1 Soares_leslis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9002	22081	35623	2.52	5.6E-02	BE542663.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9002	22081	35624	2.52	5.6E-02	BE542663.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10017	23055	36651	1.18	5.6E-02	AA482664.1	EST_HUMAN	n49d07.st NCL_CGAP_AV1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11963	24851		2.42	5.6E-02	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2720	18838	28948	7.33	5.6E-02	X07889.1	NT	H. sapiens gene encoding La autoantigen
3286	19490	29481	3.33	5.6E-02	9755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4332	17475	30459	0.98	5.6E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5776	18938	32272	3.49	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
8149	18988	32272	4.32	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7535	20608	34083	1.65	5.6E-02	9755902	NT	Mus musculus tufalin 1 (Tuf1), mRNA
8311	21393	34917	0.87	5.6E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8311	21393	34918	0.87	5.6E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9855	22895	36476	0.76	5.6E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9855	22895	36477	0.76	5.6E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9951	22990	36583	1.24	5.6E-02	U69482.1	NT	Mus musculus second IL1 receptor alpha chain (IL1R2) gene, exons 1 and 2
							Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhad), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
11271	24339	37977	6.31	5.6E-02	U09771.1	NT	Oryza sativa tbb3-1 gene for putative Bowman Birk trypsin inhibitor
3084	18260		0.85	5.4E-02	AJ277488.1	NT	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3509	18476		8.19	5.4E-02	BE073468.1	EST_HUMAN	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
4020	17177	30186	0.61	5.4E-02	U6806.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2513730
8318	21398		1.18	5.4E-02	Z99116.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
9271	22347	35897	0.51	5.4E-02	AF280226.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
10838	24020	37853	1.86	5.4E-02	U20790.1	NT	RC8-FN0112-190700-021-D08 FN0112 Homo sapiens cDNA
11453	24513	38180	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-190700-021-D08 FN0112 Homo sapiens cDNA
11453	24513	38181	1.36	5.4E-02	BF371289.1	EST_HUMAN	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
12463	26960		3.72	5.4E-02	U44894.1	NT	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1078	14244	27300	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1078	14244	27301	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1535	14688	27798	20.57	5.3E-02	T64769.1	EST_HUMAN	yea712.1 Stragene lung (4937210) Homo sapiens cDNA clone IMAGE:18951 5' similar to gb:K01506
2866	16691	28816	3.22	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
3008	16184	29207	0.97	5.3E-02	M58417.1	NT	Pseudomonas putida tfgS gene
3008	16184	29208	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3008	16184	29208	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3221	16395	29406	4.83	5.3E-02	AJ276408.1	NT	Pseudomonas putida tfgS gene
5200	18321	31290	7.98	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5434	18634	31812	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
5434	18634	31813	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6228	19403	32753	1.14	5.3E-02	MB5289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7024	20160	33580	4.02	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7241	20325	33760	1.37	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 103 of the complete genome
7517	20590		2.3	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8061	21073	34555	0.68	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF8-SP011 INTERGENIC REGION
8000	21681		0.68	5.3E-02	U10088.1	NT	Mus musculus 128/Sv cytalin C (cst) gene, complete cds
8325	22401	35954	1.73	5.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-ten DNA
10462	23497		0.61	5.3E-02	Y07907.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and posttranscription, 20-28 hpf)
10538	23573	37180	0.79	5.3E-02	X68432.1	NT	B. tenebionticus mRNA for transcription factor
13173	25761	31831	1.59	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2358	15489		64.04	5.2E-02	5031908	NT	Homo sapiens matriin A, alpha (PABA peptide hydrolase) (MEPIA) mRNA
3183	16358	28363	2.39	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3183	16358	28364	2.39	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4050	17208	30216	0.8	5.2E-02	AF235101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4393	17536	30515	3.31	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nco1 mRNA, complete cds
5287	18408	31373	0.66	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for tyroglobulin, complete cds
6040	19223	32545	0.64	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6233	19408		0.64	5.2E-02	A1830655.1	EST_HUMAN	wj80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1
7424	20501	33072	1.23	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8386	21470		2.39	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9331	22971	36560	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9331	22971	36561	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12725	25463		1.6	5.2E-02	Q03030	SWISSPROT	OXA LOAGETATE DECARBOXYLASE ALPHA CHAIN
2437	15865		0.98	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073.1 647 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D073.5
5161	18283	31248	0.89	5.1E-02	BE957423.2	EST_HUMAN	60165355R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361.3
5251	18372		0.96	5.1E-02	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/6
5349	18462		0.74	5.1E-02	U72397.1	NT	Bacteriophage 80 alpha holin and amidase genes, complete cds
6812	19868	33370	0.79	5.1E-02	AF280369.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6997	18516	31508	1.73	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8447	21528	35055	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8447	21528	35056	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8542	21623	35160	1.42	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrocyclohexene 3beta-reductase
9086	22165	35710	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9086	22165	35711	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10014	23032	36846	4.27	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10384	23419	37028	1.9	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
11068	24143	37778	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11068	24143	37779	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12736	25487		1.81	5.1E-02	AF062467.1	NT	Quercus melo polygalacturonase precursor (MPG3) mRNA, complete cds
495	13690	26721	2.8	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1231	14390	27452	2.82	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2047	15188	28299	5.08	5.0E-02	P02810	SWISSPROT	4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2879	14182	27244	10.88	5.0E-02	U72742.1	NT	Salivary acidic proline-rich phosphoprotein 1/2 precursor (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
3418	16587		1.36	5.0E-02	7305810	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3684	16847		1.01	5.0E-02	U32782.1	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3775	16936	28942	5.9	5.0E-02	U12769.2	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
4941	18071		1.05	5.0E-02	P40232	SWISSPROT	Antheraea pernyi period clock protein homolog mRNA, complete cds
6258	19432	32776	0.84	5.0E-02	AF086284.1	NT	CASEIN KINASE II BETA CHAIN (CK II)
6438	19605		1.28	5.0E-02	AJ242626.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7128	18554	31459	0.58	5.0E-02	P35616	SWISSPROT	Mus musculus Dmp-1 gene, exons 1-6
7709	20774	34259	10.04	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7913	20964	37045	0.67	5.0E-02	AW062464.1	EST_HUMAN	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10403	23435		1.37	5.0E-02	AF305238.1	NT	MR0-CT0084-100888-002-g10 CT0084 Homo sapiens cDNA
10855	23888		0.55	5.0E-02	BF213260.1	EST_HUMAN	Mus musculus Fes-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
11782	24772	38468	2.28	5.0E-02	U67600.1	NT	601844753F1 NIH MGC 56 Homo sapiens cDNA clone IMAGE:4070101 5'
12229	26004		4.7	5.0E-02	Q04047	SWISSPROT	Methanococcus jannaschii section 142 of 150 of the complete genome
231	13452		11.82	4.9E-02	M14230.1	NT	NO-ON-TRANSIENT A PROTEIN
380	13588	26623	4.18	4.9E-02	AF275948.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
380	13588	26624	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2937	16114	29125	0.71	4.9E-02	U32836.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3350	18532	29545	1.85	4.9E-02	P54258	SWISSPROT	Zea mays phytoene synthase (Y1) gene, complete cds
							ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3660	16823		0.85	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3681	16844	29851	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728428 3'
3681	16844	29852	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728428 3'
4964	18083	31069	2.64	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4964	18093	31070	2.64	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5498	18885	31702	1.82	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5498	18885	31703	1.82	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7292	20374	33831	1.79	4.9E-02	AE000880.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8815	21954		1.07	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8942	22021		0.61	4.9E-02	BE931832.1	EST_HUMAN	MRQ-HT0408-170800-003-a08 HT0408 Homo sapiens cDNA
8954	22033	35575	0.97	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10500	23535	37145	0.64	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
10802	23835	37459	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
10802	23835	37460	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
11087	24686	38376	3.46	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12957	25624		3.23	4.9E-02	M19384.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
340	13552	26582	1.19	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
341	13552	26582	2.61	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
501	13696	26728	11.53	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2347	15478	28610	2.08	4.8E-02	W51983.1	EST_HUMAN	zc49b02.s1 Soares senescent fibroblasts, NBHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30998 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3280	16454	29473	1.79	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4793	17928		1.08	4.8E-02	Z64280.1	NT	S. sacra gene for skeletal muscle ryanodine receptor
5237	18359	31328	0.88	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8332	21414	34940	1.41	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-221089-012-b02 ST0129 Homo sapiens cDNA
9329	22405	35957	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9329	22405	35958	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
11219	24238	37928	1.84	4.8E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
11219	24288	37929	1.84	4.8E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
12511	25350		1.46	4.8E-02	6932803	NT	Streptococcus thermophilus bacteriophage Sf19, complete genome
5122	18248	31214	0.74	4.7E-02	6981261	NT	Rattus norvegicus Neslin (Nes), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6969	20197	33623	3.34	4.7E-02	W01153.1	EST_HUMAN	yz9709.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu repetitive element
7025	20161	33581	0.69	4.7E-02	BF686825.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7025	20161	33582	0.69	4.7E-02	BF686825.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7058	20111	33527	1.71	4.7E-02	M62752.1	NT	Rat elastin-related protein (s1) gene, complete CDS
8445	21626	35053	9.44	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9154	22232	35777	1.31	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9176	22254		2.97	4.7E-02	AB026678.1	NT	Gallus gallus Wpkol-8 gene, complete cds
9428	22502	36068	7.75	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9936	22875		0.7	4.7E-02	A1873042.1	EST_HUMAN	w976r10x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11852	24841	38535	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11852	24841	38536	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12449	26182		4.31	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCCKD02 3'
281	13499	26531	0.69	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
758	13639	26984	2.89	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1320	14476					EST_HUMAN	em60402.s1 Johnabn frontal cortex Homo sapiens cDNA clone IMAGE:1538970 3' similar to TR:P00533
1390	14644	27620	1.49	4.6E-02	A1014255.1	EST_HUMAN	P90533 LIMA, contains element LTR1 repetitive element
			5.39	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HT0339 Homo sapiens cDNA
2557	15682	28807	2.34	4.6E-02	AW236023.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1
2869	13499	26531	1.78	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3073	16249	29270	0.64	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3410	16249	29270	0.59	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3583	16249	29270	0.84	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4239	17385		0.92	4.6E-02	AF220385.1	NT	Mus musculus nucleolar RNA hairpin (ddx21) gene, complete cds
5852	19042	32348	1.57	4.6E-02	AF070982.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6359	19529	32887	3.67	4.6E-02	X61624.1	NT	C. reinhardtii ap2 (atpB) mRNA
6359	19529	32888	3.67	4.6E-02	X61624.1	NT	C. reinhardtii ap2 (atpB) mRNA
6938	20251	33687	1.41	4.6E-02	A1148574.1	EST_HUMAN	q660506.x1 Soares placenta, 8to9weeks_2NbHP609W Homo sapiens cDNA clone IMAGE:1719971 3'
8007	21057	34569	0.83	4.6E-02	6978720	NT	similar to contains L1.13 L1 repetitive element
8556	21835	35472	3.81	4.6E-02	BE154006.1	EST_HUMAN	Rattus norvegicus Cathepsin H (Ctsh), mRNA
11689	24587	38377	3.39	4.6E-02	A4913328.1	EST_HUMAN	PM0-HT0339-080400-009-G12 HT0339 Homo sapiens cDNA
						EST_HUMAN	ol27h08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13079	25708		3.14	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
460	13655	26993	2.24	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozlin VP35 gene, complete cds
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozlin VP35 gene, complete cds
1847	14953	28095	4.93	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2177	15312	28440	2.2	4.5E-02	AE003964.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3817	16977	29681	5.04	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6360	19530	32889	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6636	19796	33184	0.84	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7018	20154	33574	0.59	4.5E-02	L26487.1	NT	Methanococcus jensenii carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
7018	20154	33574	0.59	4.5E-02	L26487.1	NT	Methanococcus jensenii carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8587	21668	35207	2.24	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10155	23192	36788	4.2	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
10305	23340	36946	0.47	4.5E-02	X95508.1	NT	A. europaeum mRNA for legumin-like protein
10421	23468	37061	0.78	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12442	25313	32089	2.61	4.5E-02	AA181013.1	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
12891	26051	31684	3.79	4.5E-02	AA181097.1	EST_HUMAN	Z14311.1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
227	13449		4.35	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_B2 Homo sapiens cDNA clone IMAGE:3935388 5'
1050	14216	27273	0.77	4.4E-02	L19295.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2163	15269		6.82	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2559	15884	28809	1.81	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3730	16891	28895	1.68	4.4E-02	AF159160.1	NT	Mycobacterium xenopus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4750	17885	30866	1.33	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4750	17885	30867	1.33	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7287	20350	33802	0.69	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7287	20350	33803	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8952	22031	35572	2.34	4.4E-02	AA736869.1	EST_HUMAN	ntw13h03.st NCJ_CGAP_SS1 Homo sapiens cDNA clone IMAGE:7239221 3'
11328	24389	38034	2.64	4.4E-02	AF060689.1	NT	Hepatitis E virus strain HEV-JS2 polypeptide (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11477	24536	38206	3.08	4.4E-02	AA498739.1	EST_HUMAN	ae33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12158	25126		4.55	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1483 protein, partial cds
12347	26102		1.65	4.4E-02	BF241245.1	EST_HUMAN	Homo sapiens mRNA for KIAA1483 protein, partial cds
802	13982	27034	7.26	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2634	15757	28871	1.55	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3516	16892	29663	9.18	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3749	16910		1.21	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6625	19785	33172	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6625	19785	33173	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6871	20023	33433	0.8	4.3E-02	AA652286.1	EST_HUMAN	ns08c12.a1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188888
8711	21791	35327	0.69	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9001	22080	35621	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
9001	22080	35622	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
12412	25291		1.2	4.3E-02	AL136077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/6
845	14023	27081	1.74	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
889	14085		2.4	4.2E-02	AU123327.1	EST_HUMAN	w34q01.x1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
919	14094	27159	1.51	4.2E-02	AW003645.1	EST_HUMAN	L1 RETROPOSON, ORF2 MRNA, contains L1.13 L1 L1 repetitive element;
1758	14907		1.37	4.2E-02	AL445086.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
1819	14968	28060	0.99	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3754	16915	28918	1.66	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4865	17698	30982	0.99	4.2E-02	BF342895.1	EST_HUMAN	60207105F1 NCL_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4152672 5'
5735	18928	32224	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18928	32225	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7122	18548	31460	0.61	4.2E-02	BE268285.1	EST_HUMAN	601124566F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2889319 5'
7695	20760	34244	4.35	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7717	20781	34267	0.61	4.2E-02	AF730347.1	EST_HUMAN	AF730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
8010	22089	35631	3.82	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10367	23402	37013	1.46	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BRAIN PROTEIN 1) (TBR-1) (TES-56)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11285	24361	38002	1.52	4.2E-02	AA976118.1	EST_HUMAN	on33b11.s1 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65290
11587	24640	38320	2.83	4.2E-02	BE816822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11587	24640	38321	2.83	4.2E-02	BE816822.1	EST_HUMAN	PM3-BN0174-260500-009-d10 BN0174 Homo sapiens cDNA
11795	24795	38483	1.52	4.2E-02	AF178458.1	NT	PM3-BN0174-260500-009-d10 BN0174 Homo sapiens cDNA
12728	26109		6.04	4.2E-02	AF683494.1	EST_HUMAN	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
13076	25705		1.17	4.2E-02	D147111.1	NT	w49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
523	13716	26743	1.86	4.1E-02	AF200629.1	NT	Staphylococcus aureus HSP10 and HSP60 genes
2741	15958	28970	1.06	4.1E-02	AE002330.2	NT	Homo sapiens HPS1 gene, intron 5
4005	17162	30168	0.61	4.1E-02	BE297236.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
4005	17162	30169	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177607F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3333353 5'
4595	17732		8.4	4.1E-02	AW893484.1	EST_HUMAN	601177607F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3333353 5'
5228	18351		0.61	4.1E-02	X83890.1	NT	QV1-NN0012-180400-164-108 NN0012 Homo sapiens cDNA
5759	18951	32253	1.08	4.1E-02	BE251894.1	EST_HUMAN	L monocytogenes type 3 partial lap gene (strain 449)
5759	18951	32254	1.06	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7022	20158		0.98	4.1E-02	X76881.1	NT	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7248	20331	33778	1.38	4.1E-02	AE002132.1	NT	A. italiana mRNA for plasma membrane intrinsic protein 1a
7682	20747	34228	1.79	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7778	20834	34325	20.08	4.1E-02	L02110.1	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
						NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7942	20992	34502	2.81	4.1E-02	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mibis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8402	21483	35011	0.74	4.1E-02	P97857	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
8845	21924	35462	0.79	4.1E-02	P34687	SWISSPROT	MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
9355	22430	35988	0.87	4.1E-02	AA372398.1	EST_HUMAN	CUTICLE COLLAGEN 34
13112	26110	31666	9.91	4.1E-02	AJ271809.1	NT	EST84281 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3316	16489	29507	3.85	4.0E-02	AB040904.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3900	17059	30058	1.09	4.0E-02	L11910.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
						NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
						NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5495	18994	31710	5.31	4.0E-02	AF280107.1	NT	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6343	19513	32870	0.98	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:076286 075286
7867	20921	34428	5.99	4.0E-02	L23838.1	NT	R29124_1.1; Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7929	20979		0.71	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7943	20953	34503	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7943	20953	34504	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7980	21029	34543	0.61	4.0E-02	AF288153.1	NT	Homo sapiens erythrocyte tropomodulin (E-TMOD) gene, exon 7
8914	21993	35532	2.52	4.0E-02	P08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN
9844	22884		0.63	4.0E-02	BF679376.1	EST_HUMAN	GLUCOHYDROLASE)
9863	22909	36495	2.46	4.0E-02	AJ000941.1	NT	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
10190	23227		1.08	4.0E-02	D43949.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thid:fumarate reductase subunit A
12073	25054		1.52	4.0E-02	AJ001018.1	NT	Human mRNA for KIAA0082 gene, partial cds
12333	25909	31859	16.34	4.0E-02	AJ001058.1	NT	Kluyveromyces fragilis gene for Car+ ATPase
1144	14309	27366	2.79	3.9E-02	BF516149.1	EST_HUMAN	Ovis aries mRNA for acetyl-coA carboxylase
1375	14530	27603	2.15	3.9E-02	P41047	SWISSPROT	UI-H-BW1-anx-h08-Q-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
2016	15156	28261	3.22	3.9E-02	AJ403386.1	NT	FAS ANTIGEN LIGAND
2769	15884		1.97	3.9E-02	4506862	NT	M.musculus DNA for desamin-binding fragment DesD7
5246	18387	31334	0.67	3.9E-02	AW392417.1	EST_HUMAN	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC)
5279	18398	31356	0.9	3.9E-02	8924019	NT	mRNA
5279	18398	31367	0.6	3.9E-02	8924019	NT	RC6-ST0258-171199-021-Q09 S10258 Homo sapiens cDNA
5949	19039	32346	1	3.9E-02	BE969841.1	EST_HUMAN	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5977	19162	32482	0.65	3.9E-02	BF676203.1	EST_HUMAN	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
7203	20068	33478	0.97	3.9E-02	BE271437.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833642 5'
8023	21106	34623	1.44	3.9E-02	BF238613.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
8250	21332	34849	0.6	3.9E-02	AJ229041.1	NT	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3046830 5'
8250	21332	34850	0.6	3.9E-02	AJ229041.1	NT	601808848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
11695	21071	34562	1.56	3.9E-02	P48778	SWISSPROT	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:4134779 5'
12184	25039		3.54	3.9E-02	AB042553.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
							ANTIGEN GOR
							Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12898	25595		2.35	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HYB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY3, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
13036	25979		64.89	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, nrmxq28orf
5556	18754	31792	0.8	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6212	19387	32736	1.04	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7471	20546	34018	1.72	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8864	21943		1.51	3.8E-02	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
10786	23822	37446	0.64	3.8E-02	7662563	NT	Homo sapiens PRO0514 protein (PRO0514), mRNA
10888	23972	37603	1.71	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1018	14187	27248	4.05	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2310	15442	28577	6.19	3.7E-02	A1994806.1	EST_HUMAN	wrs5e08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2645	15768	28883	0.97	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3115	16291	29306	1.13	3.7E-02	P78944	SWISSPROT	EOMESODERMIN
3117	16293	29307	4.33	3.7E-02	BF312963.1	EST_HUMAN	601898233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3543	16708		0.91	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
7226	26216		0.95	3.7E-02	AF000053.1	NT	Aeropyrum pernix genomic DNA, section 6/7
7889	20923	34430	0.81	3.7E-02	AE003973.1	NT	Xyella fastidiosa, section 121 of 229 of the complete genome
10219	23255		1.01	3.7E-02	AA782516.1	EST_HUMAN	ai55c09.x1 Soares_papillary_tumor_NIHHPA Homo sapiens cDNA clone 1360912 3'
12227	25175	38837	7.41	3.7E-02	BF124874.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12061	25945	31764	3.71	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
13089	25689		1.23	3.7E-02	11487432	NT	Odontella shenensis chloroplast, complete genome
3744	16905	28909	0.82	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3752	16913	28916	0.9	3.6E-02	AL086806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5313	18430	31400	0.67	3.6E-02	AL086810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5543	18740	31758	0.61	3.6E-02	X59403.1	NT	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31774	0.61	3.6E-02	X59403.1	NT	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
5617	18811	31880	0.66	3.6E-02	AF181722.1	NT	Homo sapiens RU2AS (RU2) mRNA, complete cds
5848	19999	33408	4.48	3.6E-02	AW945516.1	EST_HUMAN	GM2-EN0013-110600-192-b10 EN0013 Homo sapiens cDNA
6846	19999	33407	4.48	3.6E-02	AW945516.1	EST_HUMAN	GM2-EN0013-110600-192-b10 EN0013 Homo sapiens cDNA
7234	20318	33761	1.79	3.6E-02	AF025962.1	NT	Chromatium vinosum sulfur globule protein C12 precursor (sgp2) gene, complete cds
7458	20534	34009	2.89	3.6E-02	AA714521.1	EST_HUMAN	rw20a05.s1 NCI CGAP GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314.1rna2
7811	20856	34360	0.84	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9591	22646	36216	2.16	3.6E-02	U20608.1	NT	Dictyostelium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9591	22646	36217	2.16	3.6E-02	U20608.1	NT	Dictyostelium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9812	22852	36431	0.84	3.6E-02	BF347588.1	EST_HUMAN	602020453F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158116 5'
11456	24516	38183	1.46	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11456	24516	38184	1.46	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
918	14033	27158	0.99	3.6E-02	U09506.1	NT	Drosophila melanogaster tigger mRNA, complete cds
1033	14202	27260	2.43	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1595	14748	27831	1.4	3.6E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1695	14748	27832	1.4	3.6E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4329	17472	30457	1.83	3.6E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4435	17575	30556	1.11	3.5E-02	P53780	SWISSPROT	CYSTATIONINE BETA-LYASE PRECURSOR (OBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6351	19521	32878	1.76	3.5E-02	J01238.1	NT	Maize actin 1 gene (Mact1), complete cds
8165	21247		0.91	3.5E-02	H29951.1	EST_HUMAN	yp44a05.r1 Soares retina N255HR Homo sapiens cDNA clone IMAGE:180256 5' similar to contains Alu repetitive element
8824	21903	35443	2.93	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
10224	23280	36848	0.94	3.5E-02	X76842.1	NT	L lactis MG1363 grpE and drak genes
10270	23305	36902	0.61	3.5E-02	BE561042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11785	24775	38471	1.79	3.6E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291298-002-h03 CT0326 Homo sapiens cDNA
11785	24775	38472	1.79	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
12676	25583		1.31	3.5E-02	AF009893.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S8P to TCRBV21S2A2 region
12955	25981		2.71	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
592	13783	26802	47.29	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
592	13783	26803	47.29	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
593	13783	26802	3.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
593	13783	26803	3.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1078	14242	27288	2.57	3.4E-02	AW274020.1	EST_HUMAN	xx26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814263 3' similar to SW:C211_HUMAN P63801 PUTATIVE SURFACE GLYCOPROTEIN C210RF1 PRECURSOR ;
1233	14392		5.43	3.4E-02	11346459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220). mRNA
2465	15592	28717	1.7	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:81280 5' similar to contains MER28 repetitive element
3517	16893	29694	1.5	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3875	17034	30032	0.81	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
4030	17188	30199	3.72	3.4E-02	AW794892.1	EST_HUMAN	RC6-UM0018-210200-021-A10 UM0015 Homo sapiens cDNA
4720	17855	30838	2.77	3.4E-02	X59799.1	NT	Mus musculus S-antigen gene promoter region
5172	18294		1.9	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5189	18311	31277	1.81	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6993	18512	31504	4.68	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8456	21637		3.15	3.4E-02	AI869628.1	EST_HUMAN	wf98d04.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
8947	22026	35567	1.18	3.4E-02	AA664886.1	EST_HUMAN	nu70f08.s1 NCL CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element contains element MER25 MER25 repetitive element ;
							zq04f11.s1 Stragene muscle 837208 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9118	22197		5.28	3.4E-02	AA194306.1	EST_HUMAN	(PISGKPLPKVTLSDRGVPLKATMRFNTEITAENLTINKESVTADAGRYEITAANSSTGTTKAFINIVLDRPG
9880	23019		0.66	3.4E-02	AI092719.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGGQVNTYLLKRETSTAVVTEVSATVARTMMKVMKL ... ;
383	13591		6.8	3.3E-02	AA398735.1	EST_HUMAN	z66h08.x1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone IMAGE:1085519 3'
1193	14355	27413	12.43	3.3E-02	AB035867.1	NT	z75e08.s1 Soares_IsleNc_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1669	14821	27904	1.23	3.3E-02	AF110763.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1778	14927		1.37	3.3E-02	AE000700.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2149	15285		2.02	3.3E-02	R09112.1	EST_HUMAN	Aquifex aeolicus section 32 of 109 of the complete genome
3445	16613	29831	0.86	3.3E-02	H02386.1	EST_HUMAN	y25e09.r1 Soares_fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:127888 5'
4293	14821	27904	3.74	3.3E-02	AF110763.1	NT	y35h02.r1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4589	17728	30709	2.24	3.3E-02	BF245995.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
6560	19722	33098	25.73	3.3E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
6560	19722	33100	25.73	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7677	20742	34223	0.63	3.3E-02	AF124162.1	NT	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9523	22598	36167	0.74	3.3E-02	BF115621.1	EST_HUMAN	Nicotiana plumbaginifolia polyadenylated synthesis sulphuryase (cns5) gene, partial cds
9523	22598	36168	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
							7m92d04.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'

Single Exon Probes Expressed in Piacenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9824	22678	36248	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
9624	22579	36249	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11383	24444	38104	3.28	3.3E-02	BF581107.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12428	25303		3.1	3.3E-02	T896545.1	EST_HUMAN	ye48f1.1.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101 5'
12657	25379		1.6	3.3E-02	AF289665.1	NT	Mus musculus E1F4H gene, partial cds; LIMK1 gene, complete cds, and ELN gene, partial cds
12591	25396		1.85	3.3E-02	M81890.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
134	13360	26394	1.79	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1150	14314	27370	6.32	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1150	14314	27371	6.32	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1812	14961	28054	1.08	3.2E-02	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TER1) gene, exons 7-16 and complete cds
2187	15322		1.09	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2902	13360	26394	0.87	3.2E-02	AJ002006.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3204	16379	29389	13.21	3.2E-02	BE867353.1	EST_HUMAN	60144231F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3806	16966	29970	0.94	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4334	17477		16.42	3.2E-02	X94768.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4890	18020	31005	3.85	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
6310	18427	31397	0.93	3.2E-02	AW650159.1	EST_HUMAN	IL3_C70210-271089-022-C04 C70219 Homo sapiens cDNA
5652	18846	32127	1.49	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
5652	18846	32128	1.49	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
6953	19812	33200	2.4	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
6656	19815		30.91	3.2E-02	T89367.1	EST_HUMAN	ye33h12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element; contains LTR1 repetitive element;
6743	19896	33290	3.7	3.2E-02	AF173845.1	NT	Sagittulus oedipus tissue kallikrein gene, complete cds
7939	20989	34409	0.92	3.2E-02	11242049	NT	Homo sapiens cytochrome P450, subfamily 11B (phenobarbital-inducible) (CYP2B), mRNA
8498	21577	36113	8.04	3.2E-02	6880565	NT	Mus musculus cytochrome P450, subfamily 11B (phenobarbital-inducible) (CYP2B), mRNA
9141	22220		0.87	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9426	22500	36065	1.2	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9428	22500	36066	1.2	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
							qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
							zg54b12.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gpl.08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10262	23297		4.51	3.2E-02	AA719705.1	EST_HUMAN	Macaaca mulatta chemokine receptor CCR5 mRNA, complete cds
10566	23601	37207	1.11	3.2E-02	U96762.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1289	14445		1.92	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1333	14430	27559	1.46	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1840	15083	28184	1.28	3.1E-02	6671684	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Aps3d), mRNA
5378	18580	31449	1.29	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5476	18678		2.8	3.1E-02	AA278478.1	EST_HUMAN	z881a06.r1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:703858 5'
5764	18955	32259	0.77	3.1E-02	BF687742.1	EST_HUMAN	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
8122	21204		0.58	3.1E-02	AV686088.1	EST_HUMAN	AV686088 GKC Homo sapiens cDNA clone GKCAVH09 5'
9142	22221	35764	0.48	3.1E-02	BE965092.2	EST_HUMAN	601658879RT NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3885291 3'
9339	22415	35868	0.48	3.1E-02	AI872302.1	EST_HUMAN	wm57d09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2440049 3'
10237	23272	36864	2.67	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1652	14805		2.41	3.0E-02	AF187125.1	NT	Pfyoiketes minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2852	15775	28888	1.08	3.0E-02	AA402242.1	EST_HUMAN	z65n03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727263 5'
3743	16904	29803	2.82	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3839	16938		0.93	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150200-040-609 ST0286 Homo sapiens cDNA
4058	17214		0.94	3.0E-02	AA364003.1	EST_HUMAN	EST74630 Pineal gland II Homo sapiens cDNA 5' end
5164	18286	31250	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5164	18286	31251	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5507	18706		3.21	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6384	19553	32910	0.87	3.0E-02	N98615.1	EST_HUMAN	z839a10.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:294903 5' similar to contains element TAR1 repetitive element
6384	19553	32911	0.87	3.0E-02	N98615.1	EST_HUMAN	z839a10.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element
6929	20244	33677	2.87	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
7047	20100	33516	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7047	20100	33517	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7218	20083	33497	1.82	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7218	20083	33498	1.82	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7380	20458	33921	1.22	3.0E-02	M86524.1	NT	Human dystrophin gene
8317	21369		0.48	3.0E-02	BF679706.1	EST_HUMAN	602164364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286554 5'
8821	21900	35439	0.55	3.0E-02	BE512670.1	EST_HUMAN	601171626F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3543047 5'
8842	21921	35459	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-280600-108-c04 HT0704 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8893	22072		1.83	3.0E-02	AF275694.1	NT	Omnithorhynchus anatinus coagulation factor X mRNA, complete cds
10677	23711	37319	2.03	3.0E-02	AE001787.1	NT	Thrombocytin section 108 of 136 of the complete genome
10770	23803	37425	0.47	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11508	24598	38243	2.26	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11889	24974	38878	7.11	3.0E-02	AA483218.1	EST_HUMAN	ne87704.st NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:311263
12536	26168	31556	1.95	3.0E-02	R32019.1	EST_HUMAN	yh63d04.st Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3
12943	25621		11.62	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-p06 NN0038 Homo sapiens cDNA
12989	26161		4.97	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Galactose 4-epimerase beta-1, 4-galactosyltransferase mRNA, complete cds
3650	16813	29826	0.8	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4039	17195	30208	0.81	2.9E-02	H72805.1	EST_HUMAN	yt07e10.r1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:233130 5'
6188	19364	32712	1.39	2.9E-02	AF060221.1	NT	Sus scrofa deoxythionuclease II mRNA, complete cds
6421	19590	32655	6.58	2.9E-02	BF032233.1	EST_HUMAN	601452961.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
7398	20476	33943	9.95	2.9E-02	BE271437.1	EST_HUMAN	601140729.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7584	20656	34133	0.65	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 282
8187	21289	34793	0.82	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schleichendallia chinensis glucanase (gnd) gene, partial cds
8187	21289	34794	0.82	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schleichendallia chinensis glucanase (gnd) gene, partial cds
9859	22899	36482	2.14	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9859	22899	36483	2.14	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10078	23116		0.65	2.9E-02	AW976597.1	EST_HUMAN	EST388708 MAGE resequences, MAGN Homo sapiens cDNA
10553	23588	37196	1.25	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 777
11303	16813	29826	1.44	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12538	26057		1.35	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5'
579	13771		0.76	2.8E-02	AW970163.1	EST_HUMAN	EST382234 MAGE resequences, MAGN Homo sapiens cDNA
3453	16620	29839	1.2	2.8E-02	AF060603.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3453	16620	29840	1.2	2.8E-02	AF060603.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4430	17570		0.78	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Map1), mRNA
5005	18800	31866	11	2.8E-02	BE741083.1	EST_HUMAN	601994078.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6948	20291	33698	1.08	2.8E-02	T78960.1	EST_HUMAN	yt21b08.r1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:108855 5'
8523	21604	35142	1.67	2.8E-02	AJ005820.1	NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9219	22297	35840	0.75	2.8E-02	AA280792.1	EST_HUMAN	zs89c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711488 5'
9409	22483	36047	1.41	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9513	22578	36144	0.76	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
9674	22636	36207	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
9674	22636	36208	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
1518	14671	27753	0.96	2.7E-02	U66059.1	NT	Human germ-line T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
3518	16694	28695	1.99	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4319	17462	30447	1.93	2.7E-02	N47258.1	EST_HUMAN	y98h12.r1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17462	30448	1.93	2.7E-02	N47258.1	EST_HUMAN	y98h12.r1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:280487 5'
5362	18565	31432	0.6	2.7E-02	BF246672.1	EST_HUMAN	601864811F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5557	18755	31793	1.43	2.7E-02	R12245.1	EST_HUMAN	y33409.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6022	19205	32525	0.69	2.7E-02	XG1670.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
6734	19690		1.02	2.7E-02	X97580.1	NT	A.bisporus pgkA gene
7213	20078	33491	1.92	2.7E-02	AA963571.1	EST_HUMAN	ol66f03.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3' contains Alu repetitive element;
8549	21630		1.36	2.7E-02	AI377036.1	EST_HUMAN	tc28g08.x1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3' contains Alu repetitive element;
8816	21895	35434	0.55	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
585	13776	26798	2.52	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1399	14553		0.89	2.6E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2439	15567	28684	2.5	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stratagene fetal retina 637202 Homo sapiens cDNA clone IMAGE:839595 3'
2441	15569	28696	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2441	15569	28697	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2982	16158		2.07	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5025	18154	31131	3.89	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5170	18298	31261	1.22	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5203	18324	31293	2.54	2.6E-02	AW241154.1	EST_HUMAN	aa52b04.x1 NCI_CGAP_Sark4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y0669_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
6011	19185		2.94	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6349	19519		6.85	2.6E-02	AI206030.1	EST_HUMAN	qq27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6555	19717	33063	2	2.6E-02	BE521748.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6960	20194	33619	0.83	2.6E-02	Z96064.1	NT	Vaccinia virus ORF1L, strain Wyeth

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6966	20194	33620	0.83	2.6E-02	Z99084.1	NT	Vaccinia virus ORF1L, strain Wyeth
7050	20103	33620	5.63	2.6E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7449	20528	33989	0.65	2.6E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
8703	21763	35316	0.73	2.6E-02	AA860946.1	EST_HUMAN	al22904.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9550	22702	36268	1.24	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9915	22955	36541	0.78	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9915	22955	36542	0.78	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10614	23648	37257	5.37	2.6E-02	AL193303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11670	24747	38547	1.59	2.6E-02	AA279351.1	EST_HUMAN	zs84c02.t1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
11861	24049	38547	1.35	2.6E-02	AW500547.1	EST_HUMAN	UHF-BN0-ak-6-10-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
12460	26150	31553	1.43	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCI CGAP Brn84 Homo sapiens cDNA clone IMAGE:4160944 5'
12583	25392		1.32	2.6E-02	11422936	NT	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
12947	25658		1.39	2.6E-02	R43678.1	EST_HUMAN	ys86f07.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22845 3' similar to contains DBR repetitive element;
545	13738	26762	1.75	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y5 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1657827 5'
545	13738	26763	1.75	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y5 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
832	14010	27068	9.54	2.5E-02	BE974314.1	EST_HUMAN	601860305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950666 3'
892	14058	27133	5.83	2.5E-02	BE974314.1	EST_HUMAN	601660305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950666 3'
2821	16935		2.53	2.5E-02	U12571.1	NT	Rattus norvegicus rapillin-3A mRNA, complete cds
3021	16197	29219	2.95	2.5E-02	X99597.1	NT	H. cartesia mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3021	16197	29220	2.95	2.5E-02	X99597.1	NT	H. cartesia mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4156	18488	30302	0.92	2.5E-02	BE701185.1	EST_HUMAN	PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA
4156	18488	30303	0.92	2.5E-02	BE701185.1	EST_HUMAN	PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA
4322	17486	30450	4.66	2.5E-02	AW592114.1	EST_HUMAN	hf36f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5530	19021	32327	0.72	2.5E-02	A1732776.1	EST_HUMAN	z83c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810354 3'
6322	19494		4.88	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.t1 L1 repetitive element;
6338	19508		3.72	2.5E-02	BE746888.1	EST_HUMAN	601575933F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6466	19633	32894	0.8	2.5E-02	L28028.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7843	20898	34400	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI CGAP Brn84 Homo sapiens cDNA clone IMAGE:4213408 5'
7843	20898	34401	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI CGAP Brn84 Homo sapiens cDNA clone IMAGE:4213408 5'
8008	21058	34570	0.64	2.5E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8167	21249	34768	0.5	2.5E-02	BE252469.1	EST_HUMAN	601108291F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5'
8025	22104	35845	0.92	2.5E-02	Q81713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9164	22242	35785	0.57	2.5E-02	AW025921.1	EST_HUMAN	wl08c10.x1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2616370 3'
10271	23306		0.63	2.5E-02	X71303.1	NT	D radicum 28S ribosomal RNA, DZ domain
10810	23843	37466	0.65	2.5E-02	A1147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1895982 3'
11048	24125	37759	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11048	24125	37760	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Ia alpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like
11120	24192		2.93	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
12065	25046		1.87	2.5E-02	AB007646.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA
12419	26072		2.17	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12621	25934		1.29	2.5E-02	11433220	NT	Dicystelium discoideum putative protein kinase MkcA (mkcA) gene, complete cds
12716	25476		1.83	2.5E-02	U60169.1	NT	601652355R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:2070166 3'
12760	25497	32032	1.58	2.5E-02	BE973327.1	EST_HUMAN	bt2607.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:2070166 3'
176	13401	28431	1.44	2.4E-02	A1378582.1	EST_HUMAN	y77611.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211149 5'
1628	14780	27865	1.89	2.4E-02	H65884.1	EST_HUMAN	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2102	16054	28363	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2102	16054	28364	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4488	17628	30609	1.69	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
6344	19514	32871	0.86	2.4E-02	W88680.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7370	20449	33912	1.2	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX.T, Human adult Rhadomyosarcoma cell-line Homo sapiens cDNA
7386	20464	33928	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7386	20464	33929	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8074	21168		0.75	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-h06 ST0186 Homo sapiens cDNA
8129	21211		0.57	2.4E-02	M16780.1	NT	Human retinoblastoma 3' long terminal repeat
8636	21716		0.57	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares_fetal_liver_spleen_1NfLS Homo sapiens cDNA clone IMAGE:233376 3' similar to contains Alu repetitive element; contains A3R repetitive element
8725	21808	35344	11.69	2.4E-02	N69442.1	EST_HUMAN	zh35g11.s1 Soares_fetal_liver_spleen_1NfLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gblK02909RATSR7K Rat (rRNA); contains A3R.b1 A3R repetitive element
9187	22265	35806	0.78	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
							Zu91c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb.i04422 ISLET
9211	22269	35831	0.81	2.4E-02	AA825660.1	EST_HUMAN	ANYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9893	22933	36516	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopter in synthase sulphurylase (cns6) gene, complete cds
9893	22933	36517	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopter in synthase sulphurylase (cns6) gene, complete cds
10011	23049	36643	2.76	2.4E-02	AF692854.1	EST_HUMAN	AV692854 GKC Homo sapiens cDNA clone GKDCSC03 5'
10186	23223	36817	2.82	2.4E-02	AA493894.1	EST_HUMAN	nt07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element;
10839	23872		0.6	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902 5'
11874	24862	38557	2.45	2.4E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11874	24862	38558	2.45	2.4E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12210	25163		3.98	2.4E-02	9627809	NT	Bacteriophage bil97, complete genome
12362	25260	32118	4.45	2.4E-02	6753635	NT	Mus musculus DhhB homolog 1 (E. coli) (Dhhb1), mRNA
12478	25330	32055	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12478	25330	32096	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12668	25445		10.87	2.4E-02	AB008569.1	NT	Ceenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12697	25464		1.28	2.4E-02	N42980.1	EST_HUMAN	y08a06.t1 Scarsa melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:270610 5'
12883	25900	31858	1.25	2.4E-02	AA179693.1	EST_HUMAN	zp13h01.t1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608361 5'
1921	15094		5.25	2.3E-02	W05340.1	EST_HUMAN	z884g08.t1 Scarsa_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289284 5'
1936	15079		16.26	2.3E-02	U94166.1	NT	4 Homo sapiens mammary tumor-associated protein INT 6 (INT6) gene, exon 4
2065	15205	28321	0.99	2.3E-02	AW797356.1	EST_HUMAN	CM2-UM0038-260400-172-b11 UM0038 Homo sapiens cDNA
2426	15554	28681	2.68	2.3E-02	Z74293.1	EST_HUMAN	S.cerevisiae chromosome IV reading frame ORF YDL245c
3773	16934	28940	7.02	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
3807	16987		0.67	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3'end
4267	17412	30398	1.17	2.3E-02	L24769.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4267	17412	30399	1.17	2.3E-02	L24769.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4540	17678	30660	1.08	2.3E-02	AW889107.1	EST_HUMAN	CM4-NN0080-290400-180-b04 NN0080 Homo sapiens cDNA
4571	17709	30689	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4571	17709	30690	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4572	18469	30691	1.2	2.3E-02	AW563693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	18469	30692	1.2	2.3E-02	AW593693.1	EST_HUMAN	xs26408.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4717	17852	30835	3.01	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3955386 5'
4717	17852	30836	3.01	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3955386 5'
5144	18267	31237	0.9	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-280100-011-a07 CN0051 Homo sapiens cDNA
5265	18384	31349	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5265	18384	31350	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5491	18690	31707	3.86	2.3E-02	U88303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6365	19535	32894	0.62	2.3E-02	BF108464.1	EST_HUMAN	601822921R1 NIH_MGC 77 Homo sapiens cDNA clone IMAGE:4042829 3'
6755	19911	33306	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7119	18545	31456	0.69	2.3E-02	BE141475.1	EST_HUMAN	MRO-HT0080-011089-002-c06 HT0080 Homo sapiens cDNA
7619	20669	34164	0.63	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8060	21143	34661	4.52	2.3E-02	U83610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8667	21747	35285	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8667	21747	35286	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8894	21973	35509	0.76	2.3E-02	AI695380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8894	21973	35510	0.76	2.3E-02	AI695380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9338	22414	35967	0.84	2.3E-02	P41966	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10063	23101	36704	0.94	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10236	23271	36862	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10236	23271	36863	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11022	24101	37739	2.38	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE)(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12338	25919		3.61	2.3E-02	BE278331.1	EST_HUMAN	601179958F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3546567 5'
12801	25535	32011	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181464 5'
12801	25535	32012	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181464 5'
12919	25604	31974	2.47	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12975	26195		1.88	2.3E-02	U11077.1	NT	Dicystostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
756	13937	26982	3.59	2.2E-02	AF018287.1	NT	Calumba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1786	14936		1.79	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1800	14949	28042	2.84	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1800	14949	28043	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2072	15212	28329	2.17	2.2E-02	Z82001.1	NT	S.pneumoniae popA gene and open reading frames
3521	16687		2.03	2.2E-02	AA577785.1	EST_HUMAN	nm24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3736	16897		4.09	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3956	17114	30110	0.98	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-803 BT0340 Homo sapiens cDNA
4028	17185	30185	0.99	2.2E-02	Z74288.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5177	18299	31262	1.37	2.2E-02	Z73997.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7396	20474	33941	3.43	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8666	21647	35188	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8568	21647	35189	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9009	22088	35830	0.82	2.2E-02	X79468.1	NT	P.vulgate alpha tub 2 mRNA
9856	22868	36478	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and Intron 5
9856	22868	36478	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and Intron 5
9888	22928	36511	2.73	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9888	22928	36512	2.73	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10409	23444		1.25	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12625	25421		6.8	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
432	13827		4.48	2.1E-02	AV781602.1	EST_HUMAN	AV781602 MDS Homo sapiens cDNA clone MDSADG01 5'
482	13857		6.62	2.1E-02	AF029728.1	NT	Dicystellum discoidium histidine kinase C (dhkC) mRNA, complete cds
1292	14448	27514	6.65	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), and spore coat protein CotM (cotM) genes, complete cds
1418	14571	27844	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1418	14571	27645	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1823	14972	28065	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28068	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28087	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2019	15159	28264	0.97	2.1E-02	AF190899.1	NT	Tegula aureolincta major aerosol protein precursor (TMAP) mRNA, complete cds
2062	15232	28354	1.16	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
2082	15232	28355	1.16	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
2877	13980	27032	3.12	2.1E-02	N28266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:284641 5'
3674	18837	29847	1.01	2.1E-02	AA461271.1	EST_HUMAN	z68b09.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4249	17395	30384	0.88	2.1E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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4427	17587	30549	0.89	2.1E-02	BF343655.1	EST_HUMAN	602015306F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151161 5'
4567	17706	30885	2.14	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, ospC and ospD genes, complete cds; and unknown genes
4577	17714	30888	1.64	2.1E-02	A1768127.1	EST_HUMAN	wg81d1.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4831	17964	30953	5.95	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4852	17985	30973	0.76	2.1E-02	AA685737.1	EST_HUMAN	ag55g12.a1 Gesler Wilms tumor Homo sapiens cDNA clone IMAGE:1128918 3'
4940	18070	31048	0.89	2.1E-02	A1823432.1	EST_HUMAN	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5315	18432	31402	0.91	2.1E-02	BF028405.1	EST_HUMAN	60167141F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954410 5'
5756	18948	32250	0.6	2.1E-02	AW379529.1	EST_HUMAN	CN4-HT0244-111199-040-h05 HT0244 Homo sapiens cDNA
7212	20077	33490	0.73	2.1E-02	BF088199.1	EST_HUMAN	QV3-GN0058-120900-328-a12 GN0058 Homo sapiens cDNA
8716	21796	35333	0.66	2.1E-02	9780238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9703	22752	36322	0.54	2.1E-02	AA984286.1	EST_HUMAN	am83e07.e1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MIER11 repetitive element;
9831	22871	36453	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 6-HT4 receptor gene, exons 2 to 5
9831	22871	36454	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10189	23226	36820	1.15	2.1E-02	L29324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
10266	23301	36899	0.75	2.1E-02	AA984286.1	EST_HUMAN	am83e07.e1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MIER11 repetitive element;
10856	23899	37508	0.49	2.1E-02	AP001519.1	NT	Bacillus halodurans genomic DNA, section 131.4
11787	24777	38474	1.48	2.1E-02	6754255	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp4a), mRNA
12063	25044	38752	1.42	2.1E-02	AW844320.1	EST_HUMAN	RC4-GN0050-130200-012-h04_1 GN0050 Homo sapiens cDNA
12602	18493		11.16	2.1E-02	Y19213.1	NT	Homo sapiens putative psinHbA pseudogene for hair keratin, exons 2 to 7
12647	25915	31862	1.22	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
13091	25712	31938	3.82	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds
19	13257	26257	1.28	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MIER1 13
20	13258	26258	14.95	2.0E-02	AW895605.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
269	13488	26518	5.03	2.0E-02	6753635	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
306	13622	26556	2.95	2.0E-02	AA456533.1	EST_HUMAN	art5b10.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
821	14000	27064	3.63	2.0E-02	6763635	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
1111	14276	27333	0.98	2.0E-02	AL098805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p36.33) of Homo sapiens
1226	14386	27448	0.91	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1226	14386	27449	0.91	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1922	15065	28168	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1922	15065	28169	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2859	15073		2.09	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3148	13257	26257	1.56	2.0E-02	BF002932.1	EST_HUMAN	Tg51c08.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309898 3' similar to contains MER1.3
3213	16387		1.13	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 9B
3298	16473		1.99	2.0E-02	AF085588.1	NT	(Sema6b), mRNA
4113	17267	30267	1.57	2.0E-02	M18095.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5219	18341		0.74	2.0E-02	A1271995.1	EST_HUMAN	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
6018	19201	32520	0.59	2.0E-02	L35321.2	NT	q183e03.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1866076 3'
7723	20787	34275	0.95	2.0E-02	AF000004.1	NT	Dictyostellium discoideum class VII unconventional myosin (myoI) gene, complete cds
7723	20787	34276	0.95	2.0E-02	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
10081	23119		2.39	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
10570	23605	37210	1.84	2.0E-02	A1640342.1	EST_HUMAN	Japanese encephalitis virus envelope protein mRNA, partial cds
10878	23954	37592	1.65	2.0E-02	Z73968.1	NT	wa17b02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
11653	24732	38423	1.91	2.0E-02	D88184.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11978	24963	38664	2.04	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxysteroid 17-20-lyase, complete cds
11978	24963	38665	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12149	18499	31535	1.8	2.0E-02	AA456538.1	EST_HUMAN	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12644	15973		2.26	2.0E-02	AL161532.2	NT	aat15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
13186	25771		5.63	2.0E-02	T80037.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
711	13893	26926	2.42	1.9E-02	AA572784.1	EST_HUMAN	y00409.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:24676 5'
2097	15237	28358	4.85	1.9E-02	AL163303.2	NT	repetitive element;
2097	15237	28359	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2870	15148	29164	9.15	1.9E-02	AA713856.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3018	16194	29217	1.92	1.9E-02	AV648668.1	EST_HUMAN	nm04105.e1 NCL_CGAP_SST1 Homo sapiens cDNA clone IMAGE:1298337 3'
3332	15505		0.72	1.9E-02	AB033611.1	NT	AV048668 GLC Homo sapiens cDNA clone GLCBLH07 3'
3699	16860		1.12	1.9E-02	IN52250.1	EST_HUMAN	Utricularia talpoides mitochondrial gene for cytochrome b, complete cds
3763	16954		8.1	1.9E-02	BE738098.1	EST_HUMAN	y228b02.s1 Soares_multilaple_sclerosis_2N1bMSP Homo sapiens cDNA clone IMAGE:284331 3'
3808	16986	29971	0.83	1.9E-02	A1301183.1	EST_HUMAN	601572692F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839864 5'
							qno14c07.x1 NCL_CGAP_P15 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4158	17309	30305	1.3	1.9E-02	AF141940.1	NT	Myoplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds
4310	17453	30440	1.58	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4310	17453	30441	1.58	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4663	17798	30785	2.79	1.9E-02	AI452899.1	EST_HUMAN	h46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5125	15701	28822	4.22	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5431	18631	31609	0.96	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5585	18780	31825	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
5908	19097		0.93	1.9E-02	AB019507.1	NT	Drosophila kanehol gene for glycerol-3-phosphate dehydrogenase, complete cds
7280	20333	33780	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7280	20333	33781	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8769	21848		1.33	1.9E-02	AI62754.2	NT	Neisseria meningitidis serogroup A strain Z2401 complete genome; segment 3/7
9532	22597	36169	1.21	1.9E-02	BF316128.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9814	22854	36540	0.67	1.9E-02	L10114.1	NT	Nocdiana tabacum type II phytochrome (phyB) gene, complete cds
10251	23285	36882	1.24	1.9E-02	BF956832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10468	23493	37104	0.67	1.9E-02	DB4001.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644784
11021	24100	37738	1.91	1.9E-02	AF008938.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12372	25924	31865	4.41	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gillardin mRNA, complete cds
13006	25980		1.46	1.9E-02	L11068.1	NT	Candida albicans lambda Csa3/B fragment
356	13657	26595	1.67	1.8E-02	AW771104.1	EST_HUMAN	h52a06.x1 NCL_CGAP_Col17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER28 repetitive element;
703	13886	26918	1.81	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139883 5'
1180	14348	27406	1.43	1.8E-02	X17694.1	NT	H. fransisci mRNA for myelin basic protein (MBP)
1467	14621	27704	1.35	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encode (enc) mRNA, complete cds
2743	16960	28972	1.74	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 528 of the complete genome
3282	16456		0.94	1.8E-02	AI805829.1	EST_HUMAN	h52a06.x1 Soares_NFL_T_9BC_S1 Homo sapiens cDNA clone IMAGE:2090298 3'
3993	17160	30156	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3993	17160	30157	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4197	17347		1.01	1.8E-02	AA861446.1	EST_HUMAN	ak2404.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:14068935 3'
4500	17688	30669	1.52	1.8E-02	AW86563.1	EST_HUMAN	OV4.D10021-301269-071-b11 DT0021 Homo sapiens cDNA
5060	18197	31171	2.02	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
6949	20262	33700	4.44	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7624	20894	34170	2.3	1.8E-02	BF125690.1	EST_HUMAN	601783288F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
7650	20894	34170	0.61	1.8E-02	BF125690.1	EST_HUMAN	601783288F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8322	21404	34931	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8663	21743	35283	0.46	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-158-H09 NN1073 Homo sapiens cDNA
8710	21790	35326	0.76	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
8683	22742	36311	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
8693	22742	36312	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9842	22882		2.23	1.8E-02	AA887543.1	EST_HUMAN	aj2209.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);
10268	23303	36900	1.7	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866963 5'
10431	23466	37072	1.29	1.8E-02	X96933.1	NT	L. signals mRNA for myomodulin neuropeptide precursor
11721	23907	37530	1.76	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11721	23907	37531	1.76	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11912	24899	38002	1.55	1.8E-02	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1465000 nt, position (87)
11926	24912	38913	2.45	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
13096	25894		1.78	1.8E-02	AF202180.1	NT	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
929	14104	27167	1.34	1.7E-02	BE394869.1	EST_HUMAN	601310828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1831	14979	28075	2.12	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element;
1831	14979	28076	2.12	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element;
1920	15063		2.85	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2181	15316		13.13	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitogen-activated protein kinase 29, complete cds
2705	15823		1.36	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3062	16238	29259	0.89	1.7E-02	A1147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3602	16766		4.64	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCL_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
3716	16877		0.93	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4284	17428		1.23	1.7E-02	AA668618.1	EST_HUMAN	ec18f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4317	17460		2.02	1.7E-02	R02506.1	EST_HUMAN	y886108.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4576	17713	30697	0.74	1.7E-02	A1305279.1	EST_HUMAN	qm08g07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1831276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4649	17785	30768	1.32	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4836	17969	30957	1.91	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4834	18064		5.98	1.7E-02	AI015076.1	EST_HUMAN	ov51e02.s1 Scarses_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1640858 3'
6253	19427	32773	1.69	1.7E-02	AI769247.1	EST_HUMAN	wg38f09.x1 Scarses_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element:
6709	19867	33256	1.23	1.7E-02	AI038280.1	EST_HUMAN	cy85h03.x1 Scarses_fetal_liver_spleen_INFUS_S1 Homo sapiens cDNA clone IMAGE:1872661 3'
7195	20060	33471	1.28	1.7E-02	AF190330.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7353	20432	33994	1.9	1.7E-02	8400716	NT	Homo sapiens ribulose (NEB), mRNA
7513	20587	34060	1.08	1.7E-02	L07898.1	NT	Human apolipoprotein (a) gene, exon 1
7513	20587	34061	1.08	1.7E-02	L07898.1	NT	Human apolipoprotein (a) gene, exon 1
7921	20972		1.71	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-30
9636	21079	34591	0.89	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9000	22940	36526	1.28	1.7E-02	AL040354.1	EST_HUMAN	DKFZp4340314_r1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp4340314 5'
12093	25073	38780	1.66	1.7E-02	5802007	NT	Homo sapiens serum constituent protein (MSE56), mRNA
12891	26111	31967	2.35	1.7E-02	AW903482.1	EST_HUMAN	OM4-NN1030-040400-130-105 NN1030 Homo sapiens cDNA
13166	25757	31928	1.46	1.7E-02	AA846926.1	EST_HUMAN	oe08d04.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1 repetitive element:
524	13717		4.05	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1699	14841	27926	1.37	1.6E-02	Y18889.1	NT	Tetrahymena mallophilum flab2, flab3 and flid genes for flagellin subunit proteins and CAP protein homologue
2323	15455	28939	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2323	15455	28987	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2631	15754	28869	0.97	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ1 gene
2708	15826	28941	1.75	1.6E-02	AA484872.1	EST_HUMAN	ne81d08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910687
2769	15975		1.01	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3614	16778	29793	5.33	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-069-C07 CT0219 Homo sapiens cDNA
4291	17436		1.95	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4415	17556	30543	2.04	1.6E-02	AW875407.1	EST_HUMAN	QV2-P10012-140100-030-407 P10012 Homo sapiens cDNA
5367	18570	31438	0.59	1.6E-02	AJ281385.1	EST_HUMAN	qu42b09.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967417 3'
5741	18934	32234	1.42	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6780	19935	33331	2.16	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7071	20124	33339	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7071	20124	33540	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7888	20940	34446	0.96	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	21394	34919	0.74	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8372	21453		3.37	1.6E-02	X05151.1	NT	Human apoC-II gene for prelipoprotein C-II
10246	23281		2.97	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10633	23667	37276	1.61	1.6E-02	AA572818.1	EST_HUMAN	nt19g03.s1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. [1]
10633	23667	37277	1.61	1.6E-02	AA572818.1	EST_HUMAN	nt19g03.s1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. [1]
11149	25968	37948	2.9	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LEI0260 (=T10111))
11488	24547	38219	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	24547	38220	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11801	24791	38488	2.16	1.6E-02	A1873558.1	EST_HUMAN	q289e10.x1 Soares pregnant uterus Nb2HP Homo sapiens cDNA clone IMAGE:2042442 3'
12348	15455	28588	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12348	15455	28587	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
770	13951		9.38	1.6E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2209	15343	28469	3.58	1.6E-02	N39621.1	EST_HUMAN	y27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243926 3'
2244	15377	28505	1.6	1.6E-02	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
3128	16304	29317	1.04	1.6E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3128	16304	29318	1.04	1.6E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3818	16978	29982	1.14	1.6E-02	BF092942.1	EST_HUMAN	MR4-TN0115-060600-201-b12 TN0115 Homo sapiens cDNA
4590	17727	30710	0.72	1.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6423	19592	32957	2.07	1.6E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7472	20547		1.69	1.6E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7561	20633	34108	1.57	1.6E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8058	21141	34680	1.38	1.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8065	21147	34688	3.06	1.6E-02	11417739	NT	Homo sapiens valyl-RNA synthetase 2 (VARS2), mRNA
9030	22109	35650	1.42	1.6E-02	BF345584.1	EST_HUMAN	602018135F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154504 5'
9668	22630		0.99	1.6E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9770	22766	36337	1.59	1.6E-02	D44608.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10016	23054	36649	1.3	1.6E-02	R32687.1	EST_HUMAN	y454b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10016	23054	36650	1.3	1.6E-02	R32687.1	EST_HUMAN	y454b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10860	23693	37514	0.46	1.6E-02	T92196.1	EST_HUMAN	yel710.s1 Stratiagene lung (#937210) Homo sapiens cDNA clone IMAGE:118027 3'
11056	24133		1.78	1.6E-02	D26547.1	NT	Rice gene for thiredoxin h, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11442	24503	38171	2.21	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12576	25970		2.38	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0048-140100-011-c11 CN0049 Homo sapiens cDNA
430	13625		1.54	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1142	14307	27363	3.81	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC61225), mRNA
1285	14441		2.12	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1326	14483		2.49	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
3284	16458	29478	1.83	1.4E-02	AF160869.2	NT	Blifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds
3485	16553	29658	1.23	1.4E-02	AW074212.1	EST_HUMAN	xb08d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783 3'
3573	16738	29753	6.9	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3573	16738	29754	6.9	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3608	16772	29787	0.75	1.4E-02	4503828	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3746	16907	29911	12.14	1.4E-02	6898918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4612	17749	30729	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG Homo sapiens cDNA
4612	17749	30730	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG Homo sapiens cDNA
4908	18127	31102	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4908	18127	31103	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5911	26210		0.74	1.4E-02	X91338.1	NT	H. sapiens LeISS-B pseudogene 3
6545	19707	33083	4.52	1.4E-02	AA559030.1	EST_HUMAN	m11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1028980 3' similar to contains Alu repetitive element;
6545	19707	33084	4.52	1.4E-02	AA559030.1	EST_HUMAN	m11c04.e1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1028980 3' similar to contains Alu repetitive element;
8333	21416		1.55	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9089	22178	36722	1.44	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9366	22431	35889	1.41	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9600	22655	36227	1.66	1.4E-02	BE644561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10780	23813		0.89	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
12268	25194	38358	8.95	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12840	25430		1.84	1.4E-02	AF324885.1	NT	Arabidopsis thaliana F21J02 mRNA, complete cds
12959	25625		1.45	1.4E-02	11428968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
13075	25704		1.51	1.4E-02	AF238059.2	NT	Rheum x cultum NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1913	15056		1.19	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 6'
2010	15150	28254	2.13	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2512	15638	28759	0.98	1.3E-02	AE002445.1	NT	Neisseria meningitidis serogroup B strain MC58 section 87 of 206 of the complete genome
3285	16459	29479	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3285	16459	29480	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
4076	17232		1.22	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5275	18394		3.02	1.3E-02	D26547.1	NT	Rice gene for thioesterase h, complete cds
5360	18563	31478	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 82, mmx28orf
5360	18563	31479	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 82, mmx28orf
6293	19466	32819	1.2	1.3E-02	U60017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6327	19499	32856	1.05	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7101	18528	31481	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7101	18528	31482	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7752	20812	34303	4.9	1.3E-02	A031593.1	EST_HUMAN	ex06g05.x1 Soarea_papilloma_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1846072 3' similar to contains Alu repetitive element
8678	21768	35284	1.67	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10411	23446	37051	1.89	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10485	23520	37129	0.95	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
11239	24308	37944	3.35	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soarea_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11239	24308	37945	3.35	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soarea_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12645	26127		1.7	1.3E-02	Z89117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12753	25499		2.56	1.3E-02	9633069	NT	Human herpesvirus 8B, complete genome
12965	25885		30.16	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
219	13441		0.82	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, PP2, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
366	13675	26606	4.38	1.2E-02	AA059298.1	EST_HUMAN	zf65g01.r1 Soarea retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
465	13660	26698	1.43	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
767	13938	26983	2.67	1.2E-02	A1183522.1	EST_HUMAN	qd68e12.x1 Soarea_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 repetitive element;
2246	15379	28507	2.03	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2514	15540	28762	1.02	1.2E-02	AW172350.1	EST_HUMAN	x337c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2701	15640	28762	1.43	1.2E-02	AW172350.1	EST_HUMAN	x337c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3170	16346		7.3	1.2E-02	AA075418.1	EST_HUMAN	zn188c03.t1 Stratiogene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:646020 5'
3359	16531	29545	2.05	1.2E-02	R62805.1	EST_HUMAN	y111b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3362	16534	29548	0.69	1.2E-02	A1668694.1	EST_HUMAN	zb66a07.x8 Soares_fetal_lung_NbHL-19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
5035	18163	31139	2.02	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP13) gene, complete cds
5154	18278		1.97	1.2E-02	AB019766.1	NT	Cynops pyrrhogaster CplJbq1 mRNA, partial cds
5195	18317	31286	1.31	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5871	19051	32368	1.78	1.2E-02	D78989.1	NT	Rana rugosa mRNA for calcitriol, complete cds
6243	19417	32765	0.72	1.2E-02	AF045555.1	NT	Homo sapiens wbcrl (WBCRL1) and wbcrl5 (WBCRL5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7147	20282	33724	8.67	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7443	20520	33993	1.42	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7465	20540	34014	8.54	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC08 5'
7726	20791	34280	0.66	1.2E-02	BF216650.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095233 5'
8186	21208	34792	2.3	1.2E-02	Q11206	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT 4-B)
8321	21403	34929	0.56	1.2E-02	R68831.1	EST_HUMAN	y43706.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8321	21403	34930	0.56	1.2E-02	R68831.1	EST_HUMAN	y43706.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8386	21467	34993	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8386	21467	34994	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9091	22170		1	1.2E-02	T76987.1	EST_HUMAN	y172c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
9639	22878	36461	2.54	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9872	22912	36497	1.24	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12757	25986		1.16	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
12974	26634		6.24	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-557/006 5'
1298	14454	27520	1.22	1.1E-02	AA070364.1	EST_HUMAN	zn188c11.s1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1743	14892	27986	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1743	14892	27987	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2098	15236	28357	5.35	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCL CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153808 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2942	16119		5.31	1.1E-02	N99523.1	EST_HUMAN	zr40c05.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:295040 5'
3612	16776	26792	3.59	1.1E-02	AI653508.1	EST_HUMAN	iq55b10.r1 NCI CGAP OV23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPX_HUMAN
4222	17370		0.68	1.1E-02	AW813798.1	EST_HUMAN	Q92989 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL:
4951	18081	31057	1.27	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-q11 ST0197 Homo sapiens cDNA
							DKFZ588E0924 s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZ588E0924
6277	19451	32800	0.89	1.1E-02	U68480.1	NT	Bacillus subtilis SpoVK (spoVK), YnaA (ynaA), YnaB (ynbB), GhrR (ghrR), glutamine synthetase (ghsA), YnaA (ynaA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), xylan beta-1,4-xylosyl
7773	20830	34321	2.19	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-018-h07 HT0256 Homo sapiens cDNA
7999	21039	34551	1.25	1.1E-02	8631294	NT	Melanopus sanguinipes entomopoxvirus, complete genome
8451	21532	35061	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8451	21532	35062	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8841	21920	35458	0.69	1.1E-02	AW998160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0046 Homo sapiens cDNA
9022	22101	35641	0.7	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakemura) Homo sapiens cDNA clone 3NHC4040
9103	22182	35727	7.44	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10133	23171	36769	2.02	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10298	23334	36939	4.06	1.1E-02	AA314865.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
11224	24263	37934	2.41	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
12195	25152		4.01	1.1E-02	AA668239.1	EST_HUMAN	ab77711.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:653005 3' similar to contains
7	13245	26247	8.82	1.0E-02	AW846120.1	EST_HUMAN	Alu repetitive element
1552	14705	27785	0.97	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111099-003-s10 CT0176 Homo sapiens cDNA
2638	15701		1.71	1.0E-02	AA806389.1	EST_HUMAN	GM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3159	16334	29344	2.88	1.0E-02	BE835556.1	EST_HUMAN	cc22h08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350496 3'
3336	16506	29525	1.24	1.0E-02	BE988996.1	EST_HUMAN	RCO-FN0025-250500-021-402 FN0025 Homo sapiens cDNA
3598	16792		0.7	1.0E-02	AW846021.1	EST_HUMAN	60184987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3986	17143	30148	0.85	1.0E-02	AI065086.1	EST_HUMAN	MR0-CT0060-081099-003-H10 CT0060 Homo sapiens cDNA
4002	17159	30185	0.59	1.0E-02	AL163302.2	NT	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4899	18028	31017	5	1.0E-02	6753521	NT	Homo sapiens chromosome 21 segment HS21C102
4899	18098	31074	4.14	1.0E-02	R96557.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
5116	18243	31208	0.83	1.0E-02	AL181593.2	NT	yq54h01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:199633 5'
5242	18364	31332	1.96	1.0E-02	P06599	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5532	18729	31745	0.81	1.0E-02	H62681.1	EST_HUMAN	EXTENSIN PRECURSOR
							yu36h11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5865	19055	32362	0.66	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-A To4 (Nfatc4) gene, exons 1 and 2
8242	19418	32764	1.28	1.0E-02	AF257903.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6310	19432	32836	2.78	1.0E-02	AW577113.1	EST_HUMAN	MP4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6310	19482	32837	2.78	1.0E-02	AW577113.1	EST_HUMAN	MP4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6901	20216	33646	1.69	1.0E-02	Z29842.1	NT	Z.mays U3snRNA pseudogene
6963	22048	36219	6.34	1.0E-02	BF036331.1	EST_HUMAN	601469570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
6963	22848	36220	6.34	1.0E-02	BF036331.1	EST_HUMAN	601469570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11542	24598		2.12	1.0E-02	AF157559.1	NT	Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11573	24628		1.7	1.0E-02	AI417961.1	EST_HUMAN	tg55h07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:U15183_cds1
11648	24728	38420	1.85	1.0E-02	AV760016.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5 repetitive element
12278	26206		1.76	1.0E-02	CB2203	SWISSPROT	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12339	26941	31762	3.68	1.0E-02	AW635521.1	EST_HUMAN	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12355	28002		4.31	1.0E-02	S70330.1	NT	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12794	25974		1.4	1.0E-02	AJ278605.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12949	26060		2.91	1.0E-02	X62854.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
816	14061	27156	5.69	9.0E-03	AI796128.1	EST_HUMAN	Hi.sapiens gene for Me491/CD63 antigen
1293	14449		1.66	9.0E-03	BE781889.1	EST_HUMAN	WH42009.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:23883433 3' similar to contains element MER22 MER22 repetitive element
2469	15596	28721	2.84	9.0E-03	AL161569.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3879346 5'
2971	16147	29165	0.81	9.0E-03	AI251744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2971	16147	29166	0.81	9.0E-03	AI251744.1	EST_HUMAN	qh6009.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3768	16919	29921	0.66	9.0E-03	J05184.1	NT	qh9009.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5931	19117		1.19	9.0E-03	AI809792.1	EST_HUMAN	S.acidocalcisarius thermopsis gene, complete cds
6786	19922		4.01	9.0E-03	BE746988.1	EST_HUMAN	W77704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2381631 3'
7823	20893	34169	0.61	9.0E-03	AI24219.1	EST_HUMAN	60157343BF1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834762 5'
7840	20709	34186	0.91	9.0E-03	8922570	NT	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
8059	21142		0.8	9.0E-03	AL039991.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8443	21524		0.54	9.0E-03	AF223391.1	NT	DKFZp334L0412_r1 494 (synonym: hies3) Homo sapiens cDNA clone DKFZp334L0412 5'
10050	23088	36690	0.54	9.0E-03	P26011	SWISSPROT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10068	23104	36707	1.47	9.0E-03	P29008	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
							COLLAGEN ALPHA 1(V) CHAIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11232	24301		1.88	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11951	24937	38638	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11951	24937	38639	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12494	26208		2.07	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-c09 HT0452 Homo sapiens cDNA
12722	26200		37.58	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12838	25558	32016	1.21	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
13074	25703		17.6	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-c09 HT0452 Homo sapiens cDNA
514	13708		3.15	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pinea_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains
1013	14185	27246	12.69	8.0E-03	AF106856.1	NT	Alu repetitive element
2226	15360	28489	1.87	8.0E-03	AL163263.2	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2817	15741	28953	3.05	8.0E-03	P10268	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
3442	16610	28628	1.02	8.0E-03	AJ131016.1	NT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3766	16927	29930	1.81	8.0E-03	P32644	SWISSPROT	Homo sapiens SCL gene locus
3766	16927	29931	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4372	17515	30495	1.15	8.0E-03	BE840049.1	EST_HUMAN	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4502	17642	30827	5.73	8.0E-03	BF363327.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4839	17872	30961	0.63	8.0E-03	P03181	SWISSPROT	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
4839	17872	30962	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5271	18390	31358	0.94	8.0E-03	AU140261.1	EST_HUMAN	HYPOTHETICAL BHLF1 PROTEIN
5640	18834	31911	2.8	8.0E-03	AF110520.1	NT	ALU40261 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
6328	25823	32857	1.27	8.0E-03	AP000002.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lipasin, RalGDS-like, KE2, BINCA4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6889	20041	33450	4.4	8.0E-03	P55577	SWISSPROT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt position (2/7)
7069	20112		1.06	8.0E-03	V01109.1	NT	PROBABLE PEPTIDASE Y4NA
7357	20436	33808	1.43	8.0E-03	M17197.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7714	20778		1.8	8.0E-03	AB03287.1	NT	A.californica (marine gastropod mollusc) neurotrophin gene (bag cell), exon 1, 5' end
9084	22163	35707	0.84	8.0E-03	P98180	SWISSPROT	Turcopsis truncatus mRNA for p40-phox, complete cds
9111	22160	35734	3.53	8.0E-03	AW80892.1	EST_HUMAN	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9180	22258	35801	0.86	8.0E-03	9789898	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
10154	23191		4.75	8.0E-03	BE086509.1	EST_HUMAN	MR1-ST0111-111198-011-H06 ST0111 Homo sapiens cDNA
							Mus musculus fusion 2 (human) (Fus2), mRNA
							QV1-BT0877-04000-131-g03 BT0877 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11005	24084	37721	2.01	8.0E-03	BE788441.1	EST_HUMAN	601478619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
11231	24300		2.79	8.0E-03	Z49552.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11663	24742	38433	1.39	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11663	24742	38434	1.39	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12015	24989	38701	4.37	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C7) gene, complete cds
12205	25159		1.89	8.0E-03	M69035.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
12252	25191		7.14	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
13145	25939		1.16	8.0E-03	AI277806.1	EST_HUMAN	qim65c08.x1 Soares_placenta_81c9weeks_2NbHP81c9W Homo sapiens cDNA clone IMAGE:1882762 3'
712	13894	26930	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
712	13894	26931	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
998	14170	27231	3.28	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1140	14305	27361	3.55	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1395	14549		1.03	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/PH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1426	14590	27653	3.39	7.0E-03	AA868298.1	EST_HUMAN	ab78009.s1 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853145 3'
1532	14685	27764	3.28	7.0E-03	AW303599.1	EST_HUMAN	xx21502.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2332	16060	28598	2	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2695	15815		0.98	7.0E-03	AW772132.1	EST_HUMAN	hm97n07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032083 3' similar to contains Alu repetitive element;
3648	16811	29824	0.65	7.0E-03	AI150273.1	EST_HUMAN	qf34f02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751953 3'
3863	17023	30022	0.71	7.0E-03	AW444463.1	EST_HUMAN	UJ-H-B13-ekb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
3914	17073	30071	1.13	7.0E-03	AF198344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4128	17023	30022	0.77	7.0E-03	AW444463.1	EST_HUMAN	UJ-H-B13-ekb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4721	17856		0.98	7.0E-03	AW630898.1	EST_HUMAN	hm89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968936 5'
5103	18231		6.54	7.0E-03	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078
5940	19126		0.72	7.0E-03	H71106.1	EST_HUMAN	yf82g01.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);
6238	25821		4.42	7.0E-03	AW861059.1	EST_HUMAN	RC1-CT0286-030400-018-c08 CT0286 Homo sapiens cDNA
6444	19611	32874	1.67	7.0E-03	W68251.1	EST_HUMAN	z63310.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
6667	19826	33213	2.92	7.0E-03	AA327129.1	EST_HUMAN	EST10674 Colon 1 Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6695	19853	33243	1.05	7.0E-03	BE857385.1	EST_HUMAN	7q34p10.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7228	20133	33550	1.93	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.2 TAR1 repetitive element;
7089	20754	34238	4.76	7.0E-03	Z35938.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7089	20754	34239	4.76	7.0E-03	Z35938.1	NT	S. cerevisiae chromosome II reading frame ORF_YBL077w
8031	21114	34632	0.59	7.0E-03	AJ228043.1	NT	S. cerevisiae chromosome II reading frame ORF_YBL077w
8031	21114	34633	0.59	7.0E-03	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8302	21394	34905	2.48	7.0E-03	BE175687.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8813	21892	35433	0.58	7.0E-03	AF281074.1	NT	RC3-H10582-160300-011-D02 HT0582 Homo sapiens cDNA
9597	22652		0.64	7.0E-03	AF111168.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
							Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
							y49c10.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9794	22834	36414	0.68	7.0E-03	N92378.1	EST_HUMAN	Alu repetitive element;
9921	22961	36548	2.72	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9921	22961	36549	2.72	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10513	23548		1.34	7.0E-03	AV687379.1	EST_HUMAN	AV687379 GK6 Homo sapiens cDNA clone GKCAFC07 5'
10704	23737		0.82	7.0E-03	AJ769734.1	EST_HUMAN	wc37609.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2320840 3'
10800	23833	37456	0.47	7.0E-03	BE154643.1	EST_HUMAN	PM3-H10344-181189-002-g06 HT0344 Homo sapiens cDNA
11065	24141	37776	2.41	7.0E-03	AB008852.1	NT	Bos taurus mRNA for NDP52, complete cds
11140	24212	37838	1.55	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC3B gene, exon 1-29
11140	24212	37839	1.55	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC3B gene, exon 1-29
							Homo sapiens fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12792	26189		1.95	7.0E-03	H94065.1	EST_HUMAN	y16h01.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:3160476 5'
12800	25534		1.46	7.0E-03	BE26253.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
12808	25601		1.76	7.0E-03	Y17455.1	NT	Homo sapiens LSFR2 gene, penultimate exon
13058	26188		1.68	7.0E-03	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
							h422a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
1289	14427	27494	8.76	6.0E-03	AW511148.1	EST_HUMAN	SW:PXR_HUMAN 074469 ORPHAN NUCLEAR RECEPTOR PXR;
1289	14427	27495	8.76	6.0E-03	AW511148.1	EST_HUMAN	h422a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2831	15045	26054	0.94	6.0E-03	AF112374.1	NT	SW:PXR_HUMAN 074469 ORPHAN NUCLEAR RECEPTOR PXR;
2956	18133	28147	3.28	6.0E-03	AA759135.1	EST_HUMAN	h422a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2956	18133	28148	3.28	6.0E-03	AA759135.1	EST_HUMAN	SW:PXR_HUMAN 074469 ORPHAN NUCLEAR RECEPTOR PXR;
							Danio rerio odorant receptor gene cluster
							ah78a11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78a11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3318	16491		2.27	6.0E-03	H75690.1	EST_HUMAN	y77h04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3378	16550		0.63	6.0E-03	AF190338.1	NT	Ndancus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3469	16636	28655	1.25	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isolectin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3469	16636	28656	1.25	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isolectin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3636	16800		1.11	6.0E-03	W37695.1	EST_HUMAN	zrl3a11.1 Scarsa parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3750	16911	28914	3.73	6.0E-03	BF510986.1	EST_HUMAN	U1H-B14-epm-c-06-0.U1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3877	17036	30034	1.31	6.0E-03	8754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
4032	17188	30189	0.6	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240899-021-b10 CT0204 Homo sapiens cDNA
4067	17223		1.28	6.0E-03	BE280108.1	EST_HUMAN	800842904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859813 5'
4484	17624		1.54	6.0E-03	A016835.1	EST_HUMAN	ov33c11.x1 Scarsa testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4817	17950	30835	7.9	6.0E-03	AA324242.1	EST_HUMAN	ES9727118 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5305	18422	31392	0.8	6.0E-03	AA889972.1	EST_HUMAN	sg55g09.s1 Scarsa parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404268 3'
6281	25822	32803	0.68	6.0E-03	9627521	NT	Varidola virus, complete genome
6956	20289	33707	0.8	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6904	18513	31505	0.97	6.0E-03	BE283748.1	EST_HUMAN	801112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7399	20477	33944	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7399	20477	33945	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7824	20878	34980	0.8	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
8042	21125	34846	6.71	6.0E-03	A033980.1	EST_HUMAN	ov13a04.x1 Scarsa parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element
8161	21243	34763	2.76	6.0E-03	AW799337.1	EST_HUMAN	RC0-JM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8236	21318		1.65	6.0E-03	BF038188.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3658626 5'
9754	22692	36262	7.03	6.0E-03	D10548.1	NT	Subcutaneous sclerosing panniculitis (SSPE) virus mRNA for fusion protein
10249	23284		2.49	6.0E-03	A1432661.1	EST_HUMAN	t22a02.x1 NCJ_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10365	23400	37011	0.75	6.0E-03	AJ017849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ; Bacillus subtilis fmd gene
10503	23538		0.91	6.0E-03	AF084555.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete ccs
10515	23649	37258	0.64	6.0E-03	X68396.1	NT	M thermophilicum complete plasmid pFV1 DNA
10681	23685		0.54	6.0E-03	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
10983	24062	37687	1.56	6.0E-03	AW082164.1	EST_HUMAN	EST1374237 MAGE sequences, MAGG Homo sapiens cDNA
11049	24129		1.94	6.0E-03	11545814	NT	Homo sapiens hypochlorite zinc finger protein FLJ14011 (FLJ14011), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11226	24297		4.1	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11226	24298	37638	2.66	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3839747 5'
12321	25232		2.04	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12425	25988		1.3	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4292212 5'
12451	25928		4.65	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450286 (section 39 of 148) of the complete genome
12532	25993		2.49	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12590	25357		1.63	6.0E-03	Q62209	SWISSPROT	SYNAPTOMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12944	26622		2.41	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
13095	26018		1.61	6.0E-03	X74807.1	NT	R. norvegicus VEGP2 gene
13147	26746		1.19	6.0E-03	BF102988.1	EST_HUMAN	7336511.x1 NCI_QGAP_Lu24 Homo sapiens cDNA clone IMAGE:356564 3'
686	13871	26903	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and gprE-like protein, complete cds
686	13871	26904	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and gprE-like protein, complete cds
687	13871	26903	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and gprE-like protein, complete cds
687	13871	26904	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and gprE-like protein, complete cds
1136	14301	27357	1.47	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
1601	14754		1.08	5.0E-03	AI138977.1	EST_HUMAN	q778d05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2746	15863	28974	2.43	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
3206	16381	28392	3.87	5.0E-03	T87623.1	EST_HUMAN	y81109.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3223	16397		2.72	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3235	16409	29423	1.17	5.0E-03	R71794.1	EST_HUMAN	y85g02.s1 Soares breast 2NBHst Homo sapiens cDNA clone IMAGE:155666 3'
3351	16523		0.84	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0861 gene
3790	18951	29957	5.28	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 peritricin-binding protein 1B (porB) gene, complete cds
3854	17014	30014	0.81	5.0E-03	U36914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4079	17235		1.84	5.0E-03	AA289675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4241	17387	30374	0.85	5.0E-03	AJ002125.1	NT	Matrix domestica Zk type gene
4421	17562	30546	0.71	5.0E-03	H78355.1	EST_HUMAN	yU79g10.r1 Soares fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:240068 5'
4423	17014	30014	0.76	5.0E-03	U36914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4731	17866	30848	0.92	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4841	17974	30864	1.56	5.0E-03	AF52367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5286	18405		1.9	5.0E-03	4768747	NT	Homo sapiens myosin-binding protein C, fast-type (MYBPC2) mRNA
5916	19104	32417	5.4	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6169	19346	32691	2.82	5.0E-03	O00507	SWISSPROT	
6204	19379		0.88	5.0E-03	AE002234.2	NT	Chlamydia pneumoniae AR39, section 62 of 64 of the complete genome
6726	19882		7.34	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6888	18505	31520	7.22	5.0E-03	AB026024.1	NT	Mus musculus AVID1 gene for S-adenosylmethionine decarboxylase, complete cds
7185	20050		0.85	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7237	20321	33765	0.61	5.0E-03	6753651	NT	Mus musculus dynein, exon, heavy chain 11 (Dnaho11), mRNA
							EST103012 Fetal brain, Stragene (cat#836206) Homo sapiens cDNA clone HFBOR93 similar to EST
7654	20722	34198	0.7	5.0E-03	T05124.1	EST_HUMAN	containing Alu repeat
7774	20831		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-03T099-011-f07 CT0255 Homo sapiens cDNA
7944	20994	34505	7.18	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8415	21496	35027	0.81	5.0E-03	AW85907.1	EST_HUMAN	RC5-CT0281-08T109-011-A05 CT0281 Homo sapiens cDNA
8415	21498	35028	0.81	5.0E-03	AW85907.1	EST_HUMAN	RC5-CT0281-08T109-011-A05 CT0281 Homo sapiens cDNA
8433	21514	35045	1.89	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8811	21890		5.83	5.0E-03	M81132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
9007	22086	35629	1.21	5.0E-03	D60723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
9140	22219	35763	0.52	5.0E-03	M25080.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10044	23082	36664	1.03	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
10176	23213	36805	0.74	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10360	23395	37006	0.66	5.0E-03	AA53143.1	EST_HUMAN	U45H10.51 NCI CGAP_P18 Homo sapiens cDNA clone IMAGE:995587
10539	23574	37181	0.47	5.0E-03	7682567	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10696	23729		0.47	5.0E-03	AA653261.1	EST_HUMAN	ag48ct0.61 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
10959	24040		4.79	5.0E-03	T19586.1	EST_HUMAN	594F Heart Homo sapiens cDNA clone 604
							xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to
11181	24250	37884	2.39	5.0E-03	AW170334.1	EST_HUMAN	contains L1.12.L1 repetitive element;
11181	24250	37885	2.39	5.0E-03	AW170334.1	EST_HUMAN	xn59g06.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to
11297	24363	38004	1.76	5.0E-03	T49153.1	EST_HUMAN	contains L1.12.L1 repetitive element;
							yp09e04.r1 Stragene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11615	24666		3.41	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291622 5'
12070	25051	38759	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12070	25051	38760	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12467	26144		11.08	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12616	25414		21.79	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12718	25478		2.03	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12760	25504		1.94	5.0E-03	AA465597.1	EST_HUMAN	SW:DXA2_MOUSE P14885 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12802	25935		5.99	5.0E-03	BF57232.1	EST_HUMAN	z675a03.s1 Scarses ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:809548 3' similar to
13002	25651	31951	2.66	5.0E-03	AW449109.1	EST_HUMAN	602077774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
242	13464	26493	1.54	4.0E-03	AW500196.1	EST_HUMAN	U1H-B18-4d4-08-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
331	13545	26475	1.75	4.0E-03	R45482.1	EST_HUMAN	U1HF-BN0-akc-t-04-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
456	13651	26689	1.56	4.0E-03	P54875	SWISSPROT	Y551e04.s1 Scarses infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
616	13805	26828	4.37	4.0E-03	AA939339.1	EST_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PI3K)
900	14075	27142	1.65	4.0E-03	R46482.1	EST_HUMAN	cn75g12.s1 Scarses infant brain 1N1B Homo sapiens cDNA clone IMAGE:1562568 3'
934	14109		2.85	4.0E-03	AW749101.1	EST_HUMAN	Y551e04.s1 Scarses infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
1174	14337	27393	34.06	4.0E-03	AA098777.1	EST_HUMAN	RC8-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1196	14368	27417	1.83	4.0E-03	AW784740.1	EST_HUMAN	z181e08.r1 Stralagene colon (#837204) Homo sapiens cDNA clone IMAGE:510998 5'
1331	14488	27566	1.48	4.0E-03	AA284374.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1783	14932	28026	2.68	4.0E-03	U33472.1	NT	z559a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
2075	15215	28334	17.33	4.0E-03	AA088777.1	EST_HUMAN	Rattus norvegicus type 1 astrocyte and oligodendrocyte associated protein AT1-46 mRNA, complete cds
2321	15453		2.06	4.0E-03	BE410556.1	EST_HUMAN	z181e08.r1 Stralagene colon (#837204) Homo sapiens cDNA clone IMAGE:510998 5'
2352	15483	28616	1.53	4.0E-03	AW794740.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2639	15762	28876	1.96	4.0E-03	U92111.2	NT	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2639	15762	28876	1.96	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2755	15872	28980	2.97	4.0E-03	AJ277365.1	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2755	15872	28981	2.97	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2761	15977	28984	0.97	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3297	16471	29491	1.08	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3297	16471	28482	1.09	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-008 HT0340 Homo sapiens cDNA
3619	16783	29798	0.83	4.0E-03	AW188426.1	EST_HUMAN	X88104.x1 NCI CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2865279 3'
3619	16783	29798	0.83	4.0E-03	AW188426.1	EST_HUMAN	X88104.x1 NCI CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2865279 3'
3714	16875	29880	0.84	4.0E-03	Q13608	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4021	16875	29880	0.85	4.0E-03	Q13608	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4040	17196	30207	0.72	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4102	17256		2.18	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5339	18452	31420	0.98	4.0E-03	AW50547.1	EST_HUMAN	U1HF-BND-ak-e-10-Q-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077468 5'
5390	18592	31564	1.58	4.0E-03	AF005889.1	NT	Drosophila melanogaster anion2D7 (anon2D7) mRNA, complete cds
5815	18713	31726	27.24	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5914	19102	32418	3.1	4.0E-03	P04186	SWISSPROT	(UPRG)
5918	19106	32418	1.8	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
6003	19188	32507	0.8	4.0E-03	AL133871.1	EST_HUMAN	DKFZ7611014.1 r1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 5'
6209	19384		4.18	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6363	19533	32892	0.97	4.0E-03	AW590572.1	EST_HUMAN	Ig48c07.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2848652 3'
8439	19806	32909	1.78	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
8609	19863	33367	1.07	4.0E-03	AA813222.1	EST_HUMAN	g32711.s1 Soares_Iedle_NHT Homo sapiens cDNA clone 1382045 3'
8914	20229	33682	1.41	4.0E-03	U78408.1	NT	Lycopersicon esculentum knotted 3 protein (TKn3) mRNA, complete cds
7217	20082	33495	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7217	20082	33498	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7348	20428	33989	3.73	4.0E-03	C02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7589	20680	34136	0.98	4.0E-03	AI681483.1	EST_HUMAN	t37g12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7591	20682	34138	0.62	4.0E-03	BE670170.1	EST_HUMAN	7c31b02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7693	20758		0.85	4.0E-03	X92109.1	NT	H. sapiens hcgIX gene
8128	21210	34731	0.57	4.0E-03	Q8TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS6) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8238	21320	34838	4.51	4.0E-03	AF111944.1	NT	Dibutyryl adenosine 3',5'-bisphosphate (DBP) development protein DG1122 (DG1122) gene, partial cds
8398	21479	35008	2	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8655	21745	35284	0.67	4.0E-03	AF139827.1	NT	Plasmodium falciparum replication factor C subunit 1 (rfc1) gene, complete cds
8761	21840	35381	0.51	4.0E-03	Y12855.1	NT	Homo sapiens P2X7 gene, exon 12 and 13
8911	21980	35529	7.06	4.0E-03	AI555983.1	EST_HUMAN	ts49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
9090	22189		3.24	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9100	22179	35723	3.76	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9825	22855	36447	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9825	22855	36448	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10131	23159	36766	0.63	4.0E-03	H30664.1	EST_HUMAN	yp42g12.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
10587	23622	37228	1.35	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11283	24349	37866	1.36	4.0E-03	4759101	NT	Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8) mRNA
11394	24455	38117	5	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
12072	25053	38762	1.57	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12434	26163		5.84	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180800-002-508 BN0138 Homo sapiens cDNA
12457	25321		1.35	4.0E-03	BE298280.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028096 5'
12541	25367		1.85	4.0E-03	AW604273.1	EST_HUMAN	U1HF-BNO-4ip-8-04-0-JUL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080522 5'
12814	25543		3.33	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element/contains element MER31 repetitive element
12856	26053		2.18	4.0E-03	AW614596.1	EST_HUMAN	h102c07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR6 repetitive element
12871	25581		1.34	4.0E-03	AW619141.1	EST_HUMAN	RC3-ST0281-240400-015-003 ST0281 Homo sapiens cDNA
13202	25784	31918	1.23	4.0E-03	11436955	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
382	13590	26826	1.25	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
602	14077	27143	4.87	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1694	14846	27630	9.65	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:762984 similar to contains Alu repetitive element
2367	15496		6.37	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triphosphate isomerase
2368	15498	28624	1.14	3.0E-03	U46858.1	NT	Mus musculus intestinal trefol factor gene, partial cds
2368	15498	28625	1.14	3.0E-03	U46858.1	NT	Mus musculus intestinal trefol factor gene, partial cds
3056	16232		0.77	3.0E-03	Y08006.1	NT	Arabidopsis thaliana rpoMt gene
3152	16327	29338	3.55	3.0E-03	BE379296.1	EST_HUMAN	601237882F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3009933 5'
3220	16394	29405	2.53	3.0E-03	AW602687.1	EST_HUMAN	IL2-JM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3504	16671	29681	2.16	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3513	16679		7.5	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4086	17241	30248	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4086	17241	30249	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4147	17299	30291	1.87	3.0E-03	AI792278.1	EST_HUMAN	ar04f09.y6 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4515	17654	30642	5.53	3.0E-03	AJ011432.1	NT	Rattus norvegicus gntf gene
4641	17777	30759	4.82	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4858	17991	30978	0.99	3.0E-03	AL119067.1	EST_HUMAN	DKFZp761B0712.1 1761 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu
4955	18085	31061	2.05	3.0E-03	A1732754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:3853483 5'
4978	18107	31083	5.53	3.0E-03	BE787946.1	EST_HUMAN	repetitive element
5255	18375	31341	0.9	3.0E-03	4508414	NT	601482715F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3853483 5'
5255	18375	31342	0.9	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
							Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
							qes0b10.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745275 3' similar to
							SW:AP17_MOUSE Q00380 CLATHRIN COAT ASSEMBLY PROTEIN AP17; contains MSR1.2 MER22
5262	18381	31347	1.75	3.0E-03	A1193860.1	EST_HUMAN	repetitive element
5380	18582	31451	3.36	3.0E-03	8022499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5673	18867	32153	1.09	3.0E-03	AJ249881.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5744	18937	32237	0.83	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-
6683	19841	33231	9.72	3.0E-03	AA456701.1	EST_HUMAN	Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
7168	20301	33744	0.75	3.0E-03	D37977.1	NT	aa1310.1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7354	20433	33895	1.38	3.0E-03	AJ011419.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7691	20756	34241	3.71	3.0E-03	AB021736.1	NT	Kluyveromyces marxianus pcp3 gene for purine-cytosine permease
8124	21206	34727	0.9	3.0E-03	BF333058.1	EST_HUMAN	Oryza sativa gene for bZIP protein, complete cds
8350	21431	34955	1.4	3.0E-03	N82580.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8490	21571	35108	0.47	3.0E-03	A1866028.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8510	21591		0.63	3.0E-03	M63468.1	NT	zbt7b04.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8655	21735	35276	1.34	3.0E-03	P51989	SWISSPROT	w124d09.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2428841 3'
8679	21759	35295	1.5	3.0E-03	AL163268.2	NT	S_cerevisiae UGA35 gene, complete cds
8786	21885		1.45	3.0E-03	Q8QM81	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
9192	22270		10.8	3.0E-03	AW513774.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
9245	22322	35868	4.28	3.0E-03	AL161589.2	NT	NONSTRUCTURAL PROTEIN V
							repetitive element
							Arabis thaliana DNA chromosome 4, contig fragment No. 85
9289	22345	35898	0.96	3.0E-03	A1018731.1	EST_HUMAN	ov03d12.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:XS7138_maf
9280	22356	35906	0.53	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN)
9609	22864		0.78	3.0E-03	D90901.1	NT	602035680.F1 NCL CGAP_Bn04 Homo sapiens cDNA clone IMAGE:4183838 5'
9646	21089	34804	0.77	3.0E-03	BE154670.1	EST_HUMAN	Synedocystis sp. PGC8803 complete genome, 3/27, 271600-402289
9836	22876		0.56	3.0E-03	P03356	SWISSPROT	PM3-HT0344-071289-003-d07 HT0344 Homo sapiens cDNA
							POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9908	22948		6.51	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
10096	23137	36738	2.31	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10200	23237	36827	1.44	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10344	23379	36990	3.89	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
11085	24159		2.67	3.0E-03	5603028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11458	20756	34241	1.45	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11722	23908	37532	1.47	3.0E-03	P22531	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11732	23918	37543	1.9	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11770	24762	38457	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11770	24762	38458	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11849	24838	38532	1.36	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12077	25057		1.46	3.0E-03	AW294812.1	EST_HUMAN	U1H-B12-ah1-06-0-J1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
12199	25948		1.62	3.0E-03	AI525056.1	EST_HUMAN	primase-5.E07.1 bvtumor Homo sapiens cDNA 5'
12235	25179	38346	1.24	3.0E-03	AA893184.1	EST_HUMAN	alpha7b10.s1 Soares, total, fetus, N62HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER28 repetitive element;
12296	26090		1.78	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12481	25333	32057	1.23	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
528	13721	26746	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
528	13721	26747	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
808	16023		11.88	2.0E-03	T70874.1	EST_HUMAN	Human alpha-2-plasmin inhibitor gene, exon 8 and 7
1394	14548	27624	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exon 8 and 7
1397	14581	27626	1.42	2.0E-03	AA681605.1	EST_HUMAN	nu86101.s1 NCI_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1217593
1406	14680	27634	20.85	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1519	14672	27754	1.1	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1546	14698	27776	2.26	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1546	14698	27777	2.26	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1621	14773		6.17	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1811	14960	28053	1.27	2.0E-03	AA450139.1	EST_HUMAN	zxd2a10.r1 Soares, total, fetus, N62HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1928	15071		1.09	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT10183-061099-018-d03 HT10183 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2051	15192	28305	1.59	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2324	15458	28588	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2647	15770		4.93	2.0E-03	AY137782.1	EST_HUMAN	U1H-B11-adj-g-10-Q-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3503	16670	29680	4.92	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares_t01a1 Nb2Hf8_gw Homo sapiens cDNA clone IMAGE:789114 5'
3510	16676	29688	0.98	2.0E-03	BF588955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3756	16917	29919	5.48	2.0E-03	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
4062	17218	30226	0.92	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4229	17379	30364	2.39	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN[CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP36]
4290	17435	30423	1.02	2.0E-03	AA179693.1	EST_HUMAN	z013M01.r1 Stralagane fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
4336	17479		13.93	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4632	17670		1.99	2.0E-03	L35079.1	NT	Parine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4547	17686		1.22	2.0E-03	AW297390.1	EST_HUMAN	U1H-BW0-adj-g-03-Q-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2730413 3'
4551	17699	30870	1.05	2.0E-03	A1064748.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4668	17803	30760	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4668	17803	30791	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4828	17961	30949	1.02	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4832	17965		1.57	2.0E-03	R87773.1	EST_HUMAN	y045ec2.s1 Soares adult brain N2b-4H65Y Homo sapiens cDNA clone IMAGE:180890 3'
4962	18091	31067	1.07	2.0E-03	P11000	SWISSPROT	WALL-ASSOCIATED PROTEIN PRECURSOR
5132	18257	31223	0.84	2.0E-03	AF003328.1	NT	Homo sapiens X-linked arylsulfolipid ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5604	18799	31849	1.57	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4104692 5'
5745	18970	32238	1.83	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5826	19019	32325	2.08	2.0E-03	U63711.1	NT	Xenopus laevis xefillin mRNA, complete cds
6236	19411	32758	3.93	2.0E-03	P29477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6236	19411	32759	3.93	2.0E-03	P29477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6476	19643	33004	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6476	19643	33005	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6476	19645	33007	7.65	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121403 5'
6514	19679	33049	2.18	2.0E-03	Q9UKP4	SWISSPROT	ADAMTS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6515	19680	33050	0.75	2.0E-03	AV709075.1	EST_HUMAN	AV709075 AOC Homo sapiens cDNA clone ADCAEF09 5'
6544	19706	33082	1.45	2.0E-03	X84451.1	NT	L-eculium mRNA for lysyl-tRNA synthetase (LysRS)

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6736	19892			2.0E-03	AI991089.1	EST_HUMAN	w36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW_RL29_HUMAN P47914.60S RIBOSOMAL PROTEIN L29 ; contains element MSRT1 repetitive element ;
6775	19930	33326	1.36	0.7	2.0E-03 AA677631.1	EST_HUMAN	213a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430682 3'
7098	18625	31517	1.35	2.0E-03	AB038502.1	NT	Ceanorhabditis elegans mRNA for galestin LEC-11, complete cds
7231	20136	33554	3.3	2.0E-03	BE087986.1	EST_HUMAN	GM4-BT0366-061289-054-401 BT0368 Homo sapiens cDNA
7294	20376	33833	0.65	2.0E-03	AI298883.1	EST_HUMAN	pr98411.x1 NCI_QGAP_Lu6 Homo sapiens cDNA clone IMAGE:1896885 3'
7444	20521	33994	0.8	2.0E-03	T86669.1	EST_HUMAN	y477g10.r1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:114306 5'
7794	20860	34342	1.41	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
							h37606.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60978
8241	21323	34840	2.97	2.0E-03	AW692004.1	EST_HUMAN	Q60978.JERKY. ;
8412	21493	35023	5.49	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares_melanocyte_2NbhM_Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1 b2 L1 repetitive element ;
8412	21493	35024	5.49	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares_melanocyte_2NbhM_Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1 b2 L1 repetitive element ;
8459	21540	35069	0.64	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME I
8481	21562	35087	1.09	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8536	21617	35153	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8536	21617	35154	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8561	21642	35181	1.03	2.0E-03	AU136678.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8614	21694		0.9	2.0E-03	AJ400877.1	NT	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
8396	19018	32323	0.79	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
8396	19018	32324	0.79	2.0E-03	AW798111.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9441	22515	36079	1.07	2.0E-03	AF224698.1	NT	y985a08.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194286 3'
9726	22791	36392	0.71	2.0E-03	H60832.1	EST_HUMAN	y985a08.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194286 3'
9726	22791	36393	0.71	2.0E-03	H60832.1	EST_HUMAN	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9758	22696	36284	3.33	2.0E-03	P24821	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22808	36493	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22808	36494	1.22	2.0E-03	P48982	SWISSPROT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9924	22984	36552	0.6	2.0E-03	AJ087732.1	NT	

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9824	22984	36553	0.6	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10119	23157	36755	0.96	2.0E-03	AW884299.1	EST_HUMAN	QV3-OT0084-060400-144-e01 OT0084 Homo sapiens cDNA
10248	23283		6.26	2.0E-03	AA251376.1	EST_HUMAN	zai0a08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684764 3'
10628	23662	37270	0.49	2.0E-03	BF367386.1	EST_HUMAN	MR2-GN0030-140800-001-e05 GN0030 Homo sapiens cDNA
11265	24334		2.14	2.0E-03	M86824.1	NT	Human dyctrophin gene
11778	20850	34342	3.79	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11836	24825		2.36	2.0E-03	BF330909.1	EST_HUMAN	RC5-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11844	24833	38528	9.64	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12180	25140		3.37	2.0E-03	AI625745.1	EST_HUMAN	ly65h03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
12198	25155	38833	4.31	2.0E-03	AF157516.2	NT	Q25632 VACUOLAR ATP SYNTHASE SUBUNIT G ;
12222	25171	38838	1.71	2.0E-03	A1084325.1	EST_HUMAN	Homo sapiens SEL1L (SEL1L) gene, partial cds
12245	18497		4.86	2.0E-03	AJ245167.1	NT	cy43g06.s1 Soares_parenchymal tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to
12462	26140		4	2.0E-03	AV697968.1	EST_HUMAN	TR.PP7535 P97535 PS-PLA1 PRECURSOR ;
12581	25383	32039	1.29	2.0E-03	Y00508.1	NT	Camelus dromedarius cvnp19 gene for immunoglobulin heavy chain variable region
							AV697968 GKC Homo sapiens cDNA clone GKCX005 5'
							H. sapiens M1 gene for muscarinic acetylcholine receptor
12897	25594		1.38	2.0E-03	AF129766.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b,
13090	25927		2.46	2.0E-03	AV697968.1	EST_HUMAN	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
452	13648	26684	1.38	1.0E-03	H98471.1	EST_HUMAN	AV697968 GKC Homo sapiens cDNA clone GKCX005 5'
852	14029	27091	1.55	1.0E-03	A1720283.1	EST_HUMAN	y08c08.t1 Soares_pituitary_gland_NbHPG Homo sapiens cDNA clone IMAGE:232334 5'
							as70b08.x1 Barelead colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
852	14029	27092	1.55	1.0E-03	A1720283.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN ENOYL-COA HYDRATASE ;
1119	14284	27339	2.61	1.0E-03	A1865788.1	EST_HUMAN	as70b08.x1 Barelead colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1139	14304	27360	1.61	1.0E-03	A1864572.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN ENOYL-COA HYDRATASE ;
							w083e10.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422268 3'
1192	14354	27412	0.85	1.0E-03	A1892616.1	EST_HUMAN	w083e10.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2551242 3'
2084	15224	28348	3.42	1.0E-03	P47808	SWISSPROT	w083e10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2339440 3' similar to contains Alu
2222	15356	28483	9.52	1.0E-03	AJ131016.1	NT	repetitive element;
3044	16220	29241	1.37	1.0E-03	AB033117.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMYMI)
3280	16434	29451	2.81	1.0E-03	P18915	SWISSPROT	Homo sapiens SCL gene locus
							Homo sapiens mRNA for KIAA1291 protein, partial cds
							CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED
							CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3260	16434	29452	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3374	16546	29560	0.75	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3632	16798	29813	0.94	1.0E-03	U88061.1	NT	Human MUC2 gene, promoter region
3632	16798	29814	0.94	1.0E-03	U88061.1	NT	Human MUC2 gene, promoter region
3755	16916		1.43	1.0E-03	A8044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4034	17180	30200	0.98	1.0E-03	AW170552.1	EST_HUMAN	contains TAR1.11 TAR1 repetitive element;
4044	17200	30211	0.91	1.0E-03	Z49649.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
4656	17694	30673	2.34	1.0E-03	BE939182.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4598	17735	30715	4.89	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4785	17920	30908	0.81	1.0E-03	U28449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4945	18075	31050	2.54	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4945	18075	31051	2.54	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4946	18076		6	1.0E-03	BE164087.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5188	18310	31276	15.5	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5324	18437	31407	4.73	1.0E-03	BE219340.1	EST_HUMAN	h51802.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176955 3'
5423	18624	31600	2	1.0E-03	AA280951.1	EST_HUMAN	z944801.t1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5518	18716	31730	3.57	1.0E-03	AJ063345.1	NT	Homo sapiens KVLQ1 gene
5572	18768	31809	1.54	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5572	18768	31810	1.94	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5680	18884	32176	0.95	1.0E-03	BE708491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5696	18890	32181	1.77	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5751	18943	32244	0.8	1.0E-03	N41874.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MIER8 repetitive element;
5751	18943	32245	0.8	1.0E-03	N41874.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MIER8 repetitive element;
6033	19216		0.58	1.0E-03	BF541639.1	EST_HUMAN	60208902F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068807 5'
6144	19322		2.75	1.0E-03	X07899.1	NT	Mouse nucleolin gene
6184	19360	32708	0.85	1.0E-03	BE96939.2	EST_HUMAN	601637516T1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3875693 3'
6321	19493		8.77	1.0E-03	11626176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6464	19531	32992	1.11	1.0E-03	T87791.1	EST_HUMAN	y893a11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:115772 5'
6539	19702		1.68	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g06 NN1024 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6895	20046	33455	1.41	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric and
7302	20384	33843	2.81	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7656	20724		1.12	1.0E-03	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7817	20872	34370	1.88	1.0E-03	U52111.2	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7895	20937	34443	3.44	1.0E-03	M63376.1	NT	601491081F1 NIH_MGC 89 Homo sapiens cDNA clone IMAGE:3893278 5'
7934	20984	34492	0.79	1.0E-03	BE880044.1	EST_HUMAN	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8073	21155	34674	0.86	1.0E-03	AF274581.1	NT	Homo sapiens partial steerin-1 gene
8136	21218	34739	5.02	1.0E-03	AJ251973.1	NT	2487609.e1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1, L1 L1 repetitive element;
8337	21418	34941	1.95	1.0E-03	AA122770.1	EST_HUMAN	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8438	21519	35048	2.35	1.0E-03	AF153980.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8625	21705	35241	0.75	1.0E-03	U29397.1	NT	V. carter gene encoding volvoxapain
9144	22223		1.48	1.0E-03	Y11204.1	NT	GM3-LT0078-170200-092-e07 LT0078 Homo sapiens cDNA
9170	22248	35791	0.65	1.0E-03	AW840353.1	EST_HUMAN	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9281	22557		0.65	1.0E-03	U52111.2	NT	Human class III alcohol dehydrogenase (ADH5) c1 subunit mRNA, complete cds
9319	22395	35947	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) c1 subunit mRNA, complete cds
9319	22395	35948	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) c1 subunit mRNA, complete cds
9796	22836		0.47	1.0E-03	A1247482.1	EST_HUMAN	gbM87388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9807	22847	36424	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9807	22847	36425	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
10025	23063	36660	0.88	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10366	23401	37012	9.37	1.0E-03	AF003528.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
10372	23407		0.75	1.0E-03	AF097485.1	NT	Homo sapiens traneduch beta-like 2 (TBL2) gene, complete cds
10522	23557	37165	1.08	1.0E-03	A1024350.1	EST_HUMAN	ov7508.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643176 3' similar to contains MER39.b1
10823	23856	37478	0.5	1.0E-03	AE004782.1	NT	MER39 MER39 repetitive element;
10823	23856	37479	0.5	1.0E-03	AE004782.1	NT	Pseudomonas aeruginosa PAO1, section 323 of 529 of the complete genome
10823	23856	37479	0.5	1.0E-03	AE004782.1	NT	Pseudomonas aeruginosa PAO1, section 323 of 529 of the complete genome

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10830	23863		0.53	1.0E-03	AA706202.1	ag33112.s1 Strategene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element;
10802	23986	37617	2.01	1.0E-03	AW362393.1	RC1-CT0279-181089-011-a08 CT0279 Homo sapiens cDNA
10902	23986	37618	2.01	1.0E-03	AW362393.1	RC1-CT0279-181089-011-a09 CT0279 Homo sapiens cDNA
10988	24068	37702	2.46	1.0E-03	BE170859.1	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11062	24138		2.03	1.0E-03	AF583847.1	tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26185 Q26185 PVA1 GENE.;
11425	24486		2.63	1.0E-03	AV759949.1	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11858	24846	38543	2.17	1.0E-03	P23468	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11858	24846	38544	2.17	1.0E-03	P23468	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11824	24910	38611	1.53	1.0E-03	P13002	PROTEIN GRANY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
11824	24910	38612	1.53	1.0E-03	P13002	(TRANSCRIPTION FACTOR NTF-1)
12176	25136	38831	5.51	1.0E-03	BE894488.1	PROTEIN GRANY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
12678	26118		7.37	1.0E-03	AI347355.1	(TRANSCRIPTION FACTOR NTF-1)
12812	26142	31551	3.83	1.0E-03	BE780572.1	PROTEIN GRANY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
12889	25580		1.17	1.0E-03	11465934	601488878F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
5327	18440	31408	0.7	9.0E-04	P08548	601488878F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
5799	18989		2.08	9.0E-04	P06727	601488878F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3872035 5'
6388	19537		0.59	9.0E-04	AJ006346.1	Nicotiana tabacum chloroplast, complete genome
6615	19775	33166	1.27	9.0E-04	P02381	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9843	22883		1.46	9.0E-04	AB037203.1	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1517	14670		1.07	8.0E-04	X06469.1	Homo sapiens KVLQ1 gene
4296	17439		4.4	8.0E-04	P08547	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
4887	18017	31002	2.5	8.0E-04	U29185.1	Glycyrhiza glabra GgbA51 mRNA for beta-amylin synthase, complete cds
11412	24473		2.59	8.0E-04	AA777084.1	X. laevis mRNA for C4SR protein
11576	24631		1.87	8.0E-04	AI571098.1	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1874	15018	28127	1.11	7.0E-04	U29185.1	Homo sapiens prion protein (PrP) gene, complete cds
2472	15599	28724	1.45	7.0E-04	U29185.1	Homo sapiens prion protein (PrP) gene, complete cds
2778	15894	29004	1.33	7.0E-04	AL163210.2	Homo sapiens chromosome 21 segment HS21C010
3353	18526	29540	1.4	7.0E-04	4885170	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

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6221	18396	32745	0.93	7.0E-04	AA516212.1	EST_HUMAN	ng5g12.s1 NCI_CGAP_L1p2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 repetitive element;
6642	19801		2.33	7.0E-04	A1768331.1	EST_HUMAN	wg35109.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7376	20455		0.72	7.0E-04	AK024446.1	NT	Homo sapiens mRNA for FLJ00335 protein, partial cds
10008	23046	36839	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10008	23046	36840	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11865	24853		1.7	7.0E-04	U78027.1	NT	Homo sapiens Bruto's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11893	24881	38578	3.76	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12723	25481		9.28	7.0E-04	BE077941.1	EST_HUMAN	GM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
13001	25650		2.68	7.0E-04	R17336.1	EST_HUMAN	yg13c06.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5'
13038	25682		5.43	7.0E-04	8005835	NT	Homo sapiens Ratina-derived POU-domain factor-1 (RPE-1), mRNA
2760	15876		0.97	6.0E-04	BF341380.1	EST_HUMAN	002013339F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4149397 5'
4069	17225	30232	1.64	6.0E-04	A1862525.1	EST_HUMAN	w115a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402878 3'
4201	17350	30341	0.63	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4201	17350	30342	0.65	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4301	17444	30430	3.91	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4665	17703	30683	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
4665	17703	30684	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
8050	21133		4.58	6.0E-04	P48408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
8205	21287		0.51	6.0E-04	H92947.1	EST_HUMAN	y84c11.s1 Soares_pined_gland_N8HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element;
10185	23222		3.26	6.0E-04	AL048507.2	EST_HUMAN	DKFZp386M2024.t1 588 (synonym: huter) Homo sapiens cDNA clone DKFZp386M2024
10215	23251		0.53	6.0E-04	A1856296.1	EST_HUMAN	w135g02.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426930 3'
10285	23320	36922	2.29	6.0E-04	BE003850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10547	23582		0.84	6.0E-04	AF287478.1	NT	Lylechirus variegatus embryonic blastocoele extracellular matrix protein precursor (ECM3) mRNA, complete cds
11774	24766	38462	2.07	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11866	24854	38549	2.47	6.0E-04	AW013847.1	EST_HUMAN	U1H-B10-aab-e-09-0-J.1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11937	24823		1.62	6.0E-04	Q01788	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
12363	26007		3.31	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261189-012-008 HT0269 Homo sapiens cDNA
13226	25797		14.14	6.0E-04	A1817088.1	EST_HUMAN	w176g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;
668	13854	28882	7.86	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 28.3 KD PROTEIN (ORF92)

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1531	14884		2.03	5.0E-04	AW861844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3500	16667	29677	1.6	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3809	16969	29972	0.84	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5589	18784	31830	2.51	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6765	19921	33317	7.06	5.0E-04	AA166080.1	EST_HUMAN	z033508.t1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:589663 5'
7534	20607	34082	9.01	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
8143	21225	34745	5.58	5.0E-04	A1188882.1	EST_HUMAN	qd1306.x1 Soares_placenta_806weeks_2NbpHP869W Homo sapiens cDNA clone IMAGE:1723618 3' similar to gp-X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element
8498	21579	35116	0.95	5.0E-04	AA814519.1	EST_HUMAN	cb96602.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element
9477	22534	36098	1.67	5.0E-04	AA846545.1	EST_HUMAN	af59103.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1984357 3'
9571	22713	36281	0.59	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9718	22763	36354	0.84	6.0E-04	P28126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9809	22849	36428	4.78	5.0E-04	AW270538.1	EST_HUMAN	xe00602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768886 3'
10484	23519		0.6	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
11220	24269		1.9	5.0E-04	ALD48607.2	EST_HUMAN	DKFZp566M2024_r1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp566M2024
12012	18784	31830	15	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12301	25936		2.39	5.0E-04	AA569513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:913875
12872	25961		1.33	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
403	13600		0.75	4.0E-04	BF241482.1	EST_HUMAN	60187653.4F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4104897 5'
690	13874	26907	1.36	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
870	14046	27111	1.55	4.0E-04	A1720263.1	EST_HUMAN	as70508.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
870	14046	27112	1.55	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
1493	14946	27728	5.59	4.0E-04	AW763356.1	EST_HUMAN	as70508.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2148	15284	28410	1.87	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2202	15337		1.1	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
							DKFZp434D059_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D059 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2691	15811	28927	2.04	4.0E-04	Q96615	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3233	19407	29420	2.78	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3397	16597	29583	0.69	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
3443	16611	29629	0.6	4.0E-04	AV696624.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN ENJOY-1 COA HYDROLASE ;
4443	17583	30561	3.24	4.0E-04	AA576331.1	EST_HUMAN	AV696624 GKC Homo sapiens cDNA clone GKCFFH07 5'
4443	17583	30562	3.24	4.0E-04	AA576331.1	EST_HUMAN	nt10a10.st NCI CGAP Co1 Homo sapiens cDNA clone IMAGE:961830 3' similar to gb:M21121 T-CELL
4859	17795	30781	2.33	4.0E-04	AA088324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5199	18320	31289	3.62	4.0E-04	BE560660.1	EST_HUMAN	nt10a10.st NCI CGAP Co1 Homo sapiens cDNA clone IMAGE:961830 3' similar to gb:M21121 T-CELL
7418	20486	33965	1.55	4.0E-04	P48442	SWISSPROT	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
7705	20770	34456	0.89	4.0E-04	AL161566.2	NT	2n61.c08.st1 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:3678910 5'
7896	20948	34456	0.8	4.0E-04	AU122079.1	EST_HUMAN	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
8733	21813	35348	3.64	4.0E-04	BF240712.1	EST_HUMAN	CALCIUM-SENSING RECEPTOR
8741	21820	35354	1.68	4.0E-04	N25507.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8892	22932	36519	3.37	4.0E-04	AI025699.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001820 5'
10045	23083		1.12	4.0E-04	AF022655.1	NT	60187685F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4059700 5'
12691	25908		1.96	4.0E-04	AF254822.1	NT	yx39a12.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:264142 5'
180	13385	26415	3.21	3.0E-04	AL119426.1	EST_HUMAN	ov87h03.st1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
200	13423	26454	1.7	3.0E-04	P49259	SWISSPROT	Mus musculus neuropilin-2(alt17) mRNA, alternatively spliced, complete cds
803	14078	27144	1.63	3.0E-04	U83991.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
1886	15030	28137	1.7	3.0E-04	AI282100.1	EST_HUMAN	DKFZ761J221.1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZ761J221.1 5'
1901	15044		0.97	3.0E-04	AI398674.1	EST_HUMAN	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
3383	16554	29668	4.35	3.0E-04	P28147	SWISSPROT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
4071	17227	30234	4.64	3.0E-04	P49448	SWISSPROT	qz28a03.y1 NCI CGAP K1d11 Homo sapiens cDNA clone IMAGE:2028107 5'
4167	17317		1.38	3.0E-04	AJ271735.1	NT	nt23a02.x1 NCI CGAP P228 Homo sapiens cDNA clone IMAGE:2119082 3'
4205	17354		1.06	3.0E-04	BE140809.1	EST_HUMAN	INTERNALIN B PRECURSOR
4635	17771		1.16	3.0E-04	BE148546.1	EST_HUMAN	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4937	18067		5.2	3.0E-04	BE153778.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
5004	18133	31107	0.65	3.0E-04	AW937723.1	EST_HUMAN	RC0-HT0014-310599-028 HT0014 Homo sapiens cDNA
8271	19445		5.58	3.0E-04	AL163281.2	NT	MFO-HT0241-030200-008-e01 HT0241 Homo sapiens cDNA
6959	20187	33611	1.54	3.0E-04	AL163279.2	NT	PMD-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
							QV3-DT0045-221289-046-d09 DT0043 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C081
							Homo sapiens chromosome 21 segment HS21C078

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	18556	31471	0.67	3.0E-04	AW953981.1	EST_HUMAN	RC4-NN0027-060400-011-b08 NN0027 Homo sapiens cDNA
7765	20824	34316	0.73	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8454	21535	35065	2.16	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10124	23182	36760	1.26	3.0E-04	A4454055.1	EST_HUMAN	zx4808.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:765471 5' similar to gb:M62762
10381	23416	37025	0.46	3.0E-04	A1892139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); w756t11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10676	23710	37318	1.96	3.0E-04	AA781201.1	EST_HUMAN	el24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513276 3' RIBOSOMAL PROTEIN L7A (HUMAN); nc38e04.r1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L12 L1 repetitive element;
12249	26164	31655	2.39	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
12646	25987	31769	2.54	3.0E-04	AB018392.1	NT	DKFZp447L185_r1 847 (synonym: hibr1) Homo sapiens cDNA clone DKFZp447L185 5'
13114	25727		4.81	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
180	13403	26432	1.33	2.0E-04	AF217796.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
491	13668	26719	2.67	2.0E-04	AU146707.1	EST_HUMAN	Human dystrophin gene
930	14105	27168	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
930	14105	27169	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
1206	14368		2.78	2.0E-04	A1286021.1	EST_HUMAN	qH88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1213	14374		2.6	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1879	15023		1.71	2.0E-04	AF224288.1	NT	Mus musculus 5' flanking region of Ptx3 gene
2257	15390		1.21	2.0E-04	AA478980.1	EST_HUMAN	z339505.c1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2641	15764	28878	0.42	2.0E-04	U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
3052	16228	29248	1.23	2.0E-04	A1124628.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3415	16584	29600	0.82	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3622	16688	29697	2.96	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
4022	17178	30187	0.98	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE reassurances, MAGP Homo sapiens cDNA
4261	17406		5.5	2.0E-04	U01028.1	NT	Phasodul vulgaris nitrate reductase (PVNR2) gene, complete cds
4781	17926	30914	1.76	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4791	17926	30915	1.75	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4916	18046		1.22	2.0E-04	U09228.1	NT	Callus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5171	18293	31256	1.47	2.0E-04	AB037997.1	NT	Danio rerio hcgromo gene, exons 1 to 6, partial cds
5216	18337	31310	0.92	2.0E-04	AF057019.1	NT	Dicotyledon discoidium intercalin (abpD) gene, complete cds
5681	18855	32138	1.11	2.0E-04	AF054352.1	EST_HUMAN	AV054352 GLC Homo sapiens cDNA clone GLC04H10.3'
5674	18868	32154	1.83	2.0E-04	AI090862.1	EST_HUMAN	iq3b1.1 x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207709.3'
5966	19059	32365	0.93	2.0E-04	AA296952.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6088	19250	32578	0.92	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6386	19538	32897	1.01	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7378	20457		2.57	2.0E-04	AJ121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788.5'
7478	20553		0.84	2.0E-04	AW860963.1	EST_HUMAN	QV0-GT0387-180300-167-e10 CT0387 Homo sapiens cDNA
7798	20864		13.66	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7808	20963	34357	1.45	2.0E-04	P64296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8142	21224	34743	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8142	21224	34744	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8479	21560	35094	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8479	21560	35095	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8763	21842	35383	2.14	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8941	22020	35561	0.57	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9535	22800	36173	0.58	2.0E-04	AA725700.1	EST_HUMAN	al22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1345518.3'
9619	22874	36244	0.47	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF28.1
10180	23217	36808	1.16	2.0E-04	BE146903.1	EST_HUMAN	RC3-H10254-151089-011-505 HT0254 Homo sapiens cDNA
10223	23259	36847	2.06	2.0E-04	AA405777.1	EST_HUMAN	zlu661.1.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742964.5'
11088	24162	37798	3.88	2.0E-04	AV70373.1	EST_HUMAN	AV70373 HTF Homo sapiens cDNA clone HTFAA01.5'
11585	24638	38318	2.68	2.0E-04	AI440282.1	EST_HUMAN	t10111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289.3' similar to contains Alu repetitive element
11770	24760	38443	2.39	2.0E-04	AW136740.1	EST_HUMAN	UPH-B11-adm-c-04-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190.3'
11859	24847		2.71	2.0E-04	BE065781.1	EST_HUMAN	RC2-B10317-150200-011-104 BT0317 Homo sapiens cDNA
12108	25086	38780	32.04	2.0E-04	P21733	SWISSPROT	HYPOTHETICAL 2b.1 KD PROTEIN IN CRYB1 5'REGION (ORF2)
12121	25101	38806	2.05	2.0E-04	L19248.1	NT	Caenorhabditis elegans homeodomain protein (lin-39) mRNA, complete cds
13191	25179		1.29	2.0E-04	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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788	13987	27018	0.96	1.0E-04	H99846.1	EST_HUMAN	y26c09.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1t1 repetitive element;
1100	14205	27922	2.86	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ; ENDONUCLEASE]
1138	14303	27358	3.79	1.0E-04	AW013847.1	EST_HUMAN	U1H-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	14303	27359	3.79	1.0E-04	AW013847.1	EST_HUMAN	U1H-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1363	14517		2.65	1.0E-04	U62818.1	NT	Angiella arguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1657	14810	27894	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglyohmidine synthase, and LAMP (LAMP) genes, complete cds
1657	14810	27895	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglyohmidine synthase, and LAMP (LAMP) genes, complete cds
1909	15052	28164	2.02	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2752	15859	28978	1.06	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2752	15859	28978	1.06	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3356	16528	29543	1.18	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3829	16989	29992	0.85	1.0E-04	AI440282.1	EST_HUMAN	IQ0111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4171	17321	30314	1.72	1.0E-04	U14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4192	17342	30335	1.12	1.0E-04	AV047727.1	EST_HUMAN	AV647272 GLG Homo sapiens cDNA clone GLCBB004 3'
5207	18328	31268	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5207	18328	31299	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5980	19165	32485	1.35	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6569	19731	33109	0.95	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_P33 Homo sapiens cDNA clone IMAGE:252
6977	20205	33603	0.68	1.0E-04	AA584581.1	EST_HUMAN	nl28a04.s1 NCI_CGAP_AA11 Homo sapiens cDNA clone IMAGE:993488 3' similar to gb:U97252
7336	20417	33879	12.52	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN) contains Alu repetitive element;
7744	20417	33879	13.49	1.0E-04	A1251980.1	EST_HUMAN	qv67d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
8184	21266	34789	1.02	1.0E-04	AA630453.1	EST_HUMAN	qv67d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
9338	22603	36175	2.75	1.0E-04	A1806220.1	EST_HUMAN	ab94g05.s1 Striatagene lung (#937210) Homo sapiens cDNA clone IMAGE:954654 3'
9548	22613	36182	0.76	1.0E-04	O98959	SWISSPROT	w226a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350742 3'
9525	22680	36468	1.05	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9548	22846	36468	1.05	1.0E-04	T77153.1	NT	yc47208.r1 Soares fetal liver spymen 1N1FLS Homo sapiens cDNA clone IMAGE:113774 6'
9525	22846	36468	1.05	1.0E-04	T77153.1	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10382	23417		3.59	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10420	23455	37060	1.12	1.0E-04	P08648	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10775	23808	37431	0.46	1.0E-04	P51786	SWISSPROT	ZINC FINGER PROTEIN 157
11622	24873		2.3	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11950	24936	38637	1.81	1.0E-04	A803268.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11991	24978	38680	1.94	1.0E-04	AW289081.1	EST_HUMAN	xc49g12.x1 Sceres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12024	25008	38709	1.57	1.0E-04	Q03896	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12024	25008	38710	1.57	1.0E-04	Q03896	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
716	13898	26938	2.44	9.0E-05	AA718033.1	EST_HUMAN	chr45c11.s1 Sceres_testis_NHT Homo sapiens cDNA clone 1292468 3'
4196	17346	30338	1.13	9.0E-05	A1762209.1	EST_HUMAN	wf54c11.x1 NCI_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2394088 3' similar to contains MER.11
6084	19298	32596	1.37	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7751	20611	34301	2.44	9.0E-05	AW204958.1	EST_HUMAN	U1H-B11-aar-d-05-0-U1.s1 NCI_CGAP_Sub83 Homo sapiens cDNA clone IMAGE:2720286 3'
7751	20811	34302	2.44	9.0E-05	AW204958.1	EST_HUMAN	U1H-B11-aar-d-05-0-U1.s1 NCI_CGAP_Sub83 Homo sapiens cDNA clone IMAGE:2720286 3'
9677	22639		3.03	9.0E-05	D85606.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
9679	22841	36211	3.3	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11402	24463	38127	2.31	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_B18 Homo sapiens cDNA clone IMAGE:2588728 3' similar to contains L1 L2 L1
11518	24574	38251	1.61	9.0E-05	A1287878.1	EST_HUMAN	qv23106.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
11916	18266	32595	3.41	9.0E-05	Q60716	SWISSPROT	MIR repetitive element
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12489	26016		3.37	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLUC1, DDAH, G8b, G8c, G5b, G6a, G6b, G6f, BAT6, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
844	14022	27080	1.22	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
887	14063		3.11	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
3015	16191		1.01	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4804	17741	30719	0.78	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Sceres_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8948	22027	35568	0.51	8.0E-05	Y11686.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11419	24480	38146	2.58	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13169	26001		1.78	8.0E-05	AA279333.1	EST_HUMAN	zs8810.1.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704583 3' similar to contains Alu
357	13568	26506	3.16	7.0E-05	AW847445.1	EST_HUMAN	repetitive element/contains element MSR1 repetitive element
357	13568	26597	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220699-011-E04 CT0208 Homo sapiens cDNA
							RC3-CT0208-220699-011-E04 CT0208 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
581	13773	26793	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014
581	13773	26794	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014
1080	14246	27303	1.07	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2783	15839	29008	5.16	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3227	16401	29413	3.9	7.0E-05	AB009080.1	NT	Dicotyledonum discoidium gene for TRFA, complete cds
4168	17318		0.95	7.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4492	17632	30814	1.98	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5041	18169	31144	0.98	7.0E-05	9845300	NT	Rat cytomegalovirus Maasricht, complete genome
8420	21501	35033	1.24	7.0E-05	AA505582.1	EST_HUMAN	nt93g01.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:968098 3'
9753	22691	36261	3.6	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Striatum (cat#336206) Homo sapiens cDNA clone HFBED60
11430	24461		5.87	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2083	15223	28344	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2083	15223	28345	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2655	15778	28892	1.56	6.0E-05	AI655241.1	EST_HUMAN	w654h08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2675	13880	26912	2.54	6.0E-05	AF093630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6034	19217	32538	3.28	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6034	19217	32538	3.28	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
8533	19697	33070	1.5	6.0E-05	N72829.1	EST_HUMAN	yw50g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246212 5'
7073	20126	33542	0.74	6.0E-05	AA897680.1	EST_HUMAN	q80a03.s1 Soares NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8276	21356	34876	1.03	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
8276	21356	34877	1.03	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
8638	21718	35255	0.62	6.0E-05	AA150482.1	EST_HUMAN	z108c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element ;
8643	21723	35260	2.82	6.0E-05	AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8780	21859	35402	2.93	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9452	22568	36134	1.59	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9462	22568	36135	1.59	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9721	22786	36357	1.77	6.0E-05	T94149.1	EST_HUMAN	yw28c12.r1 Striatum lung #837210 Homo sapiens cDNA clone IMAGE:119062 5'
9822	22962	36550	0.69	6.0E-05	AW627986.1	EST_HUMAN	h137a03.x1 Soares NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2874444 3'
10987	24066	37701	2.42	6.0E-05	R75639.1	EST_HUMAN	y168c08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143536 3' similar to contains Alu repetitive element; contains LTR7 repetitive element ;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11807	24797	38496	2.7	6.0E-05	AA044015.1	EST_HUMAN	zK66f02.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12699	25999	31773	9.37	6.0E-05	AW990110.1	EST_HUMAN	MRO-NT0038-250400-001-r09 NT0038 Homo sapiens cDNA
1435	14598	27661	20.87	5.0E-05	AW392098.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1912	15055		1.07	5.0E-05	8023891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC553895), mRNA
2924	16102	29116	0.64	5.0E-05	AJ261058.1	NT	Homo sapiens MEP1A gene, promoter region and exon 1
4088	17243	30250	3.16	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5642	18836	31913	11.81	5.0E-05	X69855.1	NT	Human MLC1 gene for embryonic myosin alkaline light chain, 3'UTR
6116	19295	32830	3.58	5.0E-05	AV683544.1	EST_HUMAN	AV683544 GLC Homo sapiens cDNA clone GLCMA06 3'
6297	19470	32826	0.97	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7465	20560		1.4	5.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
12468	25503		5.26	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12759	25503		6.9	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2668	13457		2.73	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4605	17742	30720	0.76	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4605	17742	30721	0.76	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4997	18126		0.95	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5131	18256	31222	0.73	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
9723	22788		6.75	4.0E-05	AF202835.1	NT	Homo sapiens PP1200 mRNA, complete cds
10517	23651	37260	0.54	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
11007	24096	37723	4.14	4.0E-05	AW627846.1	EST_HUMAN	h86c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
12343	25248	32113	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C062
12426	25302		1.47	4.0E-05	AW117590.1	EST_HUMAN	xd83009.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
13189	25773		1.16	4.0E-05	AA417756.1	EST_HUMAN	zx01e11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746282 3'
698	13881	26914	0.8	3.0E-05	AI248061.1	EST_HUMAN	qh84ct0.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element: contains element KER repetitive element:
1084	14250	27307	1.16	3.0E-05	AW279389.1	EST_HUMAN	zx24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1550	14702	27781	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
1550	14702	27782	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3365	16537		0.7	3.0E-05	AJ288918.1	EST_HUMAN	q61g11.x1 Soares_NbHPU_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR008632
4501	17841	30625	7.91	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN ;
4501	17841	30626	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4588	17725	30707	1.11	3.0E-05	AA338878.1	EST_HUMAN	EST17996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4588	17725	30708	1.11	3.0E-05	AA368678.1	EST_HUMAN	EST76998 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4741	17878	30889	0.93	3.0E-05	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4859	13881	26914	0.7	3.0E-05	AI248061.1	EST_HUMAN	ch64c10.x1 Soares fetal liver spleen_TNFSF_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
5675	18869	32155	1.72	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2p), mRNA
6897	20047	33456	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6897	20047	33457	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8082	21164	34681	2.26	3.0E-05	BE733157.1	EST_HUMAN	601587451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8547	21628	35166	1.55	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9094	22173	35718	1.56	3.0E-05	AW770982.1	EST_HUMAN	H94e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
9098	22177	35721	1.63	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9102	22181	35726	0.59	3.0E-05	P43391	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9331	22407	36154	0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9521	22586	36154	1.4	3.0E-05	AA372582.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9863	22803	37403	3.62	3.0E-05	AI766331.1	EST_HUMAN	wg36f09.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387209 3'
10755	23788	37403	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10755	23788	37404	0.82	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12553	25255		1.61	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
12551	26374		1.37	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12613	26196		1.29	3.0E-05	AW518889.1	EST_HUMAN	xs89d06.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2776811 3'
2400	15531	28658	1.49	2.0E-05	AI286021.1	EST_HUMAN	qf68e11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3 b2 MER3 repetitive element;
2650	15773	28658	14.63	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2777	15893		6.89	2.0E-05	AA160582.1	EST_HUMAN	zq48a12.r1 Striatagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3207	16382	28393	1.29	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3428	16597	28613	1.04	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3455	16622	29643	1.12	2.0E-05	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
3583	16746		0.87	2.0E-05	X85465.1	NT	S.cerevisiae 12.8 kbp fragment of the left arm of chromosome XV
3909	17068		0.81	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5681064_r1 568 (synonym: hfrd2) Homo sapiens cDNA clone DKFZp5681064 5'
5003	18132	31106	0.8	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5876	18066	32376	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6039	19222		0.87	2.0E-05	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6092	19273	32601	0.91	2.0E-06	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6092	19273	32602	0.91	2.0E-06	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6286	19459	32811	0.79	2.0E-05	A1149272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8tc9weeks_2NHP8tc9W Homo sapiens cDNA clone IMAGE:1715114.3' similar to contains L1.b3 L1 repetitive element:
6760	19916	33311	2.11	2.0E-05	AA714330.1	EST_HUMAN	hw05d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519.3'
7042	20096	33511	1.69	2.0E-05	Y08926.1	NT	P.falciparum mRNA for AARP1 protein, partial
7054	20107	33523	1	2.0E-05	A1492980.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003.3' similar to TR:O02711
7082	20115		7.24	2.0E-05	A1991025.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN;
7303	20385	33844	2	2.0E-05	AF224262.1	NT	wu35h07.x1 Soares_Dickgraeffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077.3'
7303	20385	33845	2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7524	20597		0.77	2.0E-05	AF128847.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
8099	21151	34671	1.58	2.0E-05	A1381040.1	EST_HUMAN	Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
9487	22524	36087	0.58	2.0E-05	P49457	SWISSPROT	lg20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369.3'
9487	22524	36088	0.56	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10127	23165	36784	0.8	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10339	23374	36984	0.94	2.0E-05	BF055938.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10817	23850	37472	3.53	2.0E-05	N41751.1	EST_HUMAN	7175b05.y1 NCI_CGAP_Bn20 Homo sapiens cDNA clone IMAGE:3340576.5'
10817	23850	37473	3.53	2.0E-05	N41751.1	EST_HUMAN	yw91a08.r1 Soares_placenta_8tc9weeks_2NHP8tc9W Homo sapiens cDNA clone IMAGE:259570.5'
10881	20115		2.66	2.0E-05	A1991025.1	EST_HUMAN	yw91a08.r1 Soares_placenta_8tc9weeks_2NHP8tc9W Homo sapiens cDNA clone IMAGE:259570.5'
11738	23924	37549	1.55	2.0E-05	BE175801.1	EST_HUMAN	wu35h07.x1 Soares_Dickgraeffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077.3'
11981	24998	38688	5.74	2.0E-05	A1912713.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
12477	25921		3.7	2.0E-05	BE348228.1	EST_HUMAN	hw12h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340921.3'
12592	26104		8.13	2.0E-05	AW074604.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183592.3' similar to TR:Q12832
							Q12832 GLYCOPHORIN HEP2;
							xa89a03.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2573932.3' similar to contains L1.b3 L1 repetitive element:

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12650	25905		3.24	2.0E-05	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12825	25551	32014	2.01	2.0E-05	AU131613.1	EST_HUMAN	AU131613 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
13206	25787		1.64	2.0E-05	AJ200970.1	EST_HUMAN	qf6g11.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1756236 3'
2769	16071	28983	1.88	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3740	16901	28905	1.71	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lembo 120 Suppressor of Hairless (Su(H)) gene, partial cds
3915	17074		0.97	1.0E-05	AF223391.1	NT	Homo sapiens cadherin channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4074	17230	30236	11.88	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4288	17433	30420	1.45	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4392	17635	30614	2.14	1.0E-05	AA431119.1	EST_HUMAN	z168g04.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4975	18104	31080	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5078	18207	31179	0.86	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5084	18212	31185	0.64	1.0E-05	Z18943.1	NT	H. sapiens repeat region
6891	20043	33451	1.13	1.0E-05	AJ246003.1	NT	Homo sapiens Speal gene for spealin protein
7230	20135	33553	4.24	1.0E-05	AA641846.1	EST_HUMAN	rs19g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.11 L1
7232	20316	33759	5.19	1.0E-05	4505944	NT	L1 repetitive element;
7837	20892	34394	0.73	1.0E-05	BF222646.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7956	21006		2.03	1.0E-05	P19474	SWISSPROT	7p57a01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649845 3' similar to contains MER10.b3
8116	22195		2.39	1.0E-05	AL163227.2	NT	MER10 repetitive element;
8260	22337	35887	2.59	1.0E-05	AA452578.1	EST_HUMAN	52 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9487	22544	36107	12.29	1.0E-05	AA336110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9566	22708	36275	0.81	1.0E-05	AV732190.1	EST_HUMAN	z38h12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:788519 3' similar to
10043	23081	36682	0.78	1.0E-05	AW510802.1	EST_HUMAN	gbl02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
10043	23081	36683	0.79	1.0E-05	AW510802.1	EST_HUMAN	z305e11.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:694332 5' similar to contains Alu
10120	23168	36756	1.18	1.0E-05	AW291521.1	EST_HUMAN	repetitive element; contains element TAR1 repetitive element;
10120	23168	36757	1.18	1.0E-05	AW291521.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'
10387	23422		2.04	1.0E-05	AW468985.1	EST_HUMAN	h041b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
							OFR.11 OFR repetitive element;
							h041b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
							OFR.11 OFR repetitive element;
							UI-H-BI2-aggk-a-08-0-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							UI-H-BI2-aggk-a-08-0-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							h007c10.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1
							repetitive element;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11169	24230	37860	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11159	24230	37861	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
13023	26096	31663	1.4	1.0E-05	AL163503.2	NT	Human sapiens chromosome 21 segment HS21C103
2737	15954	28968	5.83	9.0E-06	AI583811.1	EST_HUMAN	R73a08.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3165	16340	29348	6.11	9.0E-06	AI218983.1	EST_HUMAN	cg11b08.x1 Soares_placenta_8tc9weeks_2NbHP8c9W Homo sapiens cDNA clone IMAGE:1759191 3'
3698	16859		2.56	9.0E-06	M61755.1	NT	Human alanineglyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6025	18208	32528	2.48	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7003	20139	33557	0.82	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7598	20688	34144	2.82	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7953	21003	34515	12.35	9.0E-06	AI034370.1	EST_HUMAN	cc20g01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1656812 3' similar to contains Alu repetitive element
8659	21738	35280	1.17	9.0E-06	AI163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9183	22261	35803	3.3	9.0E-06	O63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9183	22261	35804	3.3	9.0E-06	O63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9423	22497	36063	4.43	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11180	24249	37883	3.61	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2596	16065	28839	2.01	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201189-011-h11 CT0283 Homo sapiens cDNA
6728	19884	33276	2.75	8.0E-06	AA284947.1	EST_HUMAN	z22a005.s1 Soares_ovaary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:713865 3' similar to contains MER9.11 MER8 repetitive element
10761	23784	37397	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10751	23784	37398	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1002	14173		1.73	7.0E-06	AA669729.1	EST_HUMAN	ab50110.s1 Strategene lung (#637210) Homo sapiens cDNA clone IMAGE:854261 3' similar to contains MER20.11 MER20 repetitive element
1470	14624	27708	3.12	7.0E-06	7662177	NT	Homo sapiens KIAA0553 gene product (KIAA0553), mRNA
2936	16113		10.58	7.0E-06	AI368252.1	EST_HUMAN	qiv16g06.x1 NCI_CGAP_U18 Homo sapiens cDNA clone IMAGE:1991286 3' similar to contains Alu repetitive element
3654	16817		0.85	7.0E-06	AA385542.1	EST_HUMAN	EST168205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5813	18003		5.49	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062:250400-173-h01 OT0062 Homo sapiens cDNA
5925	19112	32424	0.93	7.0E-06	N98646.1	EST_HUMAN	y65607.1 Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA IMAGE:278412 5'
8989	22068	35608	0.83	7.0E-06		NT	Homo sapiens DNA segment, numerous copies, expressed probes (G31 gene) (DXF69S1E), mRNA
10104	23142		0.52	7.0E-06	Q81147	SWISSPROT	GERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	26131	31547	1.68	7.0E-06	BF215972.1	EST_HUMAN	901881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2984	19160	29177	1.17	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3784	16945	26952	1.02	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4878	19183	29206	2.13	6.0E-06	Q01466	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4983	18013	30897	2.19	6.0E-06	A1040099.1	EST_HUMAN	ox08602.x1 Soares_fetal_liver脾脏_INFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element
5465	18665	31644	2.29	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5525	18722	31739	1.16	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
10060	23098		1.99	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
13142	26742	31948	2.39	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
6186	19382	32710	3.74	6.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6467	19634	32995	1.94	6.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7382	20460	33923	1.18	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8854	21734	35274	0.58	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8654	21734	35275	0.58	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10307	23942	36947	6.06	5.0E-06	AA313620.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
10731	23764	37372	0.51	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
13011	25668	31957	5.49	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
664	13850	26877	5.47	4.0E-06	R18267.1	EST_HUMAN	ya48c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element/contains L1 repetitive element
869	14045	27110	4.73	4.0E-06	AW103354.1	EST_HUMAN	xc66g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element/contains element MER21 repetitive element
1365	14519	27593	3.18	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2036188 3'
1365	14519	27594	3.18	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2036188 3'
1503	14556	27738	1.45	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2339	15470	28605	1.56	4.0E-06	AW015401.1	EST_HUMAN	U1H-B10-aatf-05-0-U1.st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3131	16307	29321	0.89	4.0E-06	AF198349.1	NT	Galus gallus Dach2 protein (Dach2) mRNA, complete cds
4000	17157	30163	0.99	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4929	18059	31041	1.89	4.0E-06	AB86939.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
8896	21776	36308	0.68	4.0E-06	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9000	22079	35620	4.49	4.0E-06	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV/S3A2 to TCRBV12S2 region
9809	22949	36535	1.28	4.0E-06	AJ27265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11735	23821	37546	3.99	4.0E-06	AB007655.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
13149	26152		1.33	4.0E-06	AW298734.1	EST_HUMAN	xs53e01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773368 3'
2232	15366	28494	1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_infls_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.L1 L1 repetitive element;
2232	15366	28495	1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_infls_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.L1 L1 repetitive element;
2340	15471		1.48	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2688	16164	29180	0.84	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHTT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.L3 LTR1 repetitive element;
3339	16512		2.67	3.0E-06	AB57779.1	EST_HUMAN	wl22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ;contains L1.L2 L1 repetitive element ;
3883	17042	30040	1.47	3.0E-06	BE047084.1	EST_HUMAN	h664d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3883	17042	30041	1.47	3.0E-06	BE047084.1	EST_HUMAN	h664d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4597	17734	30714	0.8	3.0E-06	T50266.1	EST_HUMAN	y678b10.r1 Stralagene ovary (#637217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4684	17819	30807	5.52	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
6289	19462	32814	0.82	3.0E-06	AU159412.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7377	20456		2.14	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8274	21356	34874	0.81	3.0E-06	BE562964.1	EST_HUMAN	601338213FT NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3600314 5'
8883	21962	35496	0.75	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12650	25435		12.07	3.0E-06	AV7385282.1	EST_HUMAN	RC0-LT0001-281199-011-A03 LT0001 Homo sapiens cDNA
207	13430		2.22	2.0E-06	P54368	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1599	14752		6.39	2.0E-06	P21414	SWISSPROT	POLYPROTEIN[CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2451	15579	28707	2.58	2.0E-06	AI672138.1	EST_HUMAN	wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element;
2537	15562	28785	1.69	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2632	15755	28870	1.81	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3607	19771	29786	0.8	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFD805 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3858	17018	30017	1.54	2.0E-06	AA173518.1	EST_HUMAN	z02a05.t1 Stratigene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3868	17027	30026	0.88	2.0E-06	AW450215.1	EST_HUMAN	U1-H-B13-aky-g-05-0.U1.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2738176 3'
3876	17035	30033	1.7	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6214	19389		0.92	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6246	19420	32766	0.62	2.0E-06	AI539448.1	EST_HUMAN	te51f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537
6571	19733	33112	5.64	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7635	20704	34183	0.63	2.0E-06	AA688423.1	EST_HUMAN	W190504.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8102	21184		1.02	2.0E-06	AW669223.1	EST_HUMAN	rv59c06.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1.13 L1 repetitive element;
8281	21363	34882	0.76	2.0E-06	T12238.1	EST_HUMAN	MR3-SN067-120400-002-02 SN067 Homo sapiens cDNA
9036	22115		1.05	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9049	22128	35872	1.59	2.0E-06	H62051.1	EST_HUMAN	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9417	22451	36056	0.9	2.0E-06	AF003528.1	NT	Y37c04.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gbX74928
9417	22451	36057	0.9	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9436	22510		0.46	2.0E-06	AI473450.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9902	22942	36527	0.86	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10123	23161		0.7	2.0E-06	AV748959.1	EST_HUMAN	Y18g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
12548	26135	31540	1.34	2.0E-06	P23249	SWISSPROT	yw68e03.s1 Soares_placenta_8to6weeks_2NBHP808W Homo sapiens cDNA clone IMAGE:257212 3'
12711	25473		5.94	2.0E-06	BE328232.1	EST_HUMAN	AV748959 NPC Homo sapiens cDNA clone NPCAXD05 5'
34	13272	26276	1.16	1.0E-06	O76082	SWISSPROT	PROTEIN MOV-10
674	13860	26891	1.8	1.0E-06	AF084384.1	NT	hs9202.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144698 3' similar to contains L1.12 L1 repetitive element;
1482	14635	27719	1.8	1.0E-06	P09125	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1553	14706	27786	1	1.0E-06	AL163278.2	NT	Mus musculus D6MMSE protein (D6Mm5e) mRNA, complete cds
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
1603	14756	27838	1.19	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
							z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element;
							z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1615	14788		0.99	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2060	15191	28303	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2060	15191	28304	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4489	17629	30610	15.97	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5215	18336	31308	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5215	18336	31309	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5342	18455	31422	0.72	1.0E-06	N65946.1	EST_HUMAN	zaz27a08.s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:293750 3'
5405	18607	31579	5.14	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c08 BT0800 Homo sapiens cDNA
5430	18690	31607	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5430	18690	31608	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5592	18787	31834	1.04	1.0E-06	O60913	SWISSPROT	16 KDA SELENOPROTEIN PRECURSOR
5915	19103		0.72	1.0E-06	BE063527.1	EST_HUMAN	CN0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
7012	20148	33569	7.53	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
7923	26223		0.73	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8160	21272		0.99	1.0E-06	AA912623.1	EST_HUMAN	q28c08.s1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8468	21549	35079	1.12	1.0E-06	A347010.1	EST_HUMAN	qp54e02.x1 NCI CGAP_C08 Homo sapiens cDNA clone IMAGE:1928842 3'
8685	21765	35297	1.31	1.0E-06	A1287878.1	EST_HUMAN	qv23106.x1 NCI CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9504	22770	36341	0.91	1.0E-06	N74635.1	EST_HUMAN	MIR repetitive element ;
9579	22721	36291	0.61	1.0E-06	Q39575	SWISSPROT	zaf5e01.s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:286472 3'
9884	22924	36507	3.47	1.0E-06	L78810.1	NT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9884	22924	36508	3.47	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9829	22869	36558	5.22	1.0E-06	AA132611.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
9991	23030		3.55	1.0E-06	AA449257.1	EST_HUMAN	z04411.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:587174 5'
10705	23738		2.19	1.0E-06	AL163203.2	NT	gb:D26128 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11949	24935		3.1	1.0E-06	AW800941.1	EST_HUMAN	z04411.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:587174 5'
12599	25396	32041	8.24	1.0E-06	L78810.1	NT	Homo sapiens chromosome 21 segment HS21C003
371	13680	26613	1.95	9.0E-07	AF003529.1	NT	RC4-NT0064-120500-012-503 NT0064 Homo sapiens cDNA
371	13680	26614	1.95	9.0E-07	AF003529.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
8602	21683	36614	0.69	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
11525	24581	38257	1.83	9.0E-07	AL163281.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4893	18023	31008	4.23	8.0E-07	A1286686.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
						NT	Homo sapiens chromosome 21 segment HS21C081
						EST_HUMAN	q182q07.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4883	18023	31009	4.23	8.0E-07	AI288566.1	EST_HUMAN	q182907.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6007	19192		8.17	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8191	21273		8.44	8.0E-07	AF135418.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11021	24907		5.84	8.0E-07	T07770.1	EST_HUMAN	EST050600 Fetal brain, Strategene (cat#839206) Homo sapiens cDNA clone HFBEN89
12183	25143		6.1	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1914	15057	28167	0.97	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5636	18830	31906	0.86	7.0E-07	6003700	NT	Homo sapiens A TP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5636	18830	31907	0.86	7.0E-07	6003700	NT	Homo sapiens A TP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1902	15105	28205	3.47	6.0E-07	AW855588.1	EST_HUMAN	CM3-C10277-221099-024-e11 CT0277 Homo sapiens cDNA
2561	15685	28812	2.43	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
4080	17236		1.74	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF-4-P33 INTERGENIC REGION
9342	22418	35972	1.31	6.0E-07	BF001867.1	EST_HUMAN	7g94107.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F6L.
12115	25095	38800	1.45	6.0E-07	BE063509.1	EST_HUMAN	CM0-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
12444	26087		1.72	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
13229	25092		1.32	6.0E-07	BE223390.1	EST_HUMAN	hu11h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166329 3' similar to contains L1.b2 L1 L1 repetitive element;
338	13649		1.04	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1082	14249		2.39	5.0E-07	AA330630.1	EST_HUMAN	EST83616 Supt cells Homo sapiens cDNA 5' end
3096	16272		0.73	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4769	17904	30886	0.97	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6247	18421	32767	1.33	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7210	20076	33487	1.71	5.0E-07	AI939381.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7210	20075	33488	1.71	5.0E-07	AI939381.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7503	20578	34050	16.93	5.0E-07	AW070885.1	EST_HUMAN	xs31a02.x1 NCI_CGAP_B18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8470	21551	35081	1.02	5.0E-07	Q9WUQ1	SWISSPROT	ADAMTS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
9687	21767		0.88	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10577	23612	37217	5.47	5.0E-07	AI908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
11805	24795	38493	5.69	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11880	24868		2.08	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12256	25968		1.2	5.0E-07	AL103285.2	NT	Homo sapiens chromosome 21 segment HS21C085
12918	25966		3.06	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4109	17260	30261	1.66	4.0E-07	AW009602.1	EST_HUMAN	ws94h05.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3'
7328	20410		0.8	4.0E-07	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7417	20495	33963	0.97	4.0E-07	Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7417	20495	33964	0.97	4.0E-07	Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD6) (HISTONE DEACETYLASE MHDA1)
8107	21189	34709	0.51	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9251	22328	35875	4.9	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCL CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10332	23367	36976	0.63	4.0E-07	BE001975.1	EST_HUMAN	601676748F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3959651 5'
10332	23367	36977	0.53	4.0E-07	BE001976.1	EST_HUMAN	601676748F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3959651 5'
10531	23566	37174	0.59	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11179	24248	37881	3.88	4.0E-07	A1765528.1	EST_HUMAN	wf81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11179	24248	37882	3.88	4.0E-07	A1765528.1	EST_HUMAN	wf81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11495	24553		1.69	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
11918	24905		1.32	4.0E-07	BE967557.1	EST_HUMAN	601649083F1 NIH_MGC 73 Homo sapiens cDNA clone IMAGE:3932924 5'
13207	25788		1.71	4.0E-07	11437071	NT	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1), mRNA
454	13650	26686					Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
596	13798	26806	5.38	3.0E-07	U19719.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1405	14559	27633	1.43	3.0E-07	AJ271735.1	NT	Human polymorphic microsatellite DNA
1655	14808		3.62	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2104	15243		2.32	3.0E-07	AA528763.1	EST_HUMAN	n156b09.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.18 L1 repetitive element
2361	15492	28621	1.14	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2540	15665	28789	4.99	3.0E-07	BE005077.1	EST_HUMAN	MPO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2540	15965	28780	4.89	3.0E-07	BE005077.1	EST_HUMAN	MPO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3099	16275	29289	0.97	3.0E-07	T84704.1	EST_HUMAN	yd50f12.f1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111695 5'
3228	16402	29414	1.78	3.0E-07	P38739	SWISSPROT	HYPOPHYSICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4802	17637		0.64	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVONACROGLOBULIN)
4849	17982	30970	8.04	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLC00D01 3'
4885	18015	30999	0.7	3.0E-07	A1797236.1	EST_HUMAN	we86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347997 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5175	18297	31259	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705.3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5175	18297	31260	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705.3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5793	18075	32281	12.39	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6095	19276	32605	0.7	3.0E-07	O42280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6842	19895		5.09	3.0E-07	AA815175.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
7678	20743	34224	3.53	3.0E-07	AW797168.1	EST_HUMAN	cc04c10.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890.3'
7841	20898		1.3	3.0E-07	AI591065.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0038 Homo sapiens cDNA
9330	22406	35959	0.48	3.0E-07	P33240	SWISSPROT	tw28f11.x1 NCI CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2261037.3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
9330	22406	35960	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
13184	25777		4.26	3.0E-07	AJ132352.1	NT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
29	13267	26270	7.32	2.0E-07	AF262988.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
158	13383	26413	6.06	2.0E-07	L77569.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158	13383	26414	6.06	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
186	13408	26437	35.88	2.0E-07	U98849.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
767	13948	26985	1.48	2.0E-07	AF003530.1	NT	Fugu rubripes beta-cytoplasmic (vesicular) actin gene, complete cds
767	13948	26988	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
779	13959		1.36	2.0E-07	P11369	SWISSPROT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
							ENDONUCLEASE]
966	14139	27200	2.32	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869.3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
987	14140	27201	2.02	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790.3' similar to contains L1 repetitive element ;
1189	14351	27409	1.55	2.0E-07	Q26768	SWISSPROT	I/8 AUTOANTIGEN
1630	14782	27888	2.06	2.0E-07	Q09701	SWISSPROT	HYPOPHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3708	16899		0.63	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891.5'
3779	16940	29946	21.71	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5238	18390		0.6	2.0E-07	AW902219.1	EST_HUMAN	QV3-NN1023-260400-168-h11 NN1023 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5460	18680	31638	1.52	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6681	26829	33229	0.73	2.0E-07	AW448988.1	EST_HUMAN	UHH-B13-ake-b-01-q-UJ.st NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2734008 3'
6602	19987	33357	3.39	2.0E-07	AI208716.1	EST_HUMAN	ig56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8684	21744		3.87	2.0E-07	AV726390.1	EST_HUMAN	AV726390 HTC Homo sapiens cDNA clone HTCAEG02 5'
8893	21972	35508	1.11	2.0E-07	AA035198.1	EST_HUMAN	2427g09.g1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
9663	23002		1.44	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10474	23509	37122	6.34	2.0E-07	AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-a08 NN0003 Homo sapiens cDNA
10706	23739	37342	1.01	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
10706	23739	37343	1.01	2.0E-07	P00751	SWISSPROT	GLYCINE-RICH BETA GLYCOPROTEIN (GBG) (PBF2)
12138	26655		2.96	2.0E-07	BE153717.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12226	25967		2.38	2.0E-07	AI732482.1	EST_HUMAN	PM0-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
1126	14291		0.76	1.0E-07	AL163282.2	NT	zn55h11.x5 Stratiogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:555029 3' similar to contains THR.b2 THR repetitive element:
2888	14704	27784	2.08	1.0E-07	P09256	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
3838	14291		1.24	1.0E-07	AL163282.2	NT	GLYCOPROTEIN GPV
4408	17650	30534	2.91	1.0E-07	AV718682.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
4408	17650	30535	2.91	1.0E-07	AV718682.1	EST_HUMAN	AV718682 GLC Homo sapiens cDNA clone GLCFNF04 5'
6832	19761	33180	0.8	1.0E-07	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
7006	20142	33560	4.69	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCL CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
7006	20142	33561	4.69	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCL CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
7682	20729	34205	7.5	1.0E-07	N55081.1	EST_HUMAN	yw43c07.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7826	20881	34382	0.69	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-505 TN0024 Homo sapiens cDNA
7826	20881	34383	0.69	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-505 TN0024 Homo sapiens cDNA
7854	20906	34413	1.24	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8410	21491	35020	2.76	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8410	21491	35021	2.76	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9155	22233	35778	2.7	1.0E-07	AA693576.1	EST_HUMAN	z151e10.st Soares_fetal_liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE:434346 3'
9470	22527	36090	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9816	22856	36436	0.6	1.0E-07	BE327843.1	EST_HUMAN	huz28h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10140	23178	36776	2.35	1.0E-07	BF674624.1	EST_HUMAN	MER18 repetitive element
10149	23187	36784	1.23	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4274426 5'
10682	23716		1.22	1.0E-07	AL1632822	NT	EST185054 Brain IV Homo sapiens cDNA
12085	25065	38771	2.35	1.0E-07	AI341136.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12506	25639	31761	3.37	1.0E-07	BE048770.1	EST_HUMAN	q889a03.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2008692 3'
12859	25438		1.45	1.0E-07	X64467.1	NT	h93c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR.O95722 O95722
12862	25568		2.1	1.0E-07	X51755.1	NT	DJ1163J1.1
7433	20510	33982	0.75	9.0E-08	AI639362.1	EST_HUMAN	H. sapiens ALAD gene for porphobilinogen synthase
10091	23129	36732	2.04	9.0E-08	AV734819.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
11457	24517	38185	1.92	9.0E-08	AI891052.1	EST_HUMAN	test1606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
11965	24950	38656	2.38	9.0E-08	AL163301.2	NT	AV734819 cDNA Homo sapiens cDNA clone cdABFB08 5'
12456	25320		2.51	9.0E-08	AJ251973.1	NT	hm30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
622	16017		2.09	8.0E-08	AI911352.1	EST_HUMAN	OFR repetitive element
1075	14241		1.01	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
3634	16798		1.57	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens partial stefin-1 gene
8937	22016	35567	6.35	8.0E-08	AI752367.1	EST_HUMAN	wd18505.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8937	22016	35568	5.35	8.0E-08	AI752367.1	EST_HUMAN	601560133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
9827	22867	36449	3.03	8.0E-08	AW970693.1	EST_HUMAN	601560133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
10788	23821	37445	0.48	8.0E-08	AF111187.2	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11523	24576		1.73	8.0E-08	AF253417.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
82	13317	26345	3.91	7.0E-08	Q02367	SWISSPROT	EST382776 IMAGE resequences, MAGK Homo sapiens cDNA
1392	14546	27622	19.51	7.0E-08	X04809.1	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3688	18829	29839	0.88	7.0E-08	P15305	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
3688	18829	29840	0.88	7.0E-08	P15305	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
5332	18445	31413	0.82	7.0E-08	T65881.1	EST_HUMAN	Rat mRNA for ribosomal protein L31
11052	24129		1.73	7.0E-08	AI535743.1	EST_HUMAN	DYNEIN HEAVY CHAIN (DYHC)
11870	24955	38658	4.1	7.0E-08	U24070.1	NT	DYNEIN HEAVY CHAIN (DYHC)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12978	18829	28839	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	18829	28840	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
840	14018	27073	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
840	14018	27074	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2436	15564	28693	1.77	6.0E-08	BE144398.1	EST_HUMAN	MRO-HT0168-191188-004-g09 HT0166 Homo sapiens cDNA
3129	15309	28319	0.68	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4363	17506	30487	1.15	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8137	21219		0.59	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9529	22594		0.55	6.0E-08	AA827075.1	EST_HUMAN	gb56c06.s1 NCL CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element ;
11701	24698	38390	2.16	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
11823	24812		1.43	6.0E-08	AL163209.2	NT	ENDONUCLEASE
87	13322	26350	2.17	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C009
2309	15441	28576	3.93	5.0E-08	AA493851.1	EST_HUMAN	rh03b09.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
12185	25144		4.55	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12382	25271	32077	1.77	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1799	14948	28040	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1799	14948	28041	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2960	16127		1.08	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426.5'
3132	16308		1.01	4.0E-08	AI076417.1	EST_HUMAN	cc05a02.x1 Soares_fetal_liver_spleen_1NFUS_S1 Homo sapiens cDNA clone IMAGE:1674498 3' similar to contains Alu repetitive element;
4024	17180	30189	0.65	4.0E-08	U82698.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
5635	18698	33071	1.07	4.0E-08	P52824	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8998	22077	35617	0.9	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEIN, SERINE 2
9340	22416	35669	1.13	4.0E-08	L42571.1	NT	Chobletus griseus ribosomal transcription factor (UBP2) mRNA, complete cds
9845	22885		1.56	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10336	23571		0.85	4.0E-08	AI016342.1	EST_HUMAN	cl78d12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622303 3'
10597	23632	37241	4.75	4.0E-08	AI05027.1	EST_HUMAN	en22d10.x1 Gessler_Wilms tumor Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
11328	24391	38037	5.16	4.0E-08	AA398627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726247 5' similar to TR:G505579

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11328	24301	38038	5.16	4.0E-08	AA393927.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505679
11349	24411	38064	11.86	4.0E-08	BF592493.1	EST_HUMAN	G065579 NA/CAL-K-EXCHANGER ;
11349	24411	38005	11.86	4.0E-08	BF592493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 6'
12180	26108		1.93	4.0E-08	W76159.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12604	25568		2.01	4.0E-08	AI343353.1	EST_HUMAN	z65503.r1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
5728	18921	32216	2.27	3.0E-08	BE018348.1	EST_HUMAN	tb95a11.x1 NCL_CGAP_C016 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
7115	18541	31488	6.01	3.0E-08	AI792737.1	EST_HUMAN	MER18 MER18 repetitive element ;
7711	20776	34262	1.43	3.0E-08	AL163246.2	NT	tb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17 ;
7828	20978		3.32	3.0E-08	AI496352.1	EST_HUMAN	qs76f11.y5 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:1944045 5'
10102	23140		0.63	3.0E-08	AF055066.1	NT	Homo sapiens chromosome 21 segment HS21C046
11276	24343	37863	1.64	3.0E-08	AI218001.1	EST_HUMAN	tb93h09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
11957	24942	38646	1.32	3.0E-08	AF111187.2	NT	Homo sapiens MHC class 1 region
12156	25125		33.85	3.0E-08	R16420.1	EST_HUMAN	qh21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845294 3'
211	13434		4.16	2.0E-08	AW302996.1	EST_HUMAN	Homo sapiens Jun dimerization protein gene, partial cds; cdc gene, complete cds; and unknown gene
236	13456		5.76	2.0E-08	AA425598.1	EST_HUMAN	yq02f04.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains repetitive element ;
509	13703	26732	4.46	2.0E-08	AF198349.1	NT	xr87f06.x1 NCL_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
677	13863	26893	9.7	2.0E-08	AW868438.1	EST_HUMAN	zy48f07.r1 Soares_fetus_Nb2HF8_Bw Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER16 repetitive element ;
677	13863	26894	9.7	2.0E-08	AW868438.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
1014	14186	27602	7.75	2.0E-08	BE280477.1	EST_HUMAN	MFR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1373	14528		1.46	2.0E-08	AL163247.2	NT	MFR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1774	14923	28017	0.96	2.0E-08	AW841890.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1780	14929		2.08	2.0E-08	BE734871.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
1802	15045		6.7	2.0E-08	AW270271.1	EST_HUMAN	IL5-CN0024-030300-026-C01 GN0024 Homo sapiens cDNA
2608	15732		1.86	2.0E-08	K00216.1	NT	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 6'
3279	16453	26474	5.61	2.0E-08	O42280	SWISSPROT	xp43f11.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
							Sheep His-RNA-GUG
							WNT-14 PROTEIN PRECURSOR

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3278	16453	29475	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3862	17120		1.63	2.0E-08	AW813620.1	EST_HUMAN	RC3-STO197-161088-012-b03 ST0197 Homo sapiens cDNA
4169	17339	30332	0.62	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4525	17604		1.48	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:874380 5' similar to contains L1.12 L1 repetitive element:
5072	18200		3.5	2.0E-08	AW572881.1	EST_HUMAN	he17108.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element:
5753	18945	32247	0.85	2.0E-08	AA813204.1	EST_HUMAN	ab04111.s1 Soares_fetis_NHT Homo sapiens cDNA clone 1377189 3'
5855	19141	32457	1	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595482 3' similar to contains MER18.b3
8193	21275	34798	1.11	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element:
8301	21383	34904	1.5	2.0E-08	AA490121.1	EST_HUMAN	POL POLYPROTEIN[CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9286	22362		0.89	2.0E-08	AU139978.1	EST_HUMAN	ab02g06.e1 Stratagene fetal retina B97202 Homo sapiens cDNA clone IMAGE:839674 3'
10738	23771	37381	0.83	2.0E-08	N78097.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone IMAGE:1011719 5'
10738	23771	37381	0.83	2.0E-08	N78097.1	EST_HUMAN	W7202.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element:
12476	26328		1.77	2.0E-08	AL163284.2	NT	W7202.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element:
13065	28159		1.8	2.0E-08	11431678	NT	Homo sapiens chromosome 21 segment HS21C084
1539	16041	27770	1.05	1.0E-08	P31792	SWISSPROT	Homo sapiens hypopharyngeal protein FLJ11342 (FLJ11342), mRNA
1672	14824	27907	1.33	1.0E-08	P13002	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1672	14824	27907	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
1872	14824	27908	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
1876	14965	28058	1.96	1.0E-08	AF125348.1	NT	(TRANSCRIPTION FACTOR NTF-1)
2110	15248		2.97	1.0E-08	BE141989.1	EST_HUMAN	Homo sapiens cavedin 1 (CAV1) gene, exon 3 and partial cds
3261	16435	29453	0.95	1.0E-08	BE248844.1	EST_HUMAN	PM2-H10130-150999-001-f12 HT0130 Homo sapiens cDNA
3261	16435	29454	0.95	1.0E-08	BE248844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5716	18009	32204	4.51	1.0E-08	AJ010770.1	NT	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
7946	20998	34507	0.94	1.0E-08	P19474	SWISSPROT	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens hyperton gene, exons 1-50
8224	21308	34828	0.62	1.0E-08	AL163302.2	NT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
							Homo sapiens chromosome 21 segment HS21C102

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8320	21402	34927	0.54	1.0E-08	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8320	21402	34028	0.54	1.0E-08	AF224690.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8744	21823	35359	2.27	1.0E-08	A015304.1	EST_HUMAN	cd5a05.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9405	22479		0.56	1.0E-08	P08593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9406	22480	36043	0.85	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-402 BT0546 Homo sapiens cDNA
10171	23208	36801	0.84	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10778	23811	37434	0.87	1.0E-08	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11595	24648	38332	3.59	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
12581	25391		3.06	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
13137	25925		1.26	1.0E-08	BF375398.1	EST_HUMAN	MR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4357	17500	30481	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4357	17500	30482	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10287	23302		0.63	9.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7414	20492	33960	8.1	8.0E-09	AH163500.1	EST_HUMAN	qq42e07.x1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.1 MSR1 repetitive element:
8189	21271	34786	2.54	8.0E-09	AW900159.1	EST_HUMAN	CM0-NN1004-100300-273-a08 NN1004 Homo sapiens cDNA
9186	22267		2.53	8.0E-09	AA038892.1	EST_HUMAN	op74d08.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3695	16856		1.98	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4115	17289		0.98	7.0E-09	U90871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
8086	21198		0.58	7.0E-09	BF108755.1	EST_HUMAN	745e10.x1 Scores_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element:
8237	21319		0.99	7.0E-09	AA256200.1	EST_HUMAN	zr80c05.r1 Scores_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element:
9460	22517	36080	2.86	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10386	23421	37028	1.95	7.0E-09	BE254850.1	EST_HUMAN	80111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10554	23589		0.76	7.0E-09	AA058626.1	EST_HUMAN	zf59e07.s1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element:
10910	23993		2.01	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2221	15355		0.95	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514.r1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434C0514 5'
5095	18223	31195	6.2	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5498	18695	31711	9.33	6.0E-09	AW195784.1	EST_HUMAN	XR5H08.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8775	21854	35396	1.11	6.0E-09	BE161663.1	EST_HUMAN	MR3-HT0448-260300-201-h12 HT0446 Homo sapiens cDNA
9377	22452	36014	2.18	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10483	23518		3.4	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10669	24049	37682	1.66	6.0E-09	BF108755.1	EST_HUMAN	745610.x1 Soares_NSF_f8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12089	25080	38776	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMGS0003762 Human adult (K. Okubo) Homo sapiens cDNA
1447	14800	27677	3.47	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1900	15043	28154	7.4	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6540	19703	33075	2.22	5.0E-09	AA359454.1	EST_HUMAN	EST168746 Fetal Lung II Homo sapiens cDNA 5' end
6988	18507	31523	0.66	5.0E-09	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV7S2A1N4T, TCRBV6S1P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
8785	21864	35407	0.63	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10300	23335	35940	3.25	5.0E-09	AW799667.1	EST_HUMAN	PM2-JM0053-240300-005-c09 UM0053 Homo sapiens cDNA
11944	24930	38632	1.87	5.0E-09	AA460142.1	EST_HUMAN	z60a09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:7956880 3'
534	13727		1.64	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
987	14159		2.75	4.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C085
1497	14850	27732	1.86	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038199), mRNA
2500	15927	28747	5.32	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
8030	21113	34631	0.53	4.0E-09	AA495747.1	EST_HUMAN	z60a06.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8719	21769	35334	1.02	4.0E-09	T64942.1	EST_HUMAN	yd11a07.s1 Soares_fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66804 3'
11330	24393	38041	9.51	4.0E-09	AI886401.1	EST_HUMAN	wm94f10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
11379	24440		1.44	4.0E-09	AA195142.1	EST_HUMAN	z34a12.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:U07807 DYNAMIN-1 (HUMAN);
2427	15555	28682	4.51	3.0E-09	BE222239.1	EST_HUMAN	hu09a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;
2619	15742	28856	1.06	3.0E-09	BE222239.1	EST_HUMAN	hu09a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;
2716	15834	28944	0.66	3.0E-09	P23249	SWISSPROT	PROTEIN MOV-10
3408	16578	29593	0.9	3.0E-09	BE222239.1	EST_HUMAN	hu09a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3484	18631		0.7	3.0E-09	AA442272.1	EST_HUMAN	zif54a04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4212	17361		0.62	3.0E-09	X16674.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4546	17684	30668	3.47	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4634	17770	30751	1.19	3.0E-09	Q8Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0693)
8084	21166	34682	1.1	3.0E-09	BE465780.1	EST_HUMAN	hxb0a02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
10453	23488	37096	1.87	3.0E-09	AL163247.2	NT	Q55091 IMPACT PROTEIN.
10782	23825	37448	0.46	3.0E-09	Q10940	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
11272	24340	37978	3.15	3.0E-09	BF108943.1	EST_HUMAN	HYPOPHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X
11272	24340	37979	3.15	3.0E-09	BF108943.1	EST_HUMAN	772c08.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3627030 3'
836	14013		0.98	2.0E-09	X16674.1	NT	772c08.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3627030 3'
1287	14443	27511	4.7	2.0E-09	AL163284.2	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1691	14843		10.71	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2403	15634	28661	2.24	2.0E-09	Q8Y3R5	SWISSPROT	DKFZp761B1710_r1 761 (synonym: hama2) Homo sapiens cDNA clone DKFZp761B1710 5'
4048	17204	30214	3.01	2.0E-09	Q80241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0693)
4119	17273	30272	0.9	2.0E-09	AI263478.1	EST_HUMAN	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5284	18363	31348	0.62	2.0E-09	M23161.1	NT	q107d09.x1 Soares_NhlHMPu_S1 Homo sapiens cDNA clone IMAGE:1855783 3'
5837	19027	32333	0.67	2.0E-09	AI004062.1	EST_HUMAN	Human transposon-like element mRNA
6278	19432		0.75	2.0E-09	AL163249.2	NT	ci47b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6919	20234		0.88	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7609	20679	34155	8.81	2.0E-09	AA461430.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7692	20757	34242	0.66	2.0E-09	W28834.1	EST_HUMAN	z683h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7971	21021	34534	0.59	2.0E-09	AI24732.1	EST_HUMAN	52a11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8909	21988	35528	1.2	2.0E-09	AJ271735.1	NT	gh88g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854114 3'
10824	23857	37480	0.85	2.0E-09	AV688842.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
12746	14013		20.06	2.0E-09	X16674.1	NT	AV688842 GK Homo sapiens cDNA clone GKCA11 5'
12830	26188		1.89	2.0E-09	AA226070.1	EST_HUMAN	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1019	14190		1.19	1.0E-09	W78152.1	EST_HUMAN	nc11c02.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
1133	14258	27353	1.43	1.0E-09	5031624	NT	zif79d03.s1 Soares_fetal_heart_NhlH19W Homo sapiens cDNA clone IMAGE:348563 3' similar to gbL02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1133	14258	27354	1.43	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
							Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2571	15696		1.15	1.0E-09	AI356089.1	EST_HUMAN	qj64e11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 MER12 repetitive element ;
2854	18131	29148	2.02	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2892	15188	29184	6.17	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2892	16188	29185	6.17	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3103	16279	29283	0.99	1.0E-09	BE535440.1	EST_HUMAN	801058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4920	18050		6.15	1.0E-09	AA719297.1	EST_HUMAN	zh36b03.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
5341	18454		0.8	1.0E-09	AA921959.1	EST_HUMAN	cm44gt12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543942 3'
5620	18814	31882	0.85	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5852	19138	32454	1.29	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6272	19446	32784	3.34	1.0E-09	P26694	SWISSPROT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
8584	21685	35206	0.92	1.0E-09	AI688474.1	EST_HUMAN	wd36b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.11 MER25 repetitive element ;
10520	23555		2.72	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12642	26120	31668	1.71	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12767	25510		1.42	1.0E-09	T57368.1	EST_HUMAN	yb51g12.s1 Stratagene fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:74758 3'
13132	26020		1.68	1.0E-09	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
1337	14494	27564	1.52	9.0E-10	AW807740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2895	16074	28092	3.74	9.0E-10	AI870071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347283 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ; TR:000372 000372 PUTATIVE P1450 ;
6973	20201	33627	4.98	9.0E-10	AI452982.1	EST_HUMAN	146b09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:000372 000372 PUTATIVE P1450 ;
151	13376	26408	9.26	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3423	16592	28607	0.66	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
4318	17461	30446	5.45	8.0E-10	AA376832.1	EST_HUMAN	EST89564 Small intestine I Homo sapiens cDNA 5' and
10170	23207		2.51	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (VIP) gene, complete cds
719	13901	26941	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC61586), mRNA
719	13901	26942	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC61586), mRNA
1651	14804	27890	2.58	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2626	15749		20.25	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3197	16332	28341	2.25	7.0E-10	X00865.1	NT	H.sapiens DHFR gene, exon 3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6314	19486	32841	4.06	7.0E-10	AA345220.1	EST_HUMAN	EST151247 Gall bladder II Homo sapiens cDNA 5' end
7574	20646	34124	1.37	7.0E-10	BF352883.1	EST_HUMAN	IL3-IT00619-110700-208-D12 HT0619 Homo sapiens cDNA
7834	20889		1.85	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8163	21245	34764	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8163	21245	34765	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
936	14111	27171	8.44	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene, C11orf17 gene
2742	15859	28971	1.63	6.0E-10	A1424405.1	EST_HUMAN	h02407.x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4615	17752	30733	1.88	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4861	17894		3.15	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0264-031099-012-g12 CT0264 Homo sapiens cDNA
8983	22062	35602	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
8983	22062	35603	0.96	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)(LECAM2)
9834	22874	36458	0.48	6.0E-10	P88073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
12223	25172		1.95	6.0E-10	AW971923.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)(LECAM2)
780	13960		5.29	5.0E-10	AL046804.1	EST_HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
3564	16729	29745	1.14	5.0E-10	Q01033	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)(LECAM2) (CD62E)
5105	18233	31202	1.4	5.0E-10	AF181897.1	NT	DKFZp434N219_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5'
7475	20550		1.85	5.0E-10	BF105159.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
9736	22801	36374	2.24	5.0E-10	P34678	SWISSPROT	Homo sapiens WRN (WRN) gene, complete cds
9736	22801	36375	2.24	5.0E-10	P34678	SWISSPROT	G01822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
							HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
							HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
12040	25021	38725	1.31	5.0E-10	AF091415.1	NT	Macaca tonkeana isolate 569konkeona NADH dehydrogenase subunit 4L gene, complete cds; and NADH dehydrogenase subunit 4 gene, mitochondrial genes encoding mitochondrial proteins, partial cds
114	13345		1.09	4.0E-10	A1221083.1	EST_HUMAN	qg0009.x1 Soares, placenta, 8tc0weeks, 2Nbl-P8tc0W Homo sapiens cDNA clone IMAGE:1759049 3'
2052	15193	28308	1.4	4.0E-10	AW564709.1	EST_HUMAN	similar to contains LTR8.b2 LTR8 repetitive element ;
2640	15763	28877	6.79	4.0E-10	AL163303.2	NT	hg58g03.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
							Homo sapiens chromosome 21 segment HS21C103
7327	20409	33871	17.76	4.0E-10	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10398	23433	37039	0.71	4.0E-10	AW283243.1	EST_HUMAN	UI-H-BI2-ant-a-07-0-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10662	23696	37305	1.12	4.0E-10	AI267342.1	EST_HUMAN	sq63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10794	23827	37450	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-108 HT0521 Homo sapiens cDNA
10794	23827	37451	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-108 HT0521 Homo sapiens cDNA
936	14112	27173	2.24	3.0E-10	N36113.1	EST_HUMAN	y932106.s1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.11 L1 repetitive element;
1382	14537		5.3	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
4657	17793	30777	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4657	17793	30778	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5350	18463	31428	0.89	3.0E-10	L34070.1	NT	Human XRCC1 DNA repair gene, genomic
5571	18767	31808	0.78	3.0E-10	N50109.1	EST_HUMAN	Human XRCC1 DNA repair gene, genomic
6332	19503	32861	2.06	3.0E-10	P20350	SWISSPROT	RHOMBOD PROTEIN (VEINLET PROTEIN)
6481	19948	33010	3.62	3.0E-10	BE302970.1	EST_HUMAN	bat7d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
7937	20987	34493	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7937	20987	34498	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8928	22007	35546	1.57	3.0E-10	H87208.1	EST_HUMAN	y574b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
9249	22329	35872	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9249	22329	35873	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9541	22806		0.78	3.0E-10	A F020803.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10670	23713		1.95	3.0E-10	T65891.1	EST_HUMAN	yc11a12.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80398 5'
10820	23853		0.96	3.0E-10	AA769284.1	EST_HUMAN	ncz8g03.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12941	25619	31977	1.87	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
36	13274	26278	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
36	13274	26279	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1946	15089		1.66	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
3051	16227		0.84	2.0E-10	BF875047.1	EST_HUMAN	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5924	18111		2.3	2.0E-10	Q28640	SWISSPROT	(HPRG)
6380	19549	32905	1.56	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7537	20810	34084	0.41	2.0E-10	BE791082.1	EST_HUMAN	607586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8203	21285	34807	0.58	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8203	21285	34808	0.58	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

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9502	22658		1.06	2.0E-10	BF434565.1	EST_HUMAN	7a7d08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
11609	24662		1.33	2.0E-10	AI862153.1	EST_HUMAN	1a10f12.x1 Soares_tctat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2043695 3'
1538	14691		3.09	1.0E-10	AW867787.1	EST_HUMAN	MRO-SN0038-290300-001-101 SN0038 Homo sapiens cDNA
1637	14789	27874	3.37	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2649	15772		2.16	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-181198-058-508 CT0225 Homo sapiens cDNA
3589	16753	29768	0.9	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-181199-013-q10 TT0003 Homo sapiens cDNA
3829	16793		0.67	1.0E-10	AL041885.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3947	16793		0.76	1.0E-10	AL041885.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
4123	17277		7.33	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4245	17391	30378	16.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4245	17391	30379	16.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4253	17399	30388	1.76	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4285	17430		2.28	1.0E-10	MS0628.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5277	18396		1.01	1.0E-10	AI797745.1	EST_HUMAN	we82f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element;
7844	20713		0.58	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7860	20914	34419	0.69	1.0E-10	AU128594.1	EST_HUMAN	AU128594 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8434	21515	35046	1.14	1.0E-10	AW408990.1	EST_HUMAN	FB_6A4 Fetal brain library Homo sapiens cDNA
8855	21934		1.62	1.0E-10	AI268340.1	EST_HUMAN	qtn046f0.x1 NCL_CGAP_u6 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;
10406	23441		6.24	1.0E-10	AA081888.1	EST_HUMAN	zn23g06.r1 Syntagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11154	24225	37854	3.5	1.0E-10	AI038280.1	EST_HUMAN	cy85h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
12165	18503		1.8	1.0E-10	X87344.1	NT	H.sapiens DMA, DMB, HLA-A21, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
272	13490	26521	0.87	9.0E-11	BE145800.1	EST_HUMAN	IL2-H10203-291099-016-c08 H10203 Homo sapiens cDNA
2171	15306	28433	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3470	16637	29657	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5
3470	16637	29658	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5
4622	17759	30741	0.8	9.0E-11	AA775986.1	EST_HUMAN	ae78101.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:970267.3
5602	18886		3.05	9.0E-11	BE019780.1	EST_HUMAN	RC6-BT0027-140200-011-E08 BT0027 Homo sapiens cDNA
10357	23392	37002	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10357	23392	37003	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12556	25378	32072	2.45	9.0E-11	C16635.1	EST_HUMAN	CT6635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN:506B08.5
3185	16360		10.53	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173.3 similar to contains L1 repetitive element
4154	17306	30300	5.37	8.0E-11	N23712.1	EST_HUMAN	yw45e08.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:256288.3
5913	18101	32415	0.66	8.0E-11	AW674316.1	EST_HUMAN	ba80g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982.3
8811	18685		0.82	8.0E-11	AW166158.1	EST_HUMAN	x44f11.1x1 NCL_CGAP_Bm60 Homo sapiens cDNA clone IMAGE:2621061.3 similar to contains MER10.11 MER10 repetitive element
1479	14632	27717	2.09	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week Homo sapiens cDNA 5' end
8695	21775	35307	2.61	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10434	23489		1.37	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
425	13620	26661	6.19	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
425	13620	26662	6.19	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6802	20014	33424	0.91	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
7870	20924	34431	3.5	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8559	21640	35179	0.99	8.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCCSC06.5
9514	22579	36145	0.5	6.0E-11	BE063509.1	EST_HUMAN	GM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12	13250	26250	1	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3450	13250	26250	1.24	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6845	19804	33161	1.92	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7699	20764	34248	11.57	6.0E-11	11416799	NT	Homo sapiens prolactin beta 3 (PCLHB3), mRNA
1433	14586		1.39	4.0E-11	AA438042.1	EST_HUMAN	z01b12.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:730559.5
2851	15965	29074	9.84	4.0E-11	BE855900.1	EST_HUMAN	60150763.1F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295.5
3034	16210	29233	1.28	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4740	17675	30858	0.87	4.0E-11	D44696.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 068
6005	18765	33154	3.29	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7141	20276	33718	0.82	4.0E-11	AA442630.1	EST_HUMAN	z68f10.r1 Soares_testis_NHT: Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1055250 G1055250 PHEROMONE RECEPTOR VN4:
7532	20809		3.66	4.0E-11	AF224860.1	NT	Homo sapiens mimosinase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9595	22650		1.56	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-038 HT0256 Homo sapiens cDNA IMAGE:2105830 3' similar to WP:ZK353.1
9882	22802	36487	0.79	4.0E-11	AI609753.1	EST_HUMAN	IMAGE:2105830 3' similar to WP:ZK353.1
10859	23862	37513	0.94	4.0E-11	BF367293.1	EST_HUMAN	MR0-GN0024-180900-008-H09 GN0024 Homo sapiens cDNA
12794	25530	32008	1.71	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1521	14674	27756	4	3.0E-11	8676077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4391	17534		1.35	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
982	14165	27215	1.43	2.0E-11	AI150502.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT: Homo sapiens cDNA clone IMAGE:35144 5'
1212	14373	27434	20.98	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element:
1212	14373	27435	20.98	2.0E-11	R24807.1	EST_HUMAN	Y943e12.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:35144 5'
1644	14796	27880	4.44	2.0E-11	L17432.1	NT	Y943e12.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:35144 5'
1644	14796	27881	4.44	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3 beta) genes, complete cds
2823	15937	29047	1.09	2.0E-11	AF087913.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3 beta) genes, complete cds
3266	16440	29461	5.56	2.0E-11	P10263	SWISSPROT	Human endogenous retrovirus HERV-P.T47D
3403	16573	29568	0.92	2.0E-11	A1478617.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3448	16618	28634	0.67	2.0E-11	Q10473	SWISSPROT	IMAGE:2105830 3' similar to WP:ZK353.1
3586	16760		1.01	2.0E-11	AF020503.1	NT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
3797	16958	28962	0.94	2.0E-11	P70213	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4566	17704		1.07	2.0E-11	BE065537.1	EST_HUMAN	FRIEND VIRUS SUSCEPTIBILITY PROTEIN 1
4728	17863		0.8	2.0E-11	AL163227.2	NT	RC3-BT0316-170200-014-905 BT0316 Homo sapiens cDNA
5051	18179		1.85	2.0E-11	BE062558.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
5142	18265	31234	0.82	2.0E-11	AA307331.1	EST_HUMAN	QV2-BT0258-281099-014-901 BT0258 Homo sapiens cDNA
6263	19437	32784	1.23	2.0E-11	AW877808.1	EST_HUMAN	EST178228 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2- macroglobulin
						EST_HUMAN	QV2-P10073-280300-109-H03 PT10073 Homo sapiens cDNA

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6440	19607	32970	2	2.0E-11	AA591028.1	EST_HUMAN	nc83105.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST
7345	20425	33988	0.85	2.0E-11	BF592945.1	EST_HUMAN	P15838 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
8066	21148		0.59	2.0E-11	P37072	SWISSPROT	7197c03.r1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442665 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9424	22498		1.39	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10491	23526	37135	5.13	2.0E-11	Q13906	SWISSPROT	OLFACTORY RECEPTOR 811 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10734	23767	37376	1.09	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10734	23767	37377	1.09	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11375	24436	38094	1.84	2.0E-11	AA035389.1	EST_HUMAN	2k27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11375	24436	38095	1.84	2.0E-11	AA035389.1	EST_HUMAN	2k27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11408	24469	38133	1.4	2.0E-11	AA201959.1	EST_HUMAN	2s18b04.r1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:685519 5'
12122	25102	38807	12.19	2.0E-11	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078
12297	28105		1.85	2.0E-11	AA704195.1	EST_HUMAN	2177b03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12328	25237		1.44	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12354	25256	32115	2.15	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12641	25431		1.43	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12813	25642		3.82	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13180	25767		2.5	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA
693	13876	28909	1.57	1.0E-11	AJ131018.1	NT	Homo sapiens SCL gene locus
806	13986	27038	1.72	1.0E-11	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
1244	14403	27484	2.91	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1528	14891		1.82	1.0E-11	AF119814.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2095	15235	28356	0.94	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2195	15330	28455	3.59	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxigenase gene, complete cds
2228	15363	28492	1.1	1.0E-11	AA309318.1	EST_HUMAN	EST180185 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3588	16752	29767	0.95	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-282-d12 BN0105 Homo sapiens cDNA
5447	18647	31628	14.68	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5953	19139	32455	0.78	1.0E-11	BF222846.1	EST_HUMAN	7c57d01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:364945 3' similar to contains MER10.b3
8396	21477	35004	2.85	1.0E-11	4885546	NT	MER10 repetitive element ;
8781	21880	35403	4.81	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9248	22325	35870	1.49	1.0E-11	BF365119.1	EST_HUMAN	y73d08.r1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:28168 5'
							QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9248	22325	35871	1.49	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN149-250900-423-a03 NNT149 Homo sapiens cDNA
10526	23650		0.54	1.0E-11	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
11666	24621	38302	2.02	1.0E-11	BF690078.1	EST_HUMAN	602194807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285877 5'
12903	26879		1.37	1.0E-11	Z20377.1	EST_HUMAN	HS4AACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
3017	16193	29216	0.75	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002	23040	36632	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10002	23040	36633	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9539	22604		0.88	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
12408	26287		4.68	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4783	17918	30905	1.57	7.0E-12	Q05804	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11631	24711	38402	6.8	7.0E-12	AA704735.1	EST_HUMAN	423g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
13225	25903		1.18	7.0E-12	D16473.1	NT	Human mRNA, Xq terminal portion
3637	16801		0.96	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4488	17608	30586	9.23	6.0E-12	AA732516.1	EST_HUMAN	repetitive element;
5336	18449	31418	5.12	6.0E-12	AH459161.1	EST_HUMAN	l65g12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148438 3' similar to contains MER10.12 MER10 repetitive element;
9196	22274	35811	1.09	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9875	22637		1.81	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1367898 similar to contains MER29.12 MER29 repetitive element;
13205	25756		1.25	6.0E-12	AW886846.1	EST_HUMAN	RC4-OT0072-080400-012-11 OT0072 Homo sapiens cDNA
1068	14234	27293	2.37	5.0E-12	T06573.1	EST_HUMAN	EST04462 Fetal brain, Striagene (cat#836206) Homo sapiens cDNA clone HFB0V33
3477	16844	29963	1.28	5.0E-12	BE047778.1	EST_HUMAN	1242605.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281217 5'
3821	16981	29984	7.44	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6145	19323	32866	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6145	19323	32867	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6620	19780	33168	9.96	5.0E-12	AW974760.1	EST_HUMAN	EST386850 MAGE resequences; MAGN Homo sapiens cDNA
7176	20032	33462	1.06	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7187	20032	33462	0.93	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8424	21905	35038	1.28	5.0E-12	AA033745.1	EST_HUMAN	z01g12.s1 Soares_fetal_heart NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
8667	21946		0.56	5.0E-12	AW887037.1	EST_HUMAN	RC1-OT0088-220300-011-b07 OT0088 Homo sapiens cDNA
9195	22273		0.77	5.0E-12	AL076951.1	EST_HUMAN	DKFZp434J0426.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9308	22384	35636	2.32	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9823	22678	36247	1.22	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10452	23517		4.8	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10573	23608	37213	0.89	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10703	23626	37449	0.6	5.0E-12	6978754	NT	Rattus norvegicus Deleted in colorectal cancer (at homolog) (Dcc), mRNA
254	13474	28505	3.29	4.0E-12	AA700326.1	EST_HUMAN	Z74g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460576 3'
255	13474	28505	3.42	4.0E-12	AA700326.1	EST_HUMAN	Z74g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460576 3'
4742	17877	30860	0.88	4.0E-12	AI680984.1	EST_HUMAN	b28h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13639 Q13639 MARINER TRANPOSASE. ;
7787	20853		0.71	4.0E-12	BF445140.1	EST_HUMAN	na21b03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7 b2 MER7 repetitive element ;
8437	21518		4.81	4.0E-12	AF109507.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
11338	24401	38050	4.33	4.0E-12	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12884	25458		2.11	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
631	13818	26839	2.58	3.0E-12	AW341683.1	EST_HUMAN	Hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
631	13816	26840	2.58	3.0E-12	AW341683.1	EST_HUMAN	Hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
5276	18365	31363	0.78	3.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5568	18765	31806	1.44	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8570	21651	35193	0.5	3.0E-12	O39453	SWISSPROT	SERINE PROTEASE HEPsin
10891	23975	37606	2.32	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10891	23975	37607	2.32	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1685	14837	27921	1.24	2.0E-12	AW802131.1	EST_HUMAN	IL5-UMC071-120400-065-a05 UMC071 Homo sapiens cDNA
3556	16721	29736	0.93	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4230	17377	30366	1.29	2.0E-12	J01884.1	NT	Rat USA small nuclear RNA
4230	17377	30366	1.29	2.0E-12	J01884.1	NT	Rat USA small nuclear RNA
4541	17079		2.03	2.0E-12	BE063509.1	EST_HUMAN	GMO-BT0281-031109-087-a03 BT0281 Homo sapiens cDNA
5018	18147	31123	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BX PROTEIN 15)
5018	18147	31124	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BX PROTEIN 15)
6006	19766		2.08	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGC resequences, MAG1 Homo sapiens cDNA
7326	20408	33870	3.95	2.0E-12	T08159.1	EST_HUMAN	EST06080 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7499	20574	34047	1.33	2.0E-12	BE173035.1	EST_HUMAN	MRO-HT0559-200400-Q15-e08 HT0559 Homo sapiens cDNA
7838	20893	34395	2.19	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9508	22774		1.88	2.0E-12	AF198864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10191	23228		8.32	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-Q01 HT0487 Homo sapiens cDNA
10733	23766	37375	0.76	2.0E-12	AI334130.1	EST_HUMAN	qq0702.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1831835 3' similar to TR:Q13538
12129	25109	38813	1.53	2.0E-12	AW242934.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN.
12313	25228		1.34	2.0E-12	AL163283.2	NT	xx2703.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694965 3'
12516	25352		1.48	2.0E-12	11418248	NT	Homo sapiens chromosome 21 segment HS21C083
125	13354	28386	1.64	1.0E-12	AW627674.1	EST_HUMAN	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
2044	15185		1.78	1.0E-12	AI871728.1	EST_HUMAN	hh90a09.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11
3138	16314	28326	1.04	1.0E-12	AF000991.1	NT	MER18 repetitive element;
3138	16314	28327	1.04	1.0E-12	AF000991.1	NT	wn61107.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439483 3' similar to contains L1.b3 L1
3978	17135	30138	40.43	1.0E-12	AF000991.1	EST_HUMAN	repetitive element;
3978	17135	30139	40.43	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6088	19289		1.6	1.0E-12	U82828.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6188	18342		1.62	1.0E-12	Q8Y2G7	SWISSPROT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' -
6282	19455	32804	0.59	1.0E-12	BF642800.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6282	19455	32805	0.59	1.0E-12	BF642800.1	EST_HUMAN	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
							HYPOTHETICAL ZINC FINGER PROTEIN KIAA0981
							EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
							EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
							Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
6882	19821	33208	0.63	1.0E-12	AF229843.1	NT	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7285	20348	33800	2.53	1.0E-12	AF198864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
							qp68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to
7300	20382	33840	10.78	1.0E-12	AI248533.1	EST_HUMAN	gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10
							repetitive element;
							qp68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to
7300	20382	33841	10.78	1.0E-12	AI248533.1	EST_HUMAN	gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10
							repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8696	21766	35298	0.59	1.0E-12	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV2/51P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
8902	21981	35521	1.26	1.0E-12	AA782323.1	EST_HUMAN	ac26005.s1 Straglene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
12215	25166	38835	2.32	1.0E-12	AW982164.1	EST_HUMAN	EST374237 MAGC resequences, MAGG Homo sapiens cDNA
12437	25310		1.54	1.0E-12	AI738592.1	EST_HUMAN	wk33h08.x1 NCL_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2392095 3'
12600	26068		1.93	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12788	26168		1.19	1.0E-12	P44836	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR H10712 PRECURSOR
12951	25661		2.82	1.0E-12	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4056	17212	30223	1.21	9.0E-13	AB023900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9801	22841		2.81	9.0E-13	IN99053.1	EST_HUMAN	z626106.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:283651 3'
735	13917	26957	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
735	13917	26958	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1885	15029	28138	2.73	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p14 (btf2p-4) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
8303	21385	34906	0.83	8.0E-13	AI884398.1	EST_HUMAN	wk31h09.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8303	21385	34907	0.83	8.0E-13	AI884398.1	EST_HUMAN	wk31h09.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10350	23385		2.82	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8429	21510		0.77	7.0E-13	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12713	25474		32	7.0E-13	BE778223.1	EST_HUMAN	60146328F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886613 5'
12976	25635		1.53	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAc-T1)
2168	15303	28430	5.85	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5239	19391	31328	0.93	6.0E-13	AI267928.1	EST_HUMAN	qs44a09.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1911362 3'
3399	16569		1.15	5.0E-13	R78338.1	EST_HUMAN	y82704.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145759 5'
3484	16652		1.58	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element/contains element MER22 repetitive element:
7016	20152	33572	0.99	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11100	24173	37808	2.84	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1916	15059		4.86	4.0E-13	AW378614.1	EST_HUMAN	FN2-HT0224-221099-001-c11 HT0224 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2531	15656		1.61	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4889	18002		1.06	4.0E-13	AA454054.1	EST_HUMAN	z48d07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785469 5'
5704	18937	32189	4.47	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7355	20434	33096	1.09	4.0E-13	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7788	20844	34337	1.08	4.0E-13	AA431529.1	EST_HUMAN	z476g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
7898	20950		2.62	4.0E-13	NA4291.1	EST_HUMAN	y03g05.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995
9042	22121	35663	1.38	4.0E-13	AL043810.1	EST_HUMAN	A32995 1 complex sterility protein - mouse
9702	22751	36321	0.47	4.0E-13	AA076907.1	EST_HUMAN	DKFZp434A0128.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
10226	23262	36850	4.44	4.0E-13	AI289831.1	EST_HUMAN	7804H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7804H11
11439	24500	38167	1.54	4.0E-13	AA435819.1	EST_HUMAN	qr32d05.x1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:189945 3' similar to contains Alu repetitive element;
11438	24500	38168	1.54	4.0E-13	AA435819.1	EST_HUMAN	z476g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
184	13408		4.35	3.0E-13	AF003528.1	NT	z476g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
888	14064		1.81	3.0E-13	AA430310.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1502	14856	27737	0.96	3.0E-13	AI804151.1	EST_HUMAN	z468g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2443	15571	28700	1.53	3.0E-13	AJ271736.1	NT	GM-BT043-060296-075 BT043 Homo sapiens cDNA
2548	15673		2.28	3.0E-13	AL163210.2	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2729	15947	28957	3.69	3.0E-13	BF372962.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3256	16430		2.44	3.0E-13	AA745844.1	EST_HUMAN	GM3-FT0100-140700-242-H08 FT0100 Homo sapiens cDNA
3592	16756	29771	9.73	3.0E-13	P18616	SWISSPROT	cb18d02.s1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1324035 3'
3592	16756	29772	9.73	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5657	18851	32133	0.68	3.0E-13	AA134017.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5657	18851	32134	0.68	3.0E-13	AA134017.1	EST_HUMAN	z488h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
6114	18294	32628	0.73	3.0E-13	AW005639.1	EST_HUMAN	z488h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
8067	21149	34669	7.1	3.0E-13	U52111.2	NT	wz88c02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2665890 3' similar to TR:O75139
							O75139 KIAA0644 PROTEIN ;
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8268	21350	34965	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST0487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra- reactive factor
8268	21350	34968	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST0487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra- reactive factor
10401	23438	37043	0.58	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10915	23998		3.1	3.0E-13	A064768.1	EST_HUMAN	HA0635 Human fetal liver cDNA library Homo sapiens cDNA
11301	24367	38008	3.41	3.0E-13	BE063509.1	EST_HUMAN	CNM-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11886	24886	38985	1.62	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
154	13379	26411	3.52	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cez2/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
249	13470	26502	2.06	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1289	14455	27521	8.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3070	16245	29266	0.61	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3070	16246	29287	0.61	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3586	16760	29776	1.68	2.0E-13	AF109607.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4224	17372		2.07	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6250	19424	32770	4.34	2.0E-13	Q0852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6335	19503		0.58	2.0E-13	X79477.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6954	20267	33704	5.73	2.0E-13	X16912.1	NT	Human PKL gene for liver-type 8-phosphofructokinase (EC 2.7.1.11) exon 2
7199	20084	33474	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7199	20084	33475	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10675	23709	37317	2.41	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12368	25274		22.49	2.0E-13	AW852155.1	EST_HUMAN	GM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
302	13518	26551	1.34	1.0E-13	S74128.1	NT	FGF-1 fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	14086	27151	5.53	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1967	14521	27596	1.4	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2070	15219	28339	2.61	1.0E-13	AA720574.1	EST_HUMAN	rw21502.e1 NCI CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR, 13 THR repetitive element ;
4715	17650	30833	1.32	1.0E-13	BF340987.1	EST_HUMAN	802038003F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4185868 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8084	21176	34691	0.97	1.0E-13	AA577812.1	EST_HUMAN	m24c01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
8094	21176	34692	0.97	1.0E-13	AA577812.1	EST_HUMAN	m24c01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
10295	23330		1.04	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10508	23543	37154	0.6	1.0E-13	AF300701.1	NT	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
11861	24740	38431	0.74	1.0E-13	BF108755.1	EST_HUMAN	745e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12068	25160		1.38	1.0E-13	AV716377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DOBAIE03 5'
12920	25605		3.46	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
13077	25708		1.85	1.0E-13	X87579.1	NT	H.sapiens CD4 gene
343	13554	26583	3.76	9.0E-14	AA781159.1	EST_HUMAN	a24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
344	13555	26584	1.84	9.0E-14	AA781159.1	EST_HUMAN	a24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2569	15694		4.13	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2811	15925	29036	7.9	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3180	16355	29360	7.5	9.0E-14	AW513286.1	EST_HUMAN	xa84h05.x1 NCI_CGAP_UT1 Homo sapiens cDNA clone IMAGE:2707833 3'
3310	13554	26583	1	9.0E-14	AA781159.1	EST_HUMAN	a24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
3888	17057	30057	7.37	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4879	16010	30994	2.23	9.0E-14	AJ002153.1	NT	Sagulus oedipus gene for seminal vesicle secreted protein semenogelin I
3587	16751		1.17	8.0E-14	BE408283.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4066	17222		3.64	8.0E-14	R76269.1	EST_HUMAN	y72903.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:1447963 3'
9647	21090	34605	38.93	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9760	22698	36266	3.22	8.0E-14	AA218316.1	EST_HUMAN	zq17c10.s1 Striatogene fetal retina 637202 Homo sapiens cDNA clone IMAGE:629970 3'
11717	24767		1.79	8.0E-14	BE062668.1	EST_HUMAN	QV2-BT0288-261099-014-a01 BT0258 Homo sapiens cDNA
12611	25410	32048	2.43	8.0E-14	AJ688118.1	EST_HUMAN	wc82h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
1658	16044		4.76	7.0E-14	AW151673.1	EST_HUMAN	x87e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element;
9120	22189		0.73	7.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
378	13586	26620	12.43	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10027	23066	36662	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10027	23065	30663	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
633	13818	26942	4.17	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
9166	18288	31254	1.32	5.0E-14	AW073791.1	EST_HUMAN	xb03605.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
5650	18944	32125	5.26	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1147	16030		1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1928	15069	28174	10.15	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3847	17007		0.73	4.0E-14	AA046502.1	EST_HUMAN	2k67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4407	17549	30533	1.04	4.0E-14	N46328.1	EST_HUMAN	y73c12.x1 Soares_multiple_sclerosis_2NbHMPSP Homo sapiens cDNA clone IMAGE:279160 3' similar to contains L1.13 L1 repetitive element;
8145	21227		0.71	4.0E-14	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12043	25024	38729	5.5	4.0E-14	BE242468.1	EST_HUMAN	TCAAP1D1470 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1470
12966	26203		5.69	4.0E-14	AI886224.1	EST_HUMAN	wm08c03.x1 NCL CGAP_UK Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element
972	14145	27204	1.56	3.0E-14	X95468.1	NT	R.norvegicus mRNA for CPG2 protein
6873	20025	33434	0.93	3.0E-14	A1420786.1	EST_HUMAN	te91c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519
6873	20025	33435	0.93	3.0E-14	A1420786.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
7173	20309	33749	0.6	3.0E-14	AA386311.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
6987	22066	35606	0.86	3.0E-14	N42165.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
11512	18496	31533	5.87	3.0E-14	AW265354.1	EST_HUMAN	y07b10.r1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:270523 5'
12894	26041		1.88	3.0E-14	AL163285.2	NT	xp48f12.x1 NCL CGAP_JN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element;contains element MER9 repetitive element ;
13212	25694	31853	1.61	3.0E-14	BE891560.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
401	13598	26694	2.33	2.0E-14	AJ271736.1	NT	601435233F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920169 5'
401	13598	26635	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
708	16019	26926	11.36	2.0E-14	AL163303.2	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
							Homo sapiens chromosome 21 segment HS21C103

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2461	15588		1.04	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 3T0377 Homo sapiens cDNA
2535	15680		0.89	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2583	15718	28835	1.63	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5641	18835	31912	0.87	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5738	18931	32229	1.03	2.0E-14	AI812351.1	EST_HUMAN	ta78n01 x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.3 L1 repetitive element
5838	19028	32334	3	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7023	20159		1.04	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a08 BN0072 Homo sapiens cDNA
7437	20514	33987	1.06	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7676	20741	34221	24.46	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7676	20741	34222	24.46	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
10121	23159	36758	0.59	2.0E-14	AI978795.1	EST_HUMAN	wf58g10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element
10630	23694	37273	0.51	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBBF04 5'
11019	24098	37736	3.62	2.0E-14	AW138600.1	EST_HUMAN	UI-H-B1-adv-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12880	26045		2.5	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
13163	15860		1.26	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1082	14257	27313	2.32	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1438	14591	27664	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1438	14591	27665	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2067	15198	28312	8.9	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2258	15391	28517	6.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2480	15607	28731	6.44	1.0E-14	AF001889.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
3010	16186	29210	1.41	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3236	16410	29424	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3236	16410	29425	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3992	17149	30155	1.69	1.0E-14	AA682994.1	EST_HUMAN	ee89c12.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4596	17733	30713	2.01	1.0E-14	AW276852.1	EST_HUMAN	xx338r10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2783059 3'
5930	19116	32429	1.98	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid-CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6813	25834	33371	10.9	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
6813	25834	33372	10.9	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
1607	14780	27838	1.81	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	16376		1.38	9.0E-16	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel, a)
7666	20732	34207	4.24	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P16, P12, P30, P10]
8206	21288	34810	1.24	9.0E-15	BE903569.1	EST_HUMAN	601977760FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
13099	25716		2.87	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2872	13687		1.53	8.0E-16	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7331	20412	33874	1.13	7.0E-16	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
10650	23684		2.34	7.0E-16	AW241958.1	EST_HUMAN	XN77402.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
12270	25203		1.44	7.0E-16	AA284465.1	EST_HUMAN	zs37408.1 NCL_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gbL21834 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1:11 L1 repetitive element;
1018	14189	27250	7.51	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5263	18382		0.98	6.0E-16	AW901266.1	EST_HUMAN	GM4-NN1011-100300-170-d10 NN1011 Homo sapiens cDNA
6041	19224	32546	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
11563	26231		1.54	6.0E-15	AW836843.1	EST_HUMAN	QV1-L70036-150200-070-c10 LT0036 Homo sapiens cDNA
423	13618	28668	3.57	5.0E-16	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2819	15933	28044	1.76	5.0E-16	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5233	18355		0.91	5.0E-16	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
440	13240	28240	2.33	4.0E-16	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6804	18959	33359	0.9	4.0E-16	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11316	21065	34677	2.11	4.0E-16	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11316	21065	34678	2.11	4.0E-16	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4333	17476		7.67	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIOLILIN)
5141	18264	31232	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5141	18264	31233	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6953	20266		1.11	3.0E-15	Q84625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430	20507	33978	3.13	3.0E-15	M27695.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7430	20507	33979	3.13	3.0E-15	M27695.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10128	23167		2.38	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351704 3' similar to contains MER19.11
11033	24112	37748	8.11	3.0E-15	AB026898.1	NT	MER19 repetitive element ;
12620	26081		65.8	3.0E-15	AJ271735.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
260	13478	26511	3.71	2.0E-15	AF223391.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
379	13987	26621	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13687	26622	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1559	14712		0.99	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3599	16763	29778	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3599	16763	29779	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4745	17880		2.76	2.0E-15	AJ006335.1	EST_HUMAN	wf0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043
6311	19483	32838	1.11	2.0E-15	BE562352.1	EST_HUMAN	Q61043 NINEIN. ;
6311	19483	32839	1.11	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3577268 5'
7283	20346		1.58	2.0E-15	AJ400877.1	NT	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3577268 5'
7421	20498	33969	2.73	2.0E-15	AA704195.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7554	20926	34102	5.05	2.0E-15	W05064.1	EST_HUMAN	z77903.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
9107	22186	35730	2.86	2.0E-15	D14947.1	NT	z77903.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
9273	22349	35999	0.91	2.0E-15	AA397758.1	EST_HUMAN	WP.F44F4.8 CE02227 TRANSPOSASE ;
9273	22349	35900	0.91	2.0E-15	AA397758.1	EST_HUMAN	Human DNA, SINE repetitive element
9604	22659	36231	1.18	2.0E-15	AW379485.1	EST_HUMAN	z77908.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9604	22659	36232	1.18	2.0E-15	AW379485.1	EST_HUMAN	z77908.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
11077	24152		3.69	2.0E-15	AJ271735.1	NT	CMO-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
13016	16763	29778	3.89	2.0E-15	AF223391.1	NT	CMO-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
							Homo sapiens Xq pseudautosomal region; segment 1/2
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13016	16763	28778	3.89	2.0E-16	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2834	15948						bt2805.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
3077	16253	28275	3.03	1.0E-15	AI689984.1	EST_HUMAN	MARINER TRANSPOSASE ;
3211	16385	28396	1.42	1.0E-15	BE043584.1	EST_HUMAN	hk40902.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2869162 5'
4479	17619	30601	1.18	1.0E-15	F08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
			0.61	1.0E-15	BE182696.1	EST_HUMAN	RC3-H10649-100500-022-005 HT0649 Homo sapiens cDNA
6502	19668	33032					ye40e10.e1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains
7149	20284		1.72	1.0E-15	T95763.1	EST_HUMAN	MER6 repetitive element ;
7184	20049	33480	1.98	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
8427	21508	35040	0.79	1.0E-15	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8616	21686	35233	0.99	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8615	21695	35232	4.94	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9239	22316	35858	4.94	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9242	22319	35862	0.78	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9448	22564	38127	0.96	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
			0.99	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9832	22872	38455					ch37603.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459872 3' similar to contains L1.13 L1
11057	24134	37770	0.84	1.0E-15	AA864653.1	EST_HUMAN	repetitive element ;
			3.04	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
13104	25892	31895					bt31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element ;
4825	17762	30744	13.05	1.0E-15	AI763944.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CGAAT displacement protein) (GUTL1) mRNA
11241	24310	37947	0.93	9.0E-16	4803168	NT	HSC23F061 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
			1.41	9.0E-16	F08688.1	EST_HUMAN	qf76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
11995	24980	38685					MER10 repetitive element ;
			1.48	9.0E-16	AI244341.1	EST_HUMAN	qf76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
11995	24980	38686					MER10 repetitive element ;
5519	19009	32315	1.48	9.0E-16	AI244341.1	EST_HUMAN	qf76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
			0.85	7.0E-16	4885120	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7496	20571	34043					PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
			1.3	7.0E-16	O88807	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
7496	20571	34044					PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
			1.3	7.0E-16	O88807	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
13043	25995						ye28c12.t1 Stratiotes lung (#837210) Homo sapiens cDNA clone IMAGE:119082 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2208	15342		8.12	6.0E-16	AW972611.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
1522	14875	27757	0.96	6.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2745	15862	28973	2.21	5.0E-16	AA992178.1	EST_HUMAN	o39c04.s1 Soares total testis Nb2Hf8_3w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
11809	24799	38498	2.68	6.0E-16	BF217388.1	EST_HUMAN	contains element L1 repetitive element;
13152	25749		14.15	6.0E-16	11418127	NT	601866734F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4104129 5'
2312	15444		1.01	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2453	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
2453	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3548	16711	29722	5.29	4.0E-16	Q16883	SWISSPROT	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
4260	17405	30391	8.68	4.0E-16	BE083875.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4260	17405	30392	8.68	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g03 BT0650 Homo sapiens cDNA
5257	18377	31343	0.91	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7890	20942	34448	42.68	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9495	22552	36114	0.72	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12293	25218		1.95	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12381	25270		8.68	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
12392	25277	32079	3.23	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIA0571), mRNA
12882	25454		1.33	4.0E-16	R18591.1	EST_HUMAN	YF95111.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30489 5'
135	13361	26395	1.09	3.0E-16	AW022862.1	EST_HUMAN	d445c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
135	13361	26396	1.09	3.0E-16	AW022862.1	EST_HUMAN	d445c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
478	13873		1.58	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
488	13882		2.33	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1483	14536	27720	2.73	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
3041	18217	29237	4.71	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4711	17846	30890	0.59	3.0E-16	AW160828.1	EST_HUMAN	au76b08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to
5057	18185	31160	1.32	3.0E-16	AV661383.1	EST_HUMAN	SW/KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;
5392	18594		0.99	3.0E-16	AA077225.1	EST_HUMAN	AV661383 GLC Homo sapiens cDNA clone GLGSA01 3'
5734	18927	32223	1.87	3.0E-16	AF003529.1	NT	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
8858	21937	35473	4.25	3.0E-16	AI002836.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions am88h05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10094	23132		1.09	3.0E-16	BF90817.1	EST_HUMAN	602246538F1NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10324	23359	36989	2.59	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13187	26171	31557	3.62	3.0E-16	AL043266.2	EST_HUMAN	DKFZp434L1623_11 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5'
984	14168		1.03	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2459	15586		0.98	2.0E-16	AA621761.1	EST_HUMAN	af06004.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2763	15870		1.14	2.0E-16	J03081.1	NT	Human SSV-related endogenous retroviral LTR-like element
4294	17437	30424	1.62	2.0E-16	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
4603	17740	30718	1.27	2.0E-16	AI208733.1	EST_HUMAN	q85603.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1839187 3' similar to contains MER28.13
5299	18416	31385	0.64	2.0E-16	BE061176.1	EST_HUMAN	MER28 repetitive element;
6880	20032	33442	0.88	2.0E-16	Q31125	SWISSPROT	RC3 BT0046-131189-003-H12 BT0046 Homo sapiens cDNA HISTIDINE-RICH PROTEIN KE4
7893	20945	34451	0.99	2.0E-16	AI470723.1	EST_HUMAN	q16611.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element;
8154	21236	34757	1.67	2.0E-16	AI732837.1	EST_HUMAN	n24706.x5 NCI CGAP Pr12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN [2] TR:O08905 contains MER7.11 MER7 repetitive element;
8352	21433	34957	0.81	2.0E-16	BE658026.1	EST_HUMAN	7682H09.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3303521 3'
8352	21433	34958	0.81	2.0E-16	BE658026.1	EST_HUMAN	7682H09.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35340	0.76	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
8724	21804	35341	0.76	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
130	13411	26436	2.26	1.0E-16	AF200716.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
393	13630		22.93	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1034094 3' similar to contains OFR.12 OFR repetitive element;
2028	15169	28276	3.42	1.0E-16	BF327842.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5839	19029	32335	0.9	1.0E-16	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6565	19727		18	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds
6704	19882	33252	2.96	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7726	19727		5.39	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds
9483	22540	36103	0.81	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA
3832	18892	28994	2.08	9.0E-17	AW900048.1	EST_HUMAN	GM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
6864	20016		2.15	9.0E-17	AI382964.1	EST_HUMAN	q22c11.x1 NCI CGAP_GCL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12
							MER28 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8298	21381		3.56	9.0E-17	AW150257.1	EST_HUMAN	Xq49q12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element;
10428	23404		2.35	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1043	14209		2.43	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-401 OT0032 Homo sapiens cDNA
3988	17155		0.78	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5701	25809	32187	4.09	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7425	20502		1.73	8.0E-17	AV730769.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAGB07 5'
1487	14640		2.58	7.0E-17	6753097	NT	Mus musculus adipoprotein B editing complex 2 (Apobec2), mRNA
5438	18638		3.11	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
							Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
6826	19979	33387	7.91	7.0E-17	AF228843.1	NT	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
208	13431	28463	5.62	6.0E-17	AW998860.1	EST_HUMAN	h181-c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12
6443	18610	32973	2.06	8.0E-17	AW682772.1	EST_HUMAN	L1 repetitive element;
10490	23534	37144	0.64	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
434	13234	28234	2.37	5.0E-17	T64110.1	EST_HUMAN	y05h08.t1 Strabagene lung (8937210) Homo sapiens cDNA clone IMAGE:79839 5'
7759	20818	34308	1.81	5.0E-17	T81043.1	EST_HUMAN	y428b04.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
							x20e04.x1 NCL_CGAP_Ki48 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
9582	22704	38270	1.32	4.0E-17	AW129165.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11783	24773	38469	2.51	4.0E-17	AL163247.2	NT	Q45e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
12308	25226		1.82	4.0E-17	A1079546.1	EST_HUMAN	Q16530 PMS3 MRNA contains MER10.12 MER10 repetitive element;
2185	15300	28426	1.85	3.0E-17	AW119123.1	EST_HUMAN	x489c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3263	16437		1.17	3.0E-17	P35410	SWISSPROT	NAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3732	16893	29897	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3732	16893	29898	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
							za14b02.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.t3 PTR5 repetitive element;
8463	21544	36074	1.12	3.0E-17	N68451.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 12 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9903	22943	36528	5.19	3.0E-17	AB026898.1	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10591	23626	37234	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10591	23626	37235	0.72	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
12268	25201		4.2	3.0E-17	11417968	NT	

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13155	25751		1.23	3.0E-17	AV720204.1	EST_HUMAN	AV720204.GLC Homo sapiens cDNA clone GLC.DIF08.5
363	13574	26805	2.55	2.0E-17	AI270080.1	EST_HUMAN	q13a06.x1 NCL_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1859922.3' similar to contains Alu repetitive element
364	13574	26805	2.78	2.0E-17	AI270080.1	EST_HUMAN	q13a06.x1 NCL_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1859922.3' similar to contains Alu repetitive element
1012	14184		1.43	2.0E-17	AA722832.1	EST_HUMAN	z081d04.s1 Scores_fetal_heart_NHH18W Homo sapiens cDNA clone IMAGE:396751.3'
2518	15644	28765	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2518	15644	28766	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2896	16172	28191	6.96	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5482	18681	31686	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5482	18681	31687	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6394	19563		1.92	2.0E-17	AF055066.1	NT	Homo sapiens MHC class 1 region
6619	19779		1.39	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0610.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610.5'
8006	21056	34568	0.89	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8275	21357	34876	1.24	2.0E-17	Q86156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8651	21731	35270	1.05	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10073	23111	36715	2.71	2.0E-17	BE289886.1	EST_HUMAN	600844680F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860615.5'
10108	23146	38744	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10108	23146	36745	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10466	23501	37114	5.02	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10590	23625	37232	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10590	23625	37233	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10618	23652	37261	0.93	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719.3'
10618	23652	37262	0.93	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719.3'
769	13650	26999	2.79	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1745	14894		2.01	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
1807	14958	28050	4.83	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2184	15319	28445	2.05	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2412	15542	28669	3.16	1.0E-17	U76410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3657	18820		1.03	1.0E-17	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4256	17401		9.42	1.0E-17	R05942.1	EST_HUMAN	yf03e07.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:128388.5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6781	18946	33344	1.62	1.0E-17	AI185642.1	EST_HUMAN	q65505.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6781	19946	33346	1.62	1.0E-17	AI185642.1	EST_HUMAN	q65505.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7238	20322	33766	1.33	1.0E-17	Q16831	SWISSPROT	URDINE PHOSPHORYLASE (UDRPASE)
8792	21871	35410	1.26	1.0E-17	BE082744.1	EST_HUMAN	QV6-BT0263-101299-072-007 BT0263 Homo sapiens cDNA
10210	23246	36936	1.04	1.0E-17	AW995938.1	EST_HUMAN	QV3-BN0046-220300-129-ct10 BN0046 Homo sapiens cDNA
11703	24700	38363	1.52	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
9698	22747		3.05	9.0E-18	AI472167.1	EST_HUMAN	q65403.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3886	17045	30044	2.14	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
359	13570	26599	16.47	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NC1 CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
359	13570	26600	16.47	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
7801	20871	34146	1.09	7.0E-18	AW887642.1	EST_HUMAN	RC3-OT0091-170300-011-003 OT0091 Homo sapiens cDNA
12826	13570	26599	10.65	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NC1 CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12826	13570	26600	10.65	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
3367	16539	29552	1.23	6.0E-18	XT1791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nexin/protease nexin 1 enhancer region
4868	18001		3.99	6.0E-18	P62181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGase C) (TGC)
8444	21825		3.47	6.0E-18	11428153	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83446), mRNA
8543	21824	35161	0.78	6.0E-18	AI183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9291	22367	35916	0.48	6.0E-18	AI908256.1	EST_HUMAN	RC-BT166-020499-014 BT166 Homo sapiens cDNA
9291	22367	35917	0.48	6.0E-18	AI908256.1	EST_HUMAN	RC-BT166-020499-014 BT166 Homo sapiens cDNA
11399	24460	38124	3.63	6.0E-18	AI163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11612	24664	38351	1.69	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IAPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12634	25364	32068	3.91	6.0E-18	U87929.1	NT	Human aconitate hydratase (ACO2) gene, exon 4
1171	14334	27390	12.48	5.0E-18	AI280214.1	EST_HUMAN	qnr5g11.x1 Soares_placenta_8to6weeks_2NHP8to9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;
4433	17573	30555	0.59	5.0E-18	10946665	NT	Mus musculus gasdermin (Gsdm), mRNA
5387	18589	31561	1.29	5.0E-18	AF087813.1	NT	Human endogenous retrovirus HERV-P-T47D
8917	21990	35535	3.47	5.0E-18	BE143312.1	EST_HUMAN	MRO-HT0161-221089-002-c06 HT0161 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11223	24292	37832	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11223	24292	37833	3.43	6.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12875	28450		6.28	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
13063	28696		28.56	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLG Homo sapiens cDNA clone GLCGA02 3'
127	13355	26386	0.91	4.0E-18	BE044078.1	EST_HUMAN	hs38h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.63
							repetitive element;
127	13355	26387	0.91	4.0E-18	BE044078.1	EST_HUMAN	hs38h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.63
							repetitive element;
1754	14903	27998	52.62	4.0E-18	AA621814.1	EST_HUMAN	nc24f11.s1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26328
1938	15081		1.05	4.0E-18	AI738592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							wb33h08.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392095 3'
2274	15407	28538	1.28	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2274	15407	28537	1.28	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
3892	17051	30060	0.61	4.0E-18	AI581586.1	EST_HUMAN	ar33i06.x1 Barestead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu
5479	18878	31691	2.47	4.0E-18	AI017565.1	EST_HUMAN	repetitive element;
5479	18678	31692	2.47	4.0E-18	AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
							ou23e08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8029	21112		0.62	4.0E-18	AA746811.1	EST_HUMAN	nc84e08.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1266988 similar to contains L1.12 L1
							repetitive element;
11254	24323	37964	7.59	4.0E-18	AA371807.1	EST_HUMAN	EST36633 Pituitary gland, subcloned (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to
							EST containing O family repeat
872	14048	27114	3.81	3.0E-18	AA814196.1	EST_HUMAN	p623h11.s1 NCL_CGAP_Kk15 Homo sapiens cDNA clone IMAGE:1324681 3' similar to SW:RS5_HUMAN
963	14128	27187	2.25	3.0E-18	BE088834.1	EST_HUMAN	g4b7812.40S RIBOSOMAL PROTEIN S6 ;
4060	17216	30225	1.06	3.0E-18	AI63247.2	NT	CMO-BT0690-270300-288-g07 BT0690 Homo sapiens cDNA
6968	20196	33622	4.72	3.0E-18	BE001671.1	EST_HUMAN	PMO-BN0081-700300-001-b08 BN0081 Homo sapiens cDNA
11167	24238	37869	1.99	3.0E-18	BF218650.1	EST_HUMAN	601B84856FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103662 5'
12832	25564		4.55	3.0E-18	AW022015.1	EST_HUMAN	cd31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
261	13480	26512	74.12	2.0E-18	AW836820.1	EST_HUMAN	QV1-L1T0036-150200-070-e07 L1T0036 Homo sapiens cDNA
11793	14339		74.12	2.0E-18	BE256097.1	EST_HUMAN	601114352FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33565044 5'
1193	18368	26374	0.94	2.0E-18	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18724		4.2	2.0E-18	AA888610.1	EST_HUMAN	ek53e07.s1 Scores: testis_NHT Homo sapiens cDNA clone IMAGE:1408652 3' similar to TR:O14577
5623	18817	31886	3.51	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ;
5623	18817	31887	3.51	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5989	19184		1.84	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6294	19467	32820	0.81	2.0E-18	X60459.1	NT	602021164F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
6294	19467	32821	0.91	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6408	19577	32838	0.9	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6448	19815	32979	2.93	2.0E-18	AW665853.1	EST_HUMAN	IL3-HT0819-220700-222-C12 HT0819 Homo sapiens cDNA
7594	20665	34141	0.59	2.0E-18	AA457619.1	EST_HUMAN	h94g01.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979884 3' similar to contains MER19.12 MER19 repetitive element ;
8341	21422	34947	0.5	2.0E-18	BE439524.1	EST_HUMAN	aa68d11.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77 ;
10283	23288	36884	0.95	2.0E-18	AW151673.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA
10283	23288	36884	0.95	2.0E-18	AW151673.1	EST_HUMAN	x87e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element ;
10283	23288	36885	0.95	2.0E-18	AW151673.1	EST_HUMAN	x87e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element ;
11217	24286	37925	2.91	2.0E-18	AW470791.1	EST_HUMAN	h633d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
12031	25014	38716	4.46	2.0E-18	AW151289.1	EST_HUMAN	xg47e08.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element ;
12465	14339		12.67	2.0E-18	BE256097.1	EST_HUMAN	MER3 repetitive element ;
4537	17875		0.76	1.0E-18	T85406.1	EST_HUMAN	601114352F1 NIH_JMGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
5471	18671	31851	2.64	1.0E-18	AV653405.1	EST_HUMAN	ye43g05.1 Scores: fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ;
5888	18882	32174	3.08	1.0E-18	DO0089.1	NT	AV653405 GLC Homo sapiens cDNA clone GLDKE11 3'
5888	18882	32175	3.08	1.0E-18	DO0089.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5584	19746	33128	1.31	1.0E-18	AL163280.2	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
8637	21717	35254	1.05	1.0E-18	AI148288.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
							cd6d09.x1 Scores: senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680393 3' similar to contains L1.t1 L1 repetitive element ;
10103	23141	36740	4.93	1.0E-18	UB1328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12416	25294	32084	4.65	1.0E-18	AF003528.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
559	13752	26780	5.1	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
560	13762	26780	3.91	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
8032	21115		3.69	9.0E-19	F08668.1	EST_HUMAN	HS223F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8866	21965	35501	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8866	21965	35502	2.87	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11392	24453	38116	3.15	9.0E-19	AB032966.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12171	13762	26780	19.34	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1073	14239		1.58	8.0E-19	AW974902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
8342	21423	34948	1.12	8.0E-19	BE158936.1	EST_HUMAN	MRO-HT0404-2T0200-001-g06 HT0404 Homo sapiens cDNA
2319	15451	26583	1.74	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp-His) box polypeptide 6 (RNA helicase, 54kd) (DDX6) mRNA
6585	19747	33129	2.11	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7452	20529	34002	0.94	7.0E-19	P28444	SWISSPROT	BETA CRYSTALLIN A2
10216	23252	36841	0.54	7.0E-19	A1344951.1	EST_HUMAN	tb01c08.x1 NCL_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
12316	28163		1.72	7.0E-19	AA706684.1	EST_HUMAN	z60b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3878	17038		1.16	6.0E-19	AW852830.1	EST_HUMAN	PMD-CT0248-131089-001-g01 CT0248 Homo sapiens cDNA
4585	17722	30705	1.56	6.0E-19	P34988	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	17722	30706	1.56	6.0E-19	P34988	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	18051		1.2	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
5878	19183	32483	5.17	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC58)
6346	19516	32873	0.59	5.0E-19	AW663302.1	EST_HUMAN	hh77b06.v1 NCL_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2968787 5'
10639	23673	37283	1.18	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11829	24818	38509	8.14	5.0E-19	AW183725.1	EST_HUMAN	x87b02.k1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element;
13083	25895		1.34	5.0E-19	U66060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S6A3N2T, TCRBV13S6A2T, TCRBV6S9A2T, TCRBV6S3A2T, TCRBV13S6P, TCRBV6S3A1N1T, TCRBV6S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
568	13760	26784	0.96	4.0E-19	AB007670.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2747	15884	28975	1.15	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287874 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5512	18710	31725	1.2	4.0E-19	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3955	17113	30114	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3955	17113	30115	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4400	17543	30528	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4400	17543	30527	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4969	17707	30686	1.42	3.0E-19	AV708138.1	EST_HUMAN	AV708138 ADC Homo sapiens cDNA clone ADCAMA11 5'
5394	18596		0.69	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7543	20615		1.88	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9658	21101	34614	1.09	3.0E-19	X89685.1	NT	Mus musculus mRNA for PCR33 protein
12593	25385		16.36	3.0E-19	AF165520.1	NT	Homo sapiens photobolin 1 protein (PSI) mRNA, complete cds
2627	19750	28869	20.06	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4568	17708		1.34	2.0E-19	A1311783.1	EST_HUMAN	gc91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE;
6179	18566	32703	0.81	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7493	20568	34040	0.63	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Ktapp9-1), mRNA
8525	21608	36145	10.24	2.0E-19	AA012854.1	EST_HUMAN	ze34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10113	23151	36753	0.64	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
494	13689		1.86	1.0E-19	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3938310 5'
2293	15367	28496	1.64	1.0E-19	H30795.1	EST_HUMAN	yo79g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2782	15898		2.4	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2909	16087		6.72	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3488	16855	28569	1.18	1.0E-19	AA834967.1	EST_HUMAN	aj49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 MER37 repetitive element;
5452	18652	31631	0.73	1.0E-19	A1890866.1	EST_HUMAN	wn91608.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16530 Q16530 PMS3 MRNA;
6199	19374	32725	2.6	1.0E-19	U12186.1	NT	Oryzoblagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6337	26213		0.63	1.0E-19	AA595527.1	EST_HUMAN	nt22d03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:963093 similar to contains L1.t1 L1 repetitive element;
7806	20862	34355	1.05	1.0E-19	U08813.1	NT	Oryzoblagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7806	20862	34356	1.05	1.0E-19	U08813.1	NT	Oryzoblagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7977	25856		0.75	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8644	21724	35261	1.94	1.0E-19	M64657.1	NT	Rabbit phosphatase kinase beta subunit mRNA, complete cds
8939	22018		2.72	1.0E-19	T99920.1	EST_HUMAN	y972b02.t1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
9950	22989		0.69	1.0E-19	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10390	23426	37032	25.12	1.0E-19	AW812259.1	EST_HUMAN	RC0-ST0174-191098-031-b05 ST0174 Homo sapiens cDNA
10400	23435	37042	1.59	1.0E-19	N44631.1	EST_HUMAN	y931e09.t1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:272872 5'
11184	24253	37688	1.87	1.0E-19	BE616028.1	EST_HUMAN	601279682FT NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3811493 5'
6764	19839	33336	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6764	19839	33337	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7687	20752	34234	1.46	8.0E-20	A1221371.1	EST_HUMAN	q986109.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7687	20752	34236	1.46	8.0E-20	A1221371.1	EST_HUMAN	q986109.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3349	16521	26537	0.71	7.0E-20	BF326455.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
7134	19550	31474	5.65	7.0E-20	AL1138120.1	EST_HUMAN	DKFZp447D092.t1 647 (synonym: htfbr1) Homo sapiens cDNA clone DKFZp447D092 5'
8693	21773	35305	8.83	7.0E-20	AA557657.1	EST_HUMAN	n146c04.s1 NCL_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
8693	21773	35306	8.83	7.0E-20	AA557657.1	EST_HUMAN	n146c04.s1 NCL_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
12014	24998		2.89	7.0E-20	AA557657.1	EST_HUMAN	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3645	18808	29822	3.64	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4387	17530	30511	4.58	6.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3816231 5'
4718	17853		1.9	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCB TA01 5'
7264	20347	33789	1.42	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8131	21213	34733	6.95	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares Fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8131	21213	34734	6.95	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares Fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8295	21377	34898	0.79	5.0E-20	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9035	22114	35657	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9035	22114	35658	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9644	21087		1.13	5.0E-20	O60609	SWISSPROT	HYPOTHEICAL PROTEIN DJ845024.1
1849	14802	27889	0.94	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6765	18957		1.13	4.0E-20	Q69880	SWISSPROT	HISTONE H2B C (H2B/C)
8110	21192		5.61	4.0E-20	AI874352.1	EST_HUMAN	t664g03.x1 NCL_CGAP_OY35 Homo sapiens cDNA clone IMAGE:2283396 3'
10717	23750	37357	1.13	4.0E-20	AW837469.1	EST_HUMAN	QY3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2207	15341	28468	1.22	3.0E-20	U03888.1	NT	Human BXP21 gene
4325	17488	30455	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4747	17882	30884	1.08	3.0E-20	AA037618.1	EST_HUMAN	2436b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element
9135	22214		2.69	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10527	23562	37188	0.47	3.0E-20	BF185284.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084343 5'
10900	23984		1.59	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12331	25239	32109	6.09	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
853	14030		5.65	2.0E-20	AW303868.1	EST_HUMAN	x24e10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS6_MOUSE
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5. ; hg69h09.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
1135	14300	27356	2.49	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ; hg69h09.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
2878	14030		5.32	2.0E-20	AW303868.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ; x24e10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
5081	18189	31163	5.15	2.0E-20	Q28983	SWISSPROT	P97461 40S RIBOSOMAL PROTEIN S5. ;
5081	18189	31164	5.15	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5266	18376		0.9	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
8309	21391	34915	0.97	2.0E-20	AA308467.1	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
8391	22466	36030	2.65	2.0E-20	D10083.1	NT	EST180326 Liver III Homo sapiens cDNA 5' end
9391	22466	36031	2.65	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12743	26878	31852	2.17	2.0E-20	H55371.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
2070	15995	28327	6.61	1.0E-20	AA281951.1	EST_HUMAN	CH-R220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
4560	17698	30879	1.02	1.0E-20	BF115158.1	EST_HUMAN	z11d06.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:71281 5' similar to contains MER19.12
7034	20170	33592	0.74	1.0E-20	AF049567.1	EST_HUMAN	MER19 repetitive element ;
9384	22439	35998	2.08	1.0E-20	11418491	NT	hr84b06.x1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element ;
11847	24836	38530	2.03	1.0E-20	AF223391.1	NT	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
12461	25323		2.91	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							nc60g08.r1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2979	16166		1.18	8.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library/Homo sapiens cDNA clone MPIp12-8/J21
12174	25135		3.98	9.0E-21	AW898188.1	EST_HUMAN	RC3-NN0068-080500-021-503 NN0068 Homo sapiens cDNA
8011	22080		0.98	8.0E-21	AW674891.1	EST_HUMAN	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
11830	24819	38510	3.91	8.0E-21	AA809411.1	EST_HUMAN	Q95169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR ;
12345	25250		3.8	8.0E-21	OZ1330	SWISSPROT	ab7108.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
2130	15266	28385	3.85	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2130	15266	28386	3.85	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3792	16953	28958	1.36	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4369	17512		6.29	7.0E-21	AA046502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6564	19726	33104	0.94	7.0E-21	AL163218.2	NT	2k57a06.t1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487868 5'
8592	21653	35203	1.46	7.0E-21	AJ277557.1	NT	Homo sapiens chromosome 21 segment HS21C018
8875	21954	35490	4.94	7.0E-21	D14718.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
10319	23354	36963	1.07	7.0E-21	AW856922.1	EST_HUMAN	Human chromosomal protein HMGT related gene
10934	24016	37648	1.94	7.0E-21	AA723404.1	EST_HUMAN	RC0-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
4220	17369	30358	0.76	6.0E-21	BE408611.1	EST_HUMAN	zg73d03.s1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:398981 3' similar to
9336	22412		1.39	6.0E-21	BE162737.1	EST_HUMAN	gbM14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN) contains THR.13 OFR
947	14120	27181	1.34	5.0E-21	5902031	NT	repetitive element ;
2354	15485	28617	1.23	5.0E-21	AA928194.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
4453	17623	30604	3.21	5.0E-21	BE968833.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4809	14120	27181	1.16	5.0E-21	5902031	NT	002711 PRO-POL-DUTPASE POLYPROTEIN ;
4923	18053	31039	8.33	5.0E-21	4885474	NT	002711 PRO-POL-DUTPASE POLYPROTEIN ;
6902	20217		0.77	5.0E-21	AW440864.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN ;
7157	20291	33734	1	5.0E-21	BE859505.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN ;
10801	23834	37457	0.54	5.0E-21	O91690	SWISSPROT	002711 PRO-POL-DUTPASE POLYPROTEIN ;
10801	23834	37458	0.54	5.0E-21	O91690	SWISSPROT	002711 PRO-POL-DUTPASE POLYPROTEIN ;
12259	25186		1.28	5.0E-21	AA393574.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN ;
1772	14921	28015	1.86	4.0E-21	AA970713.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descrip ^r
7011	20147	33668	2.61	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
9983	23022	36614	0.82	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H-LA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10010	23048	36842	0.51	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1884	15028	28135	1.1	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.s1 Strategene fetal refseq 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2348	15478	28611	1.51	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3148	16324	28335	6.41	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5616	18810	31878	0.82	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5616	18810	31879	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5856	18046		0.9	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone GLCGO410 3'
6308	16480		2.74	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084945 5'
7215	20080	33493	7.52	3.0E-21	BF361083.1	EST_HUMAN	RC1-OT0083-100800-01B-g08 OT0083 Homo sapiens cDNA
9884	22634	36518	0.92	3.0E-21	AW897760.1	EST_HUMAN	CMT-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12879	26099	31665	3.58	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
150	13375		24.5	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0468-170200-080-g12 HT0468 Homo sapiens cDNA
958	14131	27189	0.61	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
958	14131	27190	0.61	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1241	14400		3.03	2.0E-21	BE084470.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
2703	15821	28937	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2703	15821	28938	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5601	18796	31846	1.66	2.0E-21	AIG24582.1	EST_HUMAN	ts30903.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854 HYPOTHETICAL 51.1 KD PROTEIN ;
5694	18888	32178	0.8	2.0E-21	AA027211.1	EST_HUMAN	z897a12.r1 Soares_fetal_heart_NBH119W Homo sapiens cDNA clone IMAGE:366910 5'
5694	18888	32179	0.8	2.0E-21	AA027211.1	EST_HUMAN	z897a12.r1 Soares_fetal_heart_NBH119W Homo sapiens cDNA clone IMAGE:366910 5'
6157	19333	32679	0.74	2.0E-21	W44483.1	EST_HUMAN	z226102.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323667 5'
6467	21548	35078	0.58	2.0E-21	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
8568	21639	35178	8.13	2.0E-21	BE141785.1	EST_HUMAN	QV04-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
9023	22102	35842	3.27	2.0E-21	AU136779.1	EST_HUMAN	AUT36779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11313	24377		2.04	2.0E-21	BE350127.1	EST_HUMAN	h03901.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER28 repetitive element ;
11599	24652	38335	2.88	2.0E-21	BE973829.1	EST_HUMAN	601880638F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11599	24652	38336	2.88	2.0E-21	BE973829.1	EST_HUMAN	601880839F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12572	25339		6.44	2.0E-21	AF176815.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds n45604.s1 NCJ_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1284	14440	27609	1.89	1.0E-21	AA567697.1	EST_HUMAN	MER29 repetitive element;
1434	14587		4.93	1.0E-21	AL601264.1	EST_HUMAN	ar68612.x1 Barstead cdon HP1RB7 Homo sapiens cDNA clone IMAGE:2152343 3'
6616	19776		2.73	1.0E-21	AL079792.1	EST_HUMAN	DKFZp434l0830_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434l0830 5'
							qq47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:MB4241.QM
7342	20422	33885	4.7	1.0E-21	AI223104.1	EST_HUMAN	PROTEIN (HUMAN);
10448	23483	37092	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10448	23483	37093	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10812	23845		1.31	1.0E-21	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
13014	25657		1.67	1.0E-21	AF046133.1	NT	Homo sapiens chromosome Xp22.410-8
4530	17698	30654	2.38	9.0E-22	AI702438.1	EST_HUMAN	b294a03.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:226204 3' similar to TR:Q15408 Q15408
8803	21882	35420	2.02	9.0E-22	AL163201.2	NT	NEUTRAL PROTEASE LARGE SUBUNIT;
8803	21882	35421	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11031	24110	37746	3.1	9.0E-22	AV761874.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
12007	24992	38696	1.39	9.0E-22	AU140368.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSGCC05 5'
971	14144		7.93	8.0E-22	BE144748.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000384 5'
8080	21192		3.36	8.0E-22	AA046502.1	EST_HUMAN	CNO-HT0178-281089-078-h05 HT0179 Homo sapiens cDNA
4398	17541	30622	3.78	7.0E-22	AL163246.2	NT	z167a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487668 5'
5150	18272	31241	0.91	7.0E-22	AB009681.1	NT	Homo sapiens chromosome 21 segment HS21C046
8988	21867		1.24	7.0E-22	AF151054.1	NT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
9032	22111	35653	2.77	7.0E-22	M78590.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
9802	22842	38418	2.05	7.0E-22	AF009660.1	NT	Homo sapiens HSPC220 mRNA, complete cds
8436	21517		1.25	6.0E-22	AW028123.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBCF07
6646	19905	33192	3.27	6.0E-22	AL163303.2	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
10525	23560	37167	2.98	5.0E-22	U60822.1	NT	wx05g07.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
							Homo sapiens chromosome 21 segment HS21C103
12833	25555		1.63	5.0E-22	BF476511.1	EST_HUMAN	Homo dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
3726	18887		0.77	4.0E-22	AJ271735.1	NT	naa27b08.x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:3255868 3' similar to contains Alu
8608	26224		2.81	4.0E-22	AL163202.2	NT	repetitive element;
10961	24042	37677	1.97	4.0E-22	BF218030.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
							Homo sapiens chromosome 21 segment HS21C002
							601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085434 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13021	25672		3.85	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
981	14154		1.34	3.0E-22	AI469879.1	EST_HUMAN	Im14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.11 L1 repetitive element;
2636	15759	28873	1.33	3.0E-22	AI659038.1	EST_HUMAN	wl0604.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429893 3' similar to SW:RL21_HUMAN
3763	16924		1.65	3.0E-22	D14718.1	NT	P48778 60S RIBOSOMAL PROTEIN L21.; Human chromosomal protein HMGT related gene
4922	16052	31038	3.18	3.0E-22	AI090125.1	EST_HUMAN	q28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8011	21091	34573	0.8	3.0E-22	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8425	21506		1.11	3.0E-22	BE166813.1	EST_HUMAN	QV0-HT0368-09020-099-112 HT0368 Homo sapiens cDNA
8430	21511	35042	1.88	3.0E-22	BE089841.1	EST_HUMAN	RC9-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8555	21636	35172	1.14	3.0E-22	X60860.1	NT	R.retus RY235 mRNA for a potential ligand-binding protein
8555	21636	35173	1.14	3.0E-22	X60860.1	NT	R.retus RY235 mRNA for a potential ligand-binding protein
2008	15148		4.04	2.0E-22	N24942.1	EST_HUMAN	yk73d05.s1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:267369 3'
2580	15715	28833	1.72	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3507	16674	29684	3.98	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4341	17484	30466	1.41	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
5973	25814	32476	1.47	2.0E-22	W39455.1	EST_HUMAN	z22001.r1 Soares_aneurysm_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6306	19478	32833	3.58	2.0E-22	BF092116.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
9904	22944	36529	1.78	2.0E-22	AI276522.1	EST_HUMAN	cl78h08.x1 Soares_NbHMPu.S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains
10001	23038	36630	0.95	2.0E-22	AA715315.1	EST_HUMAN	MER29.13 MER29 repetitive element;
10001	23039	36631	0.95	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
12056	25037	38745	1.52	2.0E-22	AW418580.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
12139	25656	31954	2.33	2.0E-22	AL163280.2	NT	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
1927	15070	28175	2.05	1.0E-22	AW865517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2651	15774	28887	2.36	1.0E-22	U50871.1	NT	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
3497	16864	29076	1.53	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
7820	20971	34478	1.09	1.0E-22	BE084667.1	EST_HUMAN	Human DNA, SINE repetitive element
10776	23809	37432	1.05	1.0E-22	AI365435.1	EST_HUMAN	MR0-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA q220h07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2 MER29 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10776	23839	37433	1.05	1.0E-23	AI368435.1	EST_HUMAN	qz09b07.x1 NCI_CGAP_COLL1 Homo sapiens cDNA clone IMAGE:2020981.3 similar to contains MER29.b2 MER29 repetitive element;
13078	26707		12.31	9.0E-23	AW802801.1	EST_HUMAN	IL2-UM0078-070400-061-F11 UM0076 Homo sapiens cDNA
3661	16824	29833	0.74	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3385	16555		2.21	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLG Homo sapiens cDNA clone GLCAW/C07.3'
11293	24359	38000	3.74	7.0E-23	5031932	NT	Homo sapiens Nds58 (D. melanogaster)-like protein (NOT58L) mRNA
3520	16686		1.83	6.0E-23	AF198333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4383	17628	30507	1.15	6.0E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
12288	25211	32097	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12283	25211	32098	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12483	25335	32058	3.18	6.0E-23	AI209130.1	EST_HUMAN	qz09b03.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1838460.3 similar to SW:MY10_MOUSE P23249 PROTEIN MOV-10.;
5560	18767	31786	4.01	5.0E-23	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
6359	25824	32898	3.69	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7695	25824	32898	2.78	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6570	19732	33110	0.67	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6570	19732	33111	0.67	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8022	21105	34622	3.26	3.0E-23	AA130185.1	EST_HUMAN	z135g09.11 Soares, pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:503988.5 similar to contains MER28.12 MER28 repetitive element;
8450	22566	36130	3.72	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9450	22566	36131	3.72	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10523	23558		1.42	3.0E-23	AW897827.1	EST_HUMAN	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA
11372	24433		1.35	3.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
683	13668	26859	3.69	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZ TEL1 gene
1168	15888		3.46	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGF) gene, complete cds
2856	15970	28079	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2856	15970	28080	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
3457	16824		1.11	2.0E-23	AI201458.1	EST_HUMAN	q873f11.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3810	16970		3.53	2.0E-23	BE165990.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
4085	17240	30246	4.43	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4085	17240	30247	4.43	2.0E-23	H59931.1	EST_HUMAN	UT16a02.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:205418 5'
							UT16a02.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds, and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8057	21140		5.28	2.0E-23	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21C103
9044	22123	35965	0.95	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12265	25199		6.7	2.0E-23	M32658.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S9A2 to TCRBV12S2 region
12844	25591		3.68	2.0E-23	AF009690.1	NT	AU133331 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
12983	26103		2.3	2.0E-23	AU133931.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
4650	17766	30769	1.97	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C010
4888	18018		5.42	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6861	20013		3.27	1.0E-23	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
							2w82c06.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12
8551	21632	35169	4.61	1.0E-23	AA448097.1	EST_HUMAN	PTR5 repetitive element ;
10909	23992	37625	2.19	1.0E-23	BE409843.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638254 5'
10909	23992	37626	2.19	1.0E-23	BE409843.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638254 5'
13082	28074	31854	1.35	1.0E-23	AW601816.1	EST_HUMAN	QV0-NN1020-170400-195-a11 NN1020 Homo sapiens cDNA
							ab75a08.a1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to
586	13758		1.67	8.0E-24	AA663213.1	EST_HUMAN	TR:E19822 E19822 CA PROTEIN. ;
4771	17908	30888	1.12	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4771	17908	30889	1.12	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
6578	19740	33121	0.95	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3976	17133		0.94	7.0E-24	AW697854.1	EST_HUMAN	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
5281	18400		16.78	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311.1 434 (synonym: htes) Homo sapiens cDNA clone DKFZp434A2311 5'
							repetitive element; contains MER19.12 MER19 repetitive element ;
10876	23961		1.91	7.0E-24	AW303317.1	EST_HUMAN	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete ccs
724	13906		2.21	8.0E-24	AB001421.1	NT	Homo sapiens chromosome 21 segment HS21C049
861	14038	27100	12.8	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
4078	17234	30241	9.39	6.0E-24	AJ22043.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7635	20885	34493	1.27	5.0E-24	AF223031.1	NT	

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4371	17514		0.9	4.0E-24	BF369469.1	EST_HUMAN	RCO-GN0090-250900-022-109 GN0090 Homo sapiens cDNA
6052	19234	32559	2.77	4.0E-24	AA564178.1	EST_HUMAN	nm31406.e1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW/POL_MLVRK
8880	21059	35404	0.71	4.0E-24	AW813711.1	EST_HUMAN	P31785 POL POLYPROTEIN ;
11454	24514	38182	2.06	4.0E-24	BES44822.1	EST_HUMAN	RC3-ST0197-130100-014-f06 STD197 Homo sapiens cDNA
12569	25446	32054	4.02	4.0E-24	AB029016.1	NT	301078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484498 5'
							Homo sapiens mRNA for KIAA1093 protein, partial cds
7229	20134	33551	0.73	3.0E-24	U68061.1	NT	Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
7229	20134	33552	0.73	3.0E-24	U68061.1	NT	Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
8818	21698		2.94	3.0E-24	AW614871.1	EST_HUMAN	hh88c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867850 3' similar to contains MER28.b2
8873	21763		1.24	3.0E-24	AW92076.1	EST_HUMAN	MER29 repetitive element ;
9685	22627	36198	3.79	3.0E-24	AL163252.2	NT	EST374149 MAGS resequences, MAGG Homo sapiens cDNA
12756	25501	32034	1.34	3.0E-24	BF127782.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
2422	15551	28678	2.55	2.0E-24	AA167539.1	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053396 5'
3899	17068		0.82	2.0E-24	AW898189.1	EST_HUMAN	zp1109.r1 Stralagene fetal retina 637202 Homo sapiens cDNA clone IMAGE:609161 5'
7515	26219		0.63	2.0E-24	AL163209.2	NT	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
7843	20712	34191	0.9	2.0E-24	AF086824.1	NT	Homo sapiens chromosome 21 segment HS21C009
7848	20717	34194	0.58	2.0E-24	AJ003536.1	EST_HUMAN	Mus musculus thofrac-interacting citron kinase (Crik) mRNA, complete cds
8938	22017	35559	3.81	2.0E-24	AL119158.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-5H13
8977	22056		0.9	2.0E-24	H69214.1	EST_HUMAN	DKFZp781L712_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781L712 5'
10058	23066	36598	1.06	2.0E-24	AJ521759.1	EST_HUMAN	Y92809.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains
10598	23066	36599	1.06	2.0E-24	AJ521759.1	EST_HUMAN	MER28 repetitive element ;
12580	26153	27972	21.43	2.0E-24	M28877.1	NT	tf77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
1731	14881		4.81	1.0E-24	7709340	NT	Human O family dispersed repeat element
2758	18555		1.65	1.0E-24	AW820194.1	EST_HUMAN	Homo sapiens CGI-127 protein (LOC51649), mRNA
3085	16261	29278	0.72	1.0E-24	D85423.1	NT	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
4385	17528		1.93	1.0E-24	AF143313.1	NT	Mus musculus mRNA for HGT keratin, partial cds
							Homo sapiens PTEN (PTEN) gene, exon 2

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6531	19695	33068	1.13	1.0E-24	7106338	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
7720	20784	34272	4.85	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7807	20969	34465	5.07	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0168-271189-005-409 HT0168 Homo sapiens cDNA
8130	21212	34732	2.29	1.0E-24	AW501164.1	EST_HUMAN	CMO-NN1010-130300-281-407 NN1010 Homo sapiens cDNA
11999	24984	38689	1.37	9.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5111	18239	31206	2.7	7.0E-25	AA483944.1	EST_HUMAN	ne92a10.s1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element.:
8413	21484	35025	3.7	7.0E-25	AA488646.1	EST_HUMAN	ne90a09.s1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element.:
12003	24988	38693	3.64	7.0E-25	AA583540.1	EST_HUMAN	n129h06.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST
7131	18597	34458	5.04	6.0E-25	W87623.1	EST_HUMAN	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.:
7899	20561	34458	11.72	8.0E-25	7305350	NT	zh65h07.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416889 5'
1683	14835	27920	1.61	5.0E-25	AW850271.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
11596	24649	38333	3.12	5.0E-25	AW979107.1	EST_HUMAN	IL3-CT0219-161199-031-DD4 CT0219 Homo sapiens cDNA
1478	14631	27716	2.66	4.0E-25	T88107.1	EST_HUMAN	EST391217 MAGS resequences, MAGP Homo sapiens cDNA
3489	16656		2.81	4.0E-25	BE170657.1	EST_HUMAN	ye56h04.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
4436	17576	36779	4.06	4.0E-25	BE170657.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
10144	23182	28516	0.83	4.0E-25	AA383873.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
2256	16389	28516	1.02	3.0E-25	BE068922.1	EST_HUMAN	EST97317 Thymus Homo sapiens cDNA 5' end similar to EST containing O family repeat
3396	16596	29581	3.12	3.0E-25	8923321	NT	RCS-BT0377-131289-031-F02 BT0377 Homo sapiens cDNA
3396	16596	29582	3.12	3.0E-25	P29922	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5015	18144	31119	0.7	3.0E-25	AL163210.2	NT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8532	21613	35149	5.42	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11287	24353	37993	2.7	3.0E-25	AA579013.1	EST_HUMAN	n130h10.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:916531 similar to contains L1.L1 L1 repetitive element.:
1378	14533	27807	4.9	2.0E-25	6032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1), mRNA
2382	15513	28641	7.33	2.0E-25	BE888016.1	EST_HUMAN	60161130F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2893	15731	28648	3.71	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30436	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30437	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9967	23008	36801	2.13	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Slavides GS) Homo sapiens cDNA
375	13583	26617	0.81	1.0E-25	AL040228.1	EST_HUMAN	DKFZp434H0313_r1 434 (synonym: hnc3) Homo sapiens cDNA clone DKFZp434H0313 5'
1277	14434		2.07	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4983	18112	31089	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-109 HT0454 Homo sapiens cDNA
5298	18415	31383	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
5298	18415	31384	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
6697	19555		0.95	1.0E-25	AA189080.1	EST_HUMAN	z445006.s1 Stragene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element;
6939	25638	33686	2.95	1.0E-25	AA582660.1	EST_HUMAN	nt64h11.s1 NCICGAP_K1d6 Homo sapiens cDNA clone IMAGE:1087749 3'
8098	21180	34698	3.56	1.0E-25	AA709079.1	EST_HUMAN	PTRE.13 PTR5 repetitive element ;
8746	22810	36388	1.32	1.0E-25	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
9746	22810	36389	1.32	1.0E-25	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
11212	24281	37920	3.11	1.0E-25	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
12280	25209	38364	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12280	25209	38363	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2563	16678	28602	1.94	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11252	24321		2.35	9.0E-26	AI905368.1	EST_HUMAN	QV-BT087-301298-008 BT087 Homo sapiens cDNA
12140	25901		5.33	9.0E-26	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C085
5811	18001		1.51	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1608	14761	27840	5.61	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4089	17244	30251	1.68	7.0E-26	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4275	17420	30407	1.92	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908386 3'
5755	18947	32249	0.84	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11688	24651		6.95	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stragene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12901	25596		5.49	7.0E-26	AW954559.1	EST_HUMAN	EST366629 IMAGE resequences, MAGC Homo sapiens cDNA
2300	15432	28565	3.83	6.0E-26	AF026308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and lymphogen gene families
3427	16595	28611	0.69	6.0E-26	AA206131.1	EST_HUMAN	zn32h04.r1 Stragene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
10753	23786	37400	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10753	23786	37401	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11979	24964	38666	2.15	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1204	14366	27426	0.89	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1204	14366	27427	0.89	5.0E-26	AF08235.1	EST_HUMAN	as38108.x1 Barstead aorta HPLR66 Homo sapiens cDNA clone IMAGE:2318519 3' similar to WP:F49C12.11 CE03371 ;
9812	22667		3.29	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10897	23981	37613	2.84	4.0E-26	BE265187.1	EST_HUMAN	901191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635210 5'
11804	24667	38342	1.38	4.0E-26	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1797	14946	28038	1.25	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2059	15200	28314	1.14	3.0E-26	AL046855.2	EST_HUMAN	DKFZp340666_r1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZp340666 5'
2086	15228		3.34	3.0E-26	AA116885.1	EST_HUMAN	zn30d08.r1 Stratiene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5'
3878	17037	30035	1.41	3.0E-26	AA192484.1	EST_HUMAN	similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3878	17037	30036	1.41	3.0E-26	AA162484.1	EST_HUMAN	zn30f10.r1 Stratiene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
7051	20104	33521	6.09	3.0E-26	BF245458.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11867	24855	38550	1.97	3.0E-26	AW876651.1	EST_HUMAN	zn30f10.r1 Stratiene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
11867	24855	38551	1.97	3.0E-26	AW876651.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11902	24890	38591	7.79	3.0E-26	AA583173.1	EST_HUMAN	zn30f10.r1 Stratiene colon (#937204) Homo sapiens cDNA clone IMAGE:4083278 5'
699	13862	26915	6.84	2.0E-26	AL163282.2	NT	G695374 THYROID RECEPTOR INTERACTOR ;
1917	15050		3.07	2.0E-26	AL038059.2	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
3303	16477	29499	5.22	2.0E-26	X86694.1	NT	601864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
10981	24070		1.93	2.0E-26	D87675.1	NT	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
							QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
							m37d05.x1 NCL_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
							OFR repetitive element ;
11493	24551	38226	2.96	2.0E-26	AI801412.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
11704	24701		2.08	2.0E-26	AF050066.1	NT	DKFZp566L171_e1 568 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566L171 3'
12389	26275		1.78	2.0E-26	AB037899.1	NT	M.musculus mRNA for asticytic phosphoprotein, PEA-15
12604	26088	31658	2.33	2.0E-26		NT	Homo sapiens DNA for amyloid precursor protein, complete cds
139	13365	28398	8.96	1.0E-26	BE170371.1	EST_HUMAN	1689a01.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu
2106	15244	28365	1.42	1.0E-26	AL039383.2	EST_HUMAN	repetitive element/contains element MER20 MER20 repetitive element ;
2751	15688		6.28	1.0E-26	AF261085.1	NT	Homo sapiens MHG class 1 region
6980	20208		2.89	1.0E-26	BE169980.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
11131	24203		1.96	1.0E-26	AL038487.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12655	26178		2.77	1.0E-26	H55083.1	EST_HUMAN	QV4-HT0538-020300-123-e02 HT0538 Homo sapiens cDNA
13175	25763		1.16	1.0E-26	AW408742.1	EST_HUMAN	DKFZp34041910_r1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZp34041910 5'
							DKFZp360C2146_r1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp360C2146 5'
							MR3-HT0487-160200-113-g01 HT0487 Homo sapiens cDNA
							DKFZp360C2146_r1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp360C2146 5'
							CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
							UI-HF-BM0-edw-d-10-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7757	20816		0.87	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9803	22769		5.02	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12143	28118		6.5	9.0E-27	BF445556.1	EST_HUMAN	na03c07.x1 NCLCGAP_P728 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.11 OFR repetitive element :
11	13249	26249	4.22	8.0E-27	AI831462.1	EST_HUMAN	wf49c04.x1 NCLCGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element :
571	13763		4.57	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1448	14601	27678	23.84	8.0E-27	AW182737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gbK00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1448	14601	27679	23.84	8.0E-27	AW182737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gbK00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2236	15369	28499	1.82	8.0E-27	AW884776.1	EST_HUMAN	PM2-SN0018-220300-002-e07 SN0018 Homo sapiens cDNA
3254	16428	29446	1.8	8.0E-27	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3434	16602	29821	0.75	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5812	19002	32308	1.07	8.0E-27	AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBC806 5'
7117	18543		2.65	8.0E-27	BE926960.1	EST_HUMAN	MR4-BT0398-260800-204-d06 BT0398 Homo sapiens cDNA
7192	20057	33467	2.49	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
9410	22484	36048	1.63	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
9410	22484	36049	1.63	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
701	13884		1.77	7.0E-27	Z70884.1	NT	Human endogenous retroviral element HC2
5201	18322		2.19	7.0E-27	AW629172.1	EST_HUMAN	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976879 3' similar to TR:076040
8058	22137		0.97	7.0E-27	D6884.1	NT	076040 ORF2: FUNCTION UNKNOWN. ;
10888	24067		3.7	7.0E-27	AJ271735.1	NT	Human mRNA for KIA0231 gene, partial cds
10964	24046	37679	3.21	6.0E-27	M26697.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
12094	25074	38781	1.55	6.0E-27	U93163.1	NT	Human nuclear protein (B23) mRNA, complete cds
7654	21004		0.73	5.0E-27	AL163033.2	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10442	23477	37081	3.21	5.0E-27	BF666614.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10442	23477	37082	3.21	5.0E-27	BF666614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6863	20035	33444	1.65	4.0E-27	9910569	NT	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
							Mus musculus sperm tail associated protein (Stap), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6125	21207		0.98	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8172	21254		1.31	4.0E-27	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9945	22984	36577	0.61	4.0E-27	AW980850.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11903	24681	38592	2.62	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
13213	26080	31855	1.17	4.0E-27	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
2099	15239	28361	7.1	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4395	17529	30510	1.55	3.0E-27	BE071924.1	EST_HUMAN	PMD-BT0527-090100-001-411 BT0527 Homo sapiens cDNA
5462	18982	31641	6.81	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9505	22771	36342	3.49	3.0E-27	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
42	13280	26289	9.28	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1944	15087		24.24	2.0E-27	AA565345.1	EST_HUMAN	hK01b10.a1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3178	16353		13.34	2.0E-27	AW629172.1	EST_HUMAN	h51h12.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:076040
3296	16470	29489	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3296	16470	29490	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6814	19987	33373	0.79	2.0E-27	H02655.1	EST_HUMAN	Y36601.1 Scieris placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8282	21394	34863	1.17	2.0E-27	AI866347.1	EST_HUMAN	SP-HMGC_MOUSE Q02591 HOMEBOX PROTEIN ;
9469	22526		2.6	2.0E-27	AA551527.1	EST_HUMAN	w128g07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
8995	23033	36625	0.83	2.0E-27	X60658.1	NT	hK08h05.a1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1
10241	23276	36868	1.45	2.0E-27	M78590.1	EST_HUMAN	repetitive element ;
10241	23276	36869	1.45	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
11197	24266	37801	3.61	2.0E-27	AU121685.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCF07
11777	15087		6.43	2.0E-27	AA565345.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCF07
12107	25087	38791	1.64	2.0E-27	AF216850.1	NT	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000748 5'
449	13645		2.34	1.0E-27	AL163246.2	NT	hK01b10.a1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
1021	14192	27251	4.97	1.0E-27	AB029898.1	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
6674	19833	33222	6.51	1.0E-27	60058551	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
							Homo sapiens chromosome 21 segment HS21C046
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
							Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
7010	20146	33566	1.85	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000085C10
7010	20146	33567	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000085C10
8809	21888	35430	1.16	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8188	22264		1.69	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA
8923	22983	36851	2.65	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
12005	24880	36694	3.05	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant bbsh mRNA, complete cds
144	13368		2.26	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
321	13535	26667	2.17	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN II ALPHAC PRECURSOR [3] TR:Q07280 TR:Q07313 ;
10601	23636	37243	0.47	9.0E-28	AA174078.1	EST_HUMAN	z018g12.61 Stratagene fetal retina 937202 Homo sapiens cDNA clone NT2RP1000443 5'
12224	25173		3.04	9.0E-28	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12563	26003		13.39	8.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
1208	14370	27430	11.5	7.0E-28	AU142750.1	EST_HUMAN	TR:O60302 O60302 KIAA0558 PROTEIN, contains element MER22 repetitive element ;
11483	24822	38192	1.65	7.0E-28	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12181	25141		5.04	7.0E-28	AV735348.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone OBFACA12 5'
9119	22188		1.28	6.0E-28	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
12886	25577		5.92	6.0E-28	AA504562.1	EST_HUMAN	aa60e03.r1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
328	13542		2.75	5.0E-28	A1921003.1	EST_HUMAN	wo18c07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element ;
4116	17270	30269	38.94	5.0E-28	R76762.1	EST_HUMAN	y88f10.r1 Scores placenta N62HP Homo sapiens cDNA clone IMAGE:148443 5'
2869	15608	28926	1.46	4.0E-28	AW195066.1	EST_HUMAN	xn33c09.x1 NCI CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2885504 3' similar to SW:GG85_HUMAN
3177	16352	28358	1.34	4.0E-28	BE409100.1	EST_HUMAN	Q08379 GOLGIN-95 ;
7483	20558	34030	3.56	4.0E-28	A1198941.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
11105	24177		4.19	4.0E-28	AF028308.1	NT	qf66f10.x1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
11255	24324		14.89	4.0E-28	AB038241.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
11278	20558	34030	4.34	4.0E-28	A1198941.1	EST_HUMAN	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
12822	25418		1.7	4.0E-28	AW854244.1	EST_HUMAN	qf66f10.x1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12773	26069		1.62	4.0E-28	AW862360.1	EST_HUMAN	RC3-CT0254-240400-210-T12 CT0254 Homo sapiens cDNA
							RC0-CT0379-070100-031-n01 CT0379 Homo sapiens cDNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No	Top Hit Database Source	Top Hit Descriptor
1312	14488		2.29	3.0E-28	AF165382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5227	18349		0.94	3.0E-28	AF009880.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8027	22106	35647	2.28	3.0E-28	BF364030.1	EST_HUMAN	MR3-HT0713-280300-013-f09 HT0713 Homo sapiens cDNA
11176	24245	37878	2.09	3.0E-28	U63688.1	NT	Homo sapiens MHC class I region
12653	25433		3.77	3.0E-28	AI831991.1	EST_HUMAN	wj9807.x1 NCL CGAP_Lym?2 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element ;
12803	25836		3.29	3.0E-28	BE082801.1	EST_HUMAN	RC2-BT0642-210200-013-f03 BT0642 Homo sapiens cDNA
12865	25578	31993	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12865	25576	31994	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
91	13326	26354	12.78	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1191	14333	27411	9.24	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2546	15671	28795	2.16	2.0E-28	AI348634.1	EST_HUMAN	q93606.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element ;
3446	16614	28632	0.81	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6437	18604	32968	1.48	2.0E-28	BF224402.1	EST_HUMAN	h76c03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element ;
8460	19627		3	2.0E-28	BF212905.1	EST_HUMAN	601814198F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8234	21316	34837	0.93	2.0E-28	AF008273.1	NT	Sus scrofa domestica submandibular apomucin mRNA, complete cds
9783	22823		2.23	2.0E-28	AW972305.1	EST_HUMAN	EST384394 IMAGE resequences, MAGL Homo sapiens cDNA
11913	24900	38603	2.52	2.0E-28	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12631	25424		1.74	2.0E-28	H06376.1	EST_HUMAN	y76c09.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:44300 5'
1508	14661	27744	2.85	1.0E-28	D36044.1	NT	Human gene for AII-receptor, exon 7-9
2294	15426	28560	3.91	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
4691	17826		0.95	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
8044	21127		1.95	1.0E-28	11426885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63081), mRNA
8208	21260		3.03	1.0E-28	8922753	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9478	22535	36099	4.75	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (metastasis to liver in mouse) [Homo sapiens cDNA 5' end similar to similar to retroviral LTR
10080	23118	36720	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
10080	23118	36721	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12186	25145		7.66	1.0E-28	AA054182.1	EST_HUMAN	z151c01.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:380448 5'
13013	25881		4.56	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13135	25122	31643	1.8	9.0E-29	AW683987.1	EST_HUMAN	h17606.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12752	25498		2.57	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 60 PROTEIN
1832	14784	27870	1.98	7.0E-29	AW966447.1	EST_HUMAN	EST378521 MAGE resequences, MAGI Homo sapiens cDNA
13197	25779		9.03	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
608	13797	26817	9.39	8.0E-29	A939748.1	EST_HUMAN	w66801.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468985 3' similar to TR:O13475
12495	25342		5.19	6.0E-29	BE940438.1	EST_HUMAN	O16475 UNNAMED HERV-H PROTEIN contains LTR7.b1 LTR7 repetitive element ;
12587	25385		2.1	6.0E-29	BF568097.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
5113	18241		2.39	5.0E-29	AL163203.2	NT	602184082FT NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
8929	22008		8.35	5.0E-29	AW887541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12795	25531		1.49	5.0E-29	BE612449.1	EST_HUMAN	RC3-OT0081-170300-011-c12 OT0081 Homo sapiens cDNA
3304	16478		2.28	4.0E-29	AJ752387.1	EST_HUMAN	601451827FT NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855726 5'
6133	18312		7.06	4.0E-29	BE164930.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8272	21354	34870	0.84	4.0E-29	A678101.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
8272	21354	34871	0.84	4.0E-29	A678101.1	EST_HUMAN	wd35g06.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8944	22023	35583	3.59	4.0E-29	J04988.1	NT	MER29.12 MER29 repetitive element ;
4536	17674	30658	1.31	3.0E-29	AB042287.1	NT	MER29.12 MER29 repetitive element ;
4855	17888	30976	1.1	3.0E-29	BF333238.1	EST_HUMAN	Human 90 kD heat shock protein gene, complete cds
6053	19235	32960	0.83	3.0E-29	BE314018.1	EST_HUMAN	Homo sapiens PTS gene for 6-pyruvoyltransferin synthase, complete cds
8931	22010	35548	3.23	3.0E-29	D38044.1	NT	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
9500	22558	38119	1.22	3.0E-29	AW303317.1	EST_HUMAN	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
9731	22796		1.49	3.0E-29	AL163246.2	NT	Human gene for Ah-receptor, exon 7-9
10164	23201		0.81	3.0E-29	BE350127.1	EST_HUMAN	xv17f03.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
11546	24802	38278	2.26	3.0E-29	AA403033.1	EST_HUMAN	repetitive element/contains MER19.12 MER19 repetitive element ;
12385	25272		1.36	3.0E-29	D63882.1	NT	Homo sapiens chromosome 21 segment HS21C048
13092	26132		1.62	3.0E-29	D63882.1	NT	MER29 repetitive element ;
505	13699	26727	0.98	2.0E-29	AF084868.1	NT	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
505	13699	26728	0.98	2.0E-29	AF084868.1	NT	MER29 repetitive element ;
							z62b01.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335769
							G1335769 GAG-POL POLYPOLYPROTEIN. ;
							Human HsLM15 mRNA for HsLM15, complete cds
							Human HsLM15 mRNA for HsLM15, complete cds
							Homo sapiens envelope protein RIC-6 (env) gene, complete cds
							Homo sapiens envelope protein RIC-6 (env) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1563	14716	27794	7.8	2.0E-29	AI663904.1	EST_HUMAN	w66d10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548 HERV-E ENVELOPE GLYCOPROTEIN;
1563	14716	27795	7.8	2.0E-29	AI663604.1	EST_HUMAN	w66d10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548 HERV-E ENVELOPE GLYCOPROTEIN;
1782	14931	28024	2.31	2.0E-29	X84900.1	NT	HERV-E ENVELOPE GLYCOPROTEIN;
1782	14931	28025	2.31	2.0E-29	X84900.1	NT	H sapiens mRNA for laminin-5, alpha3b chain
4394	17537	30516	2.55	2.0E-29	AL163268.2	NT	H sapiens mRNA for laminin-5, alpha3b chain
5946	19132	32446	0.78	2.0E-29	AI082459.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068 os71e04.x1 NCL_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1 repetitive element;
6309	19481	32835	1.49	2.0E-29	AI080418.1	EST_HUMAN	w27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;
7732	19481	32835	1.28	2.0E-29	AI080418.1	EST_HUMAN	w27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;
8164	21246	34766	1.16	2.0E-29	BE887157.1	EST_HUMAN	601442206F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3849648 5'
8777	21856	35398	0.61	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC86242), mRNA
8777	21856	35399	0.61	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC86242), mRNA
9708	22757	36327	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9708	22757	36328	2.78	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37084	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37085	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11767	24760		1.67	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnal (SPF31), mRNA
8992	22071	35611	8.27	1.0E-29	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
10850	23883	37503	2.81	1.0E-29	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
6712	19870	33261	3.53	9.0E-30	AA781215.1	EST_HUMAN	nz20c07.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element;
12268	26200		4.55	9.0E-30	11422746	NT	Homo sapiens zinc/ferritin regulated transporter-like (ZIRT), mRNA
6449	19816		10.5	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8465	21546	35076	2.26	8.0E-30	AA383973.1	EST_HUMAN	EST97917 Thymus 1 Homo sapiens cDNA 5' and similar to EST containing O family repeat
8882	21961	35495	2.79	8.0E-30	AI557072.1	EST_HUMAN	PT2.1_13 B11.1 tumor2 Homo sapiens cDNA 3'
1645	14697		1.07	7.0E-30	BE091193.1	EST_HUMAN	PM4-B10724-150400-004-d11 BT0724 Homo sapiens cDNA
1814	14983	28056	1.67	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3259	19433	29450	3.15	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
4881	19433	29450	1.02	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
10760	23793	37412	0.76	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13161	18485		1.75	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4121	17276	30274	43.22	6.0E-30	A1399992.1	EST_HUMAN	tg92g03.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5393	25928		5.79	5.0E-30	U87931.1	NT	Human acetylcholinesterase (AChE) gene, exon 7
11128	24198		2.12	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11423	24484	38148	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11423	24484	38149	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2210	15344	28470	2.38	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
2210	15344	28471	2.38	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
9108	22185	35728	1.66	4.0E-30	AW812488.1	EST_HUMAN	GM1-ST0181-091189-035-f08 ST0181 Homo sapiens cDNA
1175	14338		4.66	3.0E-30	A1338551.1	EST_HUMAN	q983c05.x1 Scores: total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element;
3853	17013	30013	1.15	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
8138	21220		0.63	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8683	21763		0.45	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10649	23683	37294	0.74	3.0E-30	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element;
11482	24541	38211	1.52	3.0E-30	P34086	SWISSPROT	TRANSCRIPTION FACTOR AP-2
682	13875	29508	1.42	2.0E-30	AW857315.1	EST_HUMAN	GM0-GT0307-310100-158-h03 GT0307 Homo sapiens cDNA
1108	14273		2.53	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1509	14662	27745	5.5	2.0E-30	BE175877.1	EST_HUMAN	RC6-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2779	15895	29005	9.93	2.0E-30	BE785232.1	EST_HUMAN	IL2-NT0101-286700-116-E04 NT0101 Homo sapiens cDNA
2986	16162	29179	6.83	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3889	17048	30048	1.95	2.0E-30	AW208661.1	EST_HUMAN	U1H-B1-af0-c-12-Q-U1.s1 NCI_CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4900	18030	31018	2.02	2.0E-30	BE288945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
4800	18030	31019	2.02	2.0E-30	BE288945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
8734	21614	35349	4.89	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-570C01 5'
8836	21915	35452	1.71	2.0E-30	BE670617.1	EST_HUMAN	7c37c12.x1 NCI_CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8838	21915	35453	1.71	2.0E-30	BE670617.1	EST_HUMAN	7c37c12.x1 NCI_CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
10201	23238	36828	3.78	2.0E-30	AW871568.1	EST_HUMAN	EST383657 MAGE resequences, MAG1 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10287	23222	36924	6.31	2.0E-30	AW470791.1	EST_HUMAN	h33306.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875495 3' similar to contains THR.b3
297	13514	26548	10.87	1.0E-30	C18939.1	EST_HUMAN	h33004.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains
551	13744	26769	1.62	1.0E-30	AW468897.1	EST_HUMAN	MER1.3 MER1 MER1 repetitive element:
734	13916	26956	5.15	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2286	15418	28550	11.56	1.0E-30	AA684377.1	EST_HUMAN	ac77008.x1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
2533	15838	28782	2.15	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157991 5'
3120	16286	28310	0.91	1.0E-30	AA315045.1	EST_HUMAN	EST188888 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
7901	20863	34460	1.96	1.0E-30	BF183230.1	EST_HUMAN	601809832F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
8176	21268	34780	0.49	1.0E-30	BE061586.1	EST_HUMAN	MRO-BT0249-091299-101-g01 BT0249 Homo sapiens cDNA
12786	26117		1.57	1.0E-30	AA298211.1	EST_HUMAN	EST11598 Uterus Homo sapiens cDNA 5' end
12937	26025		5.31	1.0E-30	H55593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3862	17022	30020	0.8	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3862	17022	30021	0.8	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8519	21600	35135	0.88	9.0E-31	R18214.1	EST_HUMAN	Y88008.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8519	21600	35136	0.88	9.0E-31	R18214.1	EST_HUMAN	Y88008.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8825	21804		1.99	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
8827	21806	35445	0.53	9.0E-31	AF078776.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
13183	25776	31934	1.29	9.0E-31	6755441	NT	Mus musculus syndecan 4 (Sdc4), mRNA
1102	14267	27325	2.52	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2484	15611		7.93	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
729	13911		1.59	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Odon adenocarcinoma IV Homo sapiens cDNA 5' end
2733	15850	28982	2.1	7.0E-31	BE325517.1	EST_HUMAN	hw05at11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2733	15850	28983	2.1	7.0E-31	BE325517.1	EST_HUMAN	hw05at11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8595	21676	35212	1.02	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8595	21676	35213	1.02	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9486	22523		1.03	7.0E-31	BE408611.1	EST_HUMAN	601304126F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
3769	18930		3.42	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8347	21428		1.39	6.0E-31	AF050661.1	NT	Homo sapiens MHC class 1 region

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8528	21607	35148	0.75	6.0E-31	BE350127.1	EST_HUMAN	h109g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
10976	24055	37389	1.43	6.0E-31	AU119105.1	EST_HUMAN	MER29 repetitive element;
12327	25236	32108	3.7	6.0E-31	AW372868.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12459	25947		2.54	6.0E-31	BE894488.1	EST_HUMAN	RC5-BT10377-091289-031-D12 BT0377 Homo sapiens cDNA
197	13420	28450	3.39	6.0E-31	M60894.1	NT	801433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	13420	28451	3.39	6.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8640	21720		1.29	6.0E-31	BF069540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
809	13798		3.02	4.0E-31	AJ271735.1	NT	710604.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13637 Q13637
							SIMILAR TO POGO ELEMENT; contains L1 L1 repetitive element;
1642	14794	27878	1.14	4.0E-31	Q10473	SWISSPROT	Homo sapiens Xq pseudautosomal region, segment 1/2
1861	15007		2.09	4.0E-31	AL163280.2	NT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-JDP
2849	16963		1.57	4.0E-31	5730038	NT	ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-
10764	23787	37402	0.46	4.0E-31	AF084484.1	NT	ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
12787	25526		1.55	4.0E-31	11430273	NT	Homo sapiens chromosome 21 segment HS21C080
12824	25609		2	4.0E-31	AB080881.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
2680	15782	28997	1.75	3.0E-31	6005871	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
7494	20569	34041	8.04	3.0E-31	4828853	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
7683	20730	34206	1.23	3.0E-31	11420329	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8355	21436		1.51	3.0E-31	AL163206.2	NT	Homo sapiens SEC83, endoplasmic reticulum translocan component (S. cerevisiae) like (SEC83L), mRNA
9779	22819	36397	2.59	3.0E-31	D14523.1	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8) mRNA
10822	23856	37477	0.65	3.0E-31	AA421242.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
10867	23952	37882	2.03	3.0E-31	P11174	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
11421	24482		3.47	3.0E-31	BF035327.1	EST_HUMAN	Horse mRNA for ferritin L-chain, complete cds
1987	15110	28211	1.58	2.0E-31	AW838171.1	EST_HUMAN	2105d04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
2288	15420	28552	1.09	2.0E-31	A1393388.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S15 (R1G PROTEIN)
2416	15645	28674	2.22	2.0E-31	AL119245.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
2511	15837	28758	4.63	2.0E-31	AA458824.1	EST_HUMAN	QV2-L T0051-260300-111-403 L T0051 Homo sapiens cDNA
5398	18591	31563	0.76	2.0E-31	AW444498.1	EST_HUMAN	Ig44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
							DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
							ae88111.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:938413 3' similar to contains
							THR12 THR repetitive element;
							UI-H-B13-akb-F09-0-U1 s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5829	19020	32326	3.43	2.0E-31	BE350127.1	EST_HUMAN	H09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER28 repetitive element:
9277	22353		1.53	2.0E-31	AA877784.1	EST_HUMAN	n0804.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.:
9408	22482	36046	3.46	2.0E-31	7661535	NT	Homo sapiens B9 protein (B9), mRNA
10110	23148	36748	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
10110	23148	36748	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
10280	23315	36914	2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
10280	23315	36915	2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12430	25305		3.49	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12578	26202		2.99	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA (MAGE-B1) genes, complete cds
17	13255	26256	9.91	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1686	14848	27932	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1696	14848	27933	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1696	14848	27934	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
5407	18609	31681	3.97	1.0E-31	AW391679.1	EST_HUMAN	MIR3-ST0220-151289-028-a08_1 ST0220 Homo sapiens cDNA
6261	19435	32761	2.57	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
7441	20518	33990	0.84	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
9006	21055	34567	1.35	1.0E-31	BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
10441	23476	37080	0.5	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11156	24227	37857	2.35	1.0E-31	AI096434.1	EST_HUMAN	q21h03.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN.:
8778	19831	33327	2.19	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAAG01 5'
7530	20603	34077	0.66	9.0E-32	L31770.1	NT	Bos taurus vacuolar H ⁺ -ATPase subunit mRNA, complete cds
7786	20825		0.91	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2139	18275	28397	5.1	8.0E-32	AI056770.1	EST_HUMAN	caf15a09.x1 Soares fetal liver spleen INFILS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5599	18794	31843	0.77	8.0E-32	AW987214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphon and neighbouring non-amplified region
12408	25285		2.98	7.0E-32	X17283.1	NT	
7523	20598		1.32	6.0E-32	BE889016.1	EST_HUMAN	601511630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12869	26181		2.5	6.0E-32	AA864653.1	EST_HUMAN	oh37c03.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:145972 3' similar to contains L1.13 L1
1059	14225	27282	10.42	6.0E-32	AF118627.1	NT	Homo sapiens PRO1181 mRNA, complete cds
954	14127		1.64	4.0E-32	AL163249.2	NT	Homo sapiens chromosome 21 segment HS210046
7779	20835	34326	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7779	20835	34327	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
6554	21635		0.93	4.0E-32	BE064410.1	EST_HUMAN	RG4-BT0311-141188-011-H03 BT0311 Homo sapiens cDNA
468	13663	26699	2.04	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1484	14637	27721	15.82	3.0E-32	AV731600.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
2973	16149	29168	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
2973	16149	29169	0.76	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
9594	22649	36221	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
9594	22649	36222	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
11198	24237	37868	3.43	3.0E-32	AA777624.1	EST_HUMAN	Z95a07.s1 Soares_fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:3139701 5'
12433	25307		7.95	3.0E-32	BE279086.1	EST_HUMAN	contains THR13 THR repetitive element;
12843	16149	29168	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
12843	16149	29169	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
13020	25971		6.47	3.0E-32	BE279086.1	EST_HUMAN	601166285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6382	19551	32907	0.89	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6608	19768	33166	5.55	2.0E-32	Z39133.1	NT	H. sapiens mRNA for myosin
6608	19768	33167	5.55	2.0E-32	Z39133.1	NT	H. sapiens mRNA for myosin
8473	21654	35085	3.34	2.0E-32	AA114294.1	EST_HUMAN	Zn66c08.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8473	21654	35086	3.34	2.0E-32	AA114294.1	EST_HUMAN	Zn66c08.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
13154	25750	31823	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
13154	25750	31824	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
3163	16938		1.25	1.0E-32	BE749289.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
7200	20065	33476	6.64	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8795	21874	35413	4.58	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	18735		4.8	9.0E-33	BE327112.1	EST_HUMAN	hw07005.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:088539 O88539 WW DOMAIN BINDING PROTEIN 11.1
6550	18712		3.17	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8998	22067	35607	1.81	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
11038	24117		4.55	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
62	13300	26320	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
62	13300	26321	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2228	15362	28491	3.04	7.0E-33	AI590115.1	EST_HUMAN	to12b09.x1 NCL_CGAP_Lu2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains ORF.t1 OFR repetitive element:
2714	15832		7.95	7.0E-33	AV730036	EST_HUMAN	HTF Homo sapiens cDNA clone HTFAVE08 5'
3314	16487		15	7.0E-33	AW971307.1	EST_HUMAN	EST3833657 MAGE resequences, MAGL Homo sapiens cDNA
9147	22228		0.87	7.0E-33	X54890.1	NT	Human HLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
11067	24142	37777	1.88	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4156670 5'
11526	24582	38258	1.59	7.0E-33	AW971569.1	EST_HUMAN	EST3833657 MAGE resequences, MAGL Homo sapiens cDNA
12413	25292	32082	9.74	7.0E-33	AA601416.1	EST_HUMAN	no18h01.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element:
3830	16990		0.93	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6192	19368	32717	0.91	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
6192	19368	32718	0.91	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8778	21657	35400	1.86	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8898	21978	35517	3.12	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277). mRNA
10214	23250	36839	2.03	6.0E-33	6755509	NT	Homo sapiens SRY-box containing gene 6 (Sox6). mRNA
10214	23250	36840	2.03	6.0E-33	6755509	NT	Mus musculus SRY-box containing gene 6 (Sox6). mRNA
1818	14957		1.9	5.0E-33	BF373515.1	EST_HUMAN	QY1-FT0168-100700-271-402 FT0169 Homo sapiens cDNA
1831	15074		1.32	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7). mRNA
1847	15090	28190	1.63	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1947	15090	28191	1.63	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2346	15477		2.92	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C086
4169	17316	30312	0.66	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
10454	23489	37097	0.82	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10454	23489	37098	0.82	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12212	25165		1.45	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1152	14316		2.25	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2194	15329	28454	3.37	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2491	15518		1.16	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2810	15734	28850	4.78	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4806	17743	30722	2.38	4.0E-33	AW293349.1	EST_HUMAN	U1-H-B12-ahc-Q3-Q-U1.s1 NCJ CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5519	18717	31731	24.75	4.0E-33	AA053053.1	EST_HUMAN	z171a08.11 Stratagene colon (4937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12871_mna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6522	18687	33060	0.79	4.0E-33	B933594	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6522	18687	33061	0.79	4.0E-33	B393894	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1113	14278		5.52	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCJ CGAP Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element;
1114	14278		5.53	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCJ CGAP Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element;
2522	16084		1.16	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLC6CF09 3'
10655	23689	37298	0.87	3.0E-33	AA891510.1	EST_HUMAN	ak32b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407847 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE.;
18	13256		1.67	2.0E-33	AI160189.1	EST_HUMAN	qb87g03.x1 Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
107	13256		5.53	2.0E-33	AI160189.1	EST_HUMAN	qb87g03.x1 Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
4539	17677		4.53	2.0E-33	BE156039.1	EST_HUMAN	MFR0-HT0405-160300-202-c08 HT0405 Homo sapiens cDNA
5100	18228	31189	8.64	2.0E-33	AA826683.1	EST_HUMAN	ab51g11.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5204	18325	31294	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5204	18325	31295	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6553	19715	33091	1.39	2.0E-33	AI277492.1	EST_HUMAN	q186d01.x1 Soares_NHHMPu_ST Homo sapiens cDNA clone IMAGE:1880167 3'
9301	22377		2.15	2.0E-33	AI052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_INF1LS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
9	13247		1.61	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7585	20637	34113	0.86	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10227	26229		1.4	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11602	24655	38340	1.56	1.0E-33	AW996818.1	EST_HUMAN	QV3-BN0047-230200-102-503 BN0047 Homo sapiens cDNA
11962	24947	38662	2.44	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12768	25511		1.25	1.0E-33	AW904491.1	EST_HUMAN	RCS-NN1055-280400-021-G03 NN1055 Homo sapiens cDNA
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12829	13247		5.7	1.0E-33	AF003528.1	NT	
12960	25626	31979	2.19	1.0E-33	AV727808.1	EST_HUMAN	AV727808 HTC Homo sapiens cDNA clone HTCCNC12.5'
13179	28706		4.77	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2240	15373	28501	0.99	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
4620	17757	30739	1.93	8.0E-34	BE062570.1	EST_HUMAN	QV2-BT0258-071299-019-g07 BT0258 Homo sapiens cDNA
7874	21024	34537	0.67	8.0E-34	BE069882.1	EST_HUMAN	NR4-BT0389-200100-001-h03 BT0389 Homo sapiens cDNA
1476	14829	27714	2.5	7.0E-34	T70845.1	EST_HUMAN	Yd15605.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320.5'
10204	14629	27714	0.54	7.0E-34	T70845.1	EST_HUMAN	Yd15605.t1 Soares placenta Nb21HP Homo sapiens cDNA clone IMAGE:108320.5'
12482	26334		3.85	7.0E-34	H12886.1	EST_HUMAN	Y14c10.t1 Soares placenta Nb21HP Homo sapiens cDNA clone IMAGE:148722.5'
483	13677	26711	1.74	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
483	13677	26712	1.74	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
5247	18368	31335	1.68	6.0E-34	AW998811.1	EST_HUMAN	PM0-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
12280	25216	32099	2.22	6.0E-34	UC3686.1	NT	Mus musculus DAB1/2J hair-specific (hact-1) gene
1928	15072		3.15	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5173	18295	31257	5.24	5.0E-34	U30883.1	NT	Human splicing factor SFRS5-1 (SFRS5) mRNA, complete cds
9067	22146	35693	1.17	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10890	23974	37605	2.02	5.0E-34	AB037650.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11532	24588		1.63	5.0E-34	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
2054	18195	28309	2.09	4.0E-34	A1804667.1	EST_HUMAN	t94c06.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2249184.3'
3241	16415	29430	0.9	4.0E-34	5803168	NT	Homo sapiens splicing factor 3a, subunit 3, 80kD (SFS3A), mRNA
6981	19169	32486	0.62	4.0E-34	AA881773.1	EST_HUMAN	ak35c01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407836.3'
9238	22315	33857	0.83	4.0E-34	BF209778.1	EST_HUMAN	601874950FT NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213.5'
6361	19531	32890	0.66	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11420	24481		2.86	3.0E-34	BF035327.1	EST_HUMAN	601458531FT NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3882088.5'
							wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170.3' similar to contains MER29.12 MER29 repetitive element
9152	22230	35774	0.75	2.0E-34	A1678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170.3' similar to contains MER29.12 MER29 repetitive element
9152	22230	35775	0.75	2.0E-34	A1678101.1	EST_HUMAN	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
11431	24492	38156	8.64	2.0E-34	P57805	SWISSPROT	

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11431	24492	38157	8.54	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1534	14887	27767	10.13	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
1738	14887		7.18	1.0E-34	AU136024.1	EST_HUMAN	AU136024 PLACE1 Homo sapiens cDNA clone PLACE1003383 5'
3764	16925	29927	2.51	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4181	17331	30323	0.78	1.0E-34	AY006397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4181	17331	30324	0.79	1.0E-34	AY006397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4602	17739		8.26	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-076-H08 B T0506 Homo sapiens cDNA
6266	19440	32787	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
6266	19440	32788	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
9527	22592	38163	0.94	1.0E-34	P23286	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
9898	22938	38923	8.07	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563 J1 564 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564A1563 5'
11469	24518	38186	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11469	24518	38187	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11473	24532	38202	2.92	1.0E-34	11438589	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12680	26125		2.44	1.0E-34	AA607097.1	EST_HUMAN	cc31c11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203
12950	26660		5.84	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FL74 PRECURSOR (HUMAN);
3735	16896	29800	1.3	9.0E-35	AW569302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
232	13453		7.21	8.0E-35	6031190	NT	hh77b06.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988787 5'
1776	14925	28019	3.63	8.0E-35	BF589837.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1776	14925	28019	3.63	8.0E-35	BF589837.1	EST_HUMAN	na53a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1776	14925	28019	3.63	8.0E-35	BF589837.1	EST_HUMAN	na53a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4989	18118	31097	2.61	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
10929	24011	37645	1.53	8.0E-35	BF378480.1	EST_HUMAN	na53a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:4040324 5'
12404	25283		5.89	8.0E-35	BF589282.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
6813	19773	33164	1.61	7.0E-35	11425417	NT	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3508513 5'
1445	14598	27675	1.06	6.0E-35	AA757115.1	EST_HUMAN	602184624F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300650 3'
2025	15166	28271	4.63	8.0E-35	6005975	NT	Homo sapiens phosphatidylinositol glycan, class L (PTGL), mRNA
4184	17314	30309	0.8	6.0E-35	AW297191.1	EST_HUMAN	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
8081	21163	34680	4.03	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8906	21985	35624	0.57	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8906	21985	35625	0.57	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8967	22907	36492	0.61	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0368 gene, partial cds
10107	23145	36743	2.97	6.0E-35	AB03786.1	NT	Human mRNA for KIAA1385 protein, partial cds
148	13373	26408	0.61	5.0E-35	AF154630.1	NT	Homo sapiens carboxyl phosphatase 1 mRNA, complete cds
1746	14895	27889	2.25	5.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2844	16958	28067	0.99	5.0E-35	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3074	16250	28271	2.87	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4529	17697	30853	1.72	5.0E-35	AF023288.1	NT	Homo sapiens cdk2 kinase (CLK2), protein 1, coter1, coter1, glucocorticoid-induced (GBA), and melanin genes, complete cds; melanin pseudogene and glucocorticoid-induced pseudogene; and thrombospondin3 (THBS3) gene, partial cds
8378	21459		4.25	5.0E-35	BE890892.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8405	21486	35015	2.17	5.0E-35	AI208765.1	EST_HUMAN	q38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
8405	21486	35016	2.17	5.0E-35	AI208765.1	EST_HUMAN	q38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
11461	24511		2.94	5.0E-35	AA001786.1	EST_HUMAN	z84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1465	14619	27703	20.46	4.0E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1682	15008	28114	11.21	4.0E-35	H61193.1	EST_HUMAN	y98a07.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
7358	20437		1.67	4.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 b3
8715	21795	35332	8.05	4.0E-35	AL040598.1	EST_HUMAN	DKFZp434L148_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
12098	25078	38786	2.5	4.0E-35	AF114186.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
1610	14763	27843	33.92	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2403	15539		2.64	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5456	18656	31634	23.43	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
5456	18656	31635	23.43	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
9689	22738		1.45	3.0E-35	AF223391.1	NT	Q9QZH7 F-BOX PROTEIN FBL2. ; Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10378	23413	37022	1.5	3.0E-35	AW003063.1	EST_HUMAN	wf03a05.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN p10266 RETROVIRUS-RELATED POL POLYPYRIN (CONTAINS: REVERSE TRANSCRIPTASE ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
111	16005	26372	1.25	2.0E-35	N88955.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1215	14376	27436	1.89	2.0E-35	T11909.1	EST_HUMAN	REPETITIVE ELEMENT
2292	15424	26558	4.56	2.0E-36	AB018413.1	NT	A071F Heart Homo sapiens cDNA clone A071
2748	16865	26976	1.13	2.0E-35	AW665005.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
3386	16556	26570	1.08	2.0E-35	6912459	NT	h186a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to
3388	16556	26571	1.08	2.0E-35	6912459	NT	SW:TR12_HUMAN Q14689 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
3947	16610		0.77	2.0E-35	AB020702.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4019	17176	30184	0.85	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens mRNA for KIAA0995 protein, partial cds
4019	17179	30185	0.85	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens
4792	17927		3.01	2.0E-35	H49239.1	EST_HUMAN	cDNA clone TCBAP4328
5700	18894	32186	1.93	2.0E-35	BF332417.1	EST_HUMAN	Y118a12.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:274079 5'
7253	20338	33785	0.6	2.0E-35	BE832636.1	EST_HUMAN	QV0-BT0701-210400-163-b04 BT0701 Homo sapiens cDNA
7253	20338	33786	0.6	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11036	24116	37749	2.93	2.0E-35	X59417.1	NT	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
12157	16556	29570	1.22	2.0E-35	6912459	NT	H. sapiens PROS-27 mRNA
12157	16556	29571	1.22	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12342	25247	32111	1.33	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12342	25247	32112	1.33	2.0E-35	BE904978.1	EST_HUMAN	601498774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12931	25614		7.22	2.0E-35	AL163210.2	NT	601498774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
13056	16005	26372	1.74	2.0E-35	N88955.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
47	13286	26296	5.76	1.0E-35	AA631949.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
47	13286	26296	5.76	1.0E-35	AA631949.1	EST_HUMAN	REPETITIVE ELEMENT
771	13952	27000	35.82	1.0E-35	AW389473.1	EST_HUMAN	hmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
771	13952	27001	35.82	1.0E-35	AW389473.1	EST_HUMAN	hmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
932	14107		1.28	1.0E-35	T67947.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
2507	15730	28847	1.89	1.0E-35	7705994	NT	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
2826	15940	29050	1.34	1.0E-35	BE350127.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
							Y63a01.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
							SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
							Homo sapiens hypofibrin protein (LOC51233), mRNA
							ht09g01.x1 NC1_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
							MER29 repetitive element ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
2826	15940	29051	1.34	1.0E-35	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.03
3212	16366	29397	1.87	1.0E-35	6006030	NT	MER29 repetitive element ;
3232	16408	29418	1.67	1.0E-35	AV650422.1	EST_HUMAN	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TOEB1L) mRNA
3232	16408	29419	1.67	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE006 3'
4542	17680	30661	4.82	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE006 3'
4542	17680	30662	4.82	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
6627	18921	31890	1.48	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
7135	18561	31475	0.74	1.0E-35	11526238	EST_HUMAN	Homo sapiens chromatin assembly factor 1, subunit B (p80) (CHAF1B), mRNA
7135	18561	31476	0.74	1.0E-35	AW608665.1	EST_HUMAN	MR1-ST0111-111199-011-407 ST0111 Homo sapiens cDNA
7652	20720	34196	0.99	1.0E-35	AB033105.1	NT	MR1-ST0111-111199-011-407 ST0111 Homo sapiens cDNA
7819	20874	34373	0.91	1.0E-35	11418002	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
9742	25661	36383	2.46	1.0E-35	AU158595.1	EST_HUMAN	Homo sapiens KIAA0845 gene product (KIA0845), mRNA
9742	25661	36384	2.46	1.0E-35	AU158595.1	EST_HUMAN	AUT58595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10805	23838	37462	0.72	1.0E-35	BF598594.1	EST_HUMAN	AUT58595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10805	23838	37463	0.72	1.0E-35	BF598594.1	EST_HUMAN	naa06d06.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
12055	25036	38743	1.49	1.0E-35	AB028990.1	NT	naa06d06.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
12055	25036	38744	1.49	1.0E-35	AB028990.1	NT	O31341 BETA-GALACTOSIDASE ;
12062	25043	31677	2.04	1.0E-35	AI525119.1	EST_HUMAN	O31341 BETA-GALACTOSIDASE ;
12188	26077		6.35	1.0E-35	11418274	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12405	25284		1.26	1.0E-35	11418110	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12806	25539		2.49	1.0E-35	BE792832.1	EST_HUMAN	promina-7.D01.7 by tumor Homo sapiens cDNA 5'
6131	19310	32650	0.67	8.0E-36	X78479.1	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
6131	19310	32650	0.67	8.0E-36	X78479.1	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
6430	22504	36070	0.76	8.0E-36	AA348480.1	EST_HUMAN	601584533F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
2697	16173	29192	1.53	7.0E-36	AW867579.1	EST_HUMAN	B.bovis BB50 mRNA for schdelin
3188	16363		5.25	7.0E-36	4537498	NT	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
6273	18392	31360	1.09	7.0E-36	Q27409	SWISSPROT	CM1-CT0315-091299-083-407 CT0315 Homo sapiens cDNA
5273	18392	31361	1.09	7.0E-36	Q27409	SWISSPROT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7832	20887	34389	6.31	7.0E-36	U06872.1	NT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
7832	20887	34390	6.31	7.0E-36	U06872.1	NT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
12570	25388	32040	27.36	7.0E-36	AF052091.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
						NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
						NT	Human sapiens glutathione transferase A4 gene, exon 1

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2060	15201	28315	1.92	6.0E-36	7706622	NT	Homo sapiens rhinovirus 2 (NINJ2), mRNA
2490	15617		5.59	6.0E-36	AB035346.1	NT	Homo sapiens TCE6 gene, exon 12
3728	16930	29894	0.59	6.0E-36	BF515101.1	EST_HUMAN	UJH-BW1-antv-c-12-O-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5446	18646	31624	7.17	6.0E-36	AI435168.1	EST_HUMAN	t193006.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb U11949 PANCAREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7258	20341	33782	3.03	6.0E-36	AW780143.1	EST_HUMAN	h006102.x1 NCI CGAP Co14 Homo sapiens cDNA clone IMAGE:3038527 3' similar to SW:IMA2_HUMAN
8853	21932	35471	4.62	6.0E-36	AF208161.1	NT	P52292 IMPORTIN ALPHA-2 SUBUNIT
10430	23485		0.63	6.0E-36	C16927.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
11841	24930	38521	3.49	6.0E-36	AI380499.1	EST_HUMAN	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
140	13566	26399	15.16	5.0E-36	AJ271735.1	NT	MER9 repetitive element
2809	15923	28033	21.08	5.0E-36	BE369436.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region: segment 1/2
3700	16861	29863	3.24	5.0E-36	AL163209.2	NT	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
4909	18039	31028	1.31	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4909	18039	31029	1.31	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
7968	21016	34528	0.59	5.0E-36	11079227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12155	13366	28399	6.11	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
12458	25322	32095	2.36	5.0E-36	5010038.1	EST_HUMAN	Homo sapiens calcitonin binding protein 1 (KIA00330), mRNA
1252	14411	27473	1.57	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1677	14829	27913	1.36	4.0E-36	BE382574.1	EST_HUMAN	601288574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2297	15429		4.14	4.0E-36	AW247772.1	EST_HUMAN	2820020 SpHme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3435	16603	29622	1.1	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3435	16603	29623	1.1	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4877	18008	30992	0.69	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5833	19024		0.96	4.0E-36	R64023.1	EST_HUMAN	Y19105.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139713 5'
6180	19356	32704	2.49	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7851	20886	34388	1.78	4.0E-36	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
8752	21831	35369	1.45	4.0E-36	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8752	21831	35370	1.45	4.0E-36	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11255	24304	37947	3.13	4.0E-36	AA400370.1	EST_HUMAN	z169c10.r1 Soares tests_NHT Homo sapiens cDNA clone IMAGE:743250 5'
12476	25328		1.91	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
12520	25951		4.27	4.0E-36	AV753628.1	EST_HUMAN	AV753628 TP Homo sapiens cDNA clone TPGABH01 5'
714	13898	26934	2.93	3.0E-36	AF099810.1	NT	Homo sapiens neuroxin II-alpha gene, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2373	15504	28630	1.19	3.0E-36	7662401	NT	Homo sapiens KIAA0982 protein (KIAA0982), mRNA
4624	17761	30743	7.5	3.0E-36	10181139	NT	Mus musculus junctional protein 1 (Jp1-pending), mRNA
11368	24428	38086	1.94	3.0E-36	BF038327.1	EST_HUMAN	601486331F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3238	16412	29427	2.5	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5074	18202	31174	10.78	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5603	18788	31848	2.88	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5970	19156	32471	3.75	2.0E-36	T08756.1	EST_HUMAN	EST06948 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBB128 5' end
6706	19864	33254	13.94	2.0E-36	T69629.1	EST_HUMAN	yc44a07.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9588	22643	36212	0.94	2.0E-36	BF512784.1	EST_HUMAN	UI-H-BW1-aru-e-11-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9749	22687	36258	0.74	2.0E-36	4607848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9749	22687	36259	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
908	14083	27148	1.74	1.0E-36	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2212	15346	28474	1.71	1.0E-36	BE145523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2212	15346	28475	1.71	1.0E-36	BE145523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2275	15408	28538	1.83	1.0E-36	BF673761.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3428	18594		3.33	1.0E-36	AF158982.1	NT	Homo sapiens human endogenous retrovirus W prc6-19 protease (pro) gene, partial cds
6847	19037	32344	0.84	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G022 5'
6020	19203	32523	1.23	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6312	19484		4.27	1.0E-36	AI867714.1	EST_HUMAN	w637c12.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6519	19684	33055	1.9	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6519	19684	33056	1.9	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6820	19973	33381	0.72	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
8147	21229	34747	4.06	1.0E-36	AA148034.1	EST_HUMAN	z651a12.r1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8147	21229	34748	4.06	1.0E-36	AA148034.1	EST_HUMAN	z651a12.r1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8243	21325	34841	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8243	21325	34842	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8373	21454	34977	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone IMAGE:1001033 5'
8373	21454	34978	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
9229	22307	38850	3.33	1.0E-36	AW103668.1	EST_HUMAN	xe2607.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10320	23355	36964	3.83	1.0E-36	BF364189.1	EST_HUMAN	QV3-NN1023-010800-199-h01 NN1023 Homo sapiens cDNA
10534	23569	37176	0.64	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10534	23569	37177	0.94	1.0E-36	AW856983.1	EST_HUMAN	RC3-CT0279-040600-017-410 CT0279 Homo sapiens cDNA
11190	24259	37895	2.55	1.0E-36	AW897639.1	EST_HUMAN	CM8-NN0061-140400-147-412 NN0061 Homo sapiens cDNA
11682	24741	38432	3.55	1.0E-36	AW504143.1	EST_HUMAN	U1HIF-BN0-ale-c-03-Q-U1.11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12048	25029		10.8	1.0E-36	11646901	NT	Homo sapiens PP3227 protein (PP3227), mRNA
12340	25245		2.93	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12835	25596		5.78	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13131	25737		2.76	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7539	20612	34087	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80507.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
7539	20612	34088	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80507.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
12619	25417		3.97	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp5081-cleaved sublibrary Homo sapiens cDNA not directional
3436	16604	29824	1.4	8.0E-37	4757979	NT	Homo sapiens chimera (chimera) 2 (CHN2) mRNA
5363	18566		1.7	8.0E-37	BE698077.1	EST_HUMAN	CW0-UT0003-050800-503-409 UT0003 Homo sapiens cDNA
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5949	19135	32449	3.48	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
5998	19183	32505	7.08	8.0E-37	AW840840.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
8068	21150	34870	6.2	8.0E-37	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1313	14469		4.92	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0422 5'
5228	18350	31320	3.04	7.0E-37	AW969823.1	EST_HUMAN	EST380369 MAGI2 sequences. MAGI2 Homo sapiens cDNA
10994	24073	37706	8.66	7.0E-37	AI817700.1	EST_HUMAN	wk25b11.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
11134	24206	37831	1.89	7.0E-37	AI536702.1	EST_HUMAN	PTR5 repetitive element;
8634	21714	35251	0.59	6.0E-37	AF169089.1	EST_HUMAN	h087g03.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2185140 3' similar to contains L1.b3 L1
12864	25575		2.3	6.0E-37	U78308.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12884	25641		4.5	6.0E-37	AF202723.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and
6218	19393	32741	4.3	5.0E-37	AA307123.1	EST_HUMAN	olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
6218	19393	32742	4.3	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
8956	22035	35576	1.03	5.0E-37	AV750211.1	EST_HUMAN	EST178035 Cdon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
11160	24231		4.02	5.0E-37	7657117	NT	EST178035 Cdon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
12335	25242		3.63	5.0E-37	AF149773.1	NT	AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'
							Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
							Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2495	15622	28741	2.97	4.0E-37	AA702784.1	EST_HUMAN	z80b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6416	19585	32947	0.68	4.0E-37	AW764502.1	EST_HUMAN	RC8-UK0014-210200-021-H05 UM0014 Homo sapiens cDNA
9556	22621	36182	0.56	4.0E-37	AA843806.1	EST_HUMAN	ak08c02.s1 Soares_perithyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2074	15214	28332	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434L2418
2074	15214	28333	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434L2418
2581	15708		1.54	3.0E-37	AW061150.1	EST_HUMAN	EST373222 MAGE resequencing, MAGF Homo sapiens cDNA
3030	16206		4.02	3.0E-37	AW061150.1	EST_HUMAN	EST373222 MAGE resequencing, MAGF Homo sapiens cDNA
5985	19170	32492	0.7	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 647 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547G067 5'
7728	20790	34279	0.72	3.0E-37	A1748952.1	EST_HUMAN	Q13537 SIMILAR TO POGO ELEMENT. ;
392	13629	26666	0.89	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
302	13629	26667	0.89	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1105	14270	27328	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1105	14270	27329	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
2021	15162	28267	1.32	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3999	17156	30162	6.71	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4360	17503	30485	0.6	2.0E-37	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
5504	18703		0.9	2.0E-37	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
6076	19835	33224	0.9	2.0E-37	11900617	NT	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
6798	19853	33353	3.72	2.0E-37	AA346720.1	EST_HUMAN	EST62931 Fetal heart II Homo sapiens cDNA 5' end
8185	21267	34780	0.47	2.0E-37	BE537784.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8185	21267	34781	0.47	2.0E-37	BE537784.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8227	21309	34829	2.32	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
11856	24844	38541	10.07	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12797	25770		1.44	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
13184	25770		4.19	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2154	15290	28417	6.95	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3287	18441		1.03	1.0E-37	AW862082.1	EST_HUMAN	RC3-GT0347-210400-016-m03 CT0347 Homo sapiens cDNA
5055	19163	31158	2.34	1.0E-37	BF371719.1	EST_HUMAN	QVQ-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
8127	19306		0.89	1.0E-37	7305360	NT	Mus musculus obogelin (Obog), mRNA
8408	21460	35019	1.12	1.0E-37	BE546032.1	EST_HUMAN	601072416F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
8933	22012	35551	3.59	1.0E-37	AA171408.1	EST_HUMAN	zp21002.1 Stratiagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1/L2 L1 repetitive element ;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10937	24019	37652	2.19	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12871	25447		1.94	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0098-140700-243-307 FT0098 Homo sapiens cDNA
5898	19086	32398	1.72	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
1248	14408	27470	1.98	8.0E-38	11436855	NT	Homo sapiens Grb2-associated binder 2 (KIA0571), mRNA
2587	15692	28817	1.21	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153692 5'
12735	14408	27470	1.37	8.0E-38	11436855	NT	Homo sapiens Grb2-associated binder 2 (KIA0571), mRNA
13210	26049		1.44	8.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2254	15387	28515	1.7	7.0E-38	AW972825.1	EST_HUMAN	EST384920 IMAGE resequences, MAGL Homo sapiens cDNA
3107	15283	29289	1.98	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3856948 5'
5706	18889	32192	0.98	6.0E-38	11428114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5705	18896	32193	0.98	6.0E-38	11428114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7482	20557	34029	0.59	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
12189	25147		4.27	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12704	25468	32025	6.66	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13160	25913	31881	1.79	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
745	13928	28987	0.9	5.0E-38	AW971819.1	EST_HUMAN	EST383908 IMAGE resequences, MAGL Homo sapiens cDNA
2525	15650	28774	4.57	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLIR gene (partial), exon 8
3798	16957	29981	0.94	5.0E-38	7548804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3671	16957	29981	0.77	5.0E-38	7548804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5288	15650	28774	0.98	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLIR gene (partial), exon 8
7172	20305	33748	1.63	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
121	13351	26380	4.28	4.0E-38	Z26466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
121	13351	26381	4.28	4.0E-38	Z26466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1183	14346	27403	1.15	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2167	15302		4.42	3.0E-38	AF003630.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3787	16948		1.49	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (HIRAIP4), mRNA
3958	17116	30119	2.48	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3958	17116	30120	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4736	17871		0.61	3.0E-38	BE278301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6893	26838	33463	5.89	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7393	20471	33937	0.58	3.0E-38	AW302461.1	EST_HUMAN	xw04061 x1 NCL_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2827009 3'
7763	20822	34313	6.53	3.0E-38	BF373684.1	EST_HUMAN	CM3-FT0181-140700-241-407 FT0181 Homo sapiens cDNA
8851	21930	38489	2.11	3.0E-38	H85494.1	EST_HUMAN	yv68804.1 Scores melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:249775 6'
8851	21930	35470	2.11	3.0E-38	H85494.1	EST_HUMAN	yv68804.1 Scores melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:249775 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10177	23214		1.84	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11598	24651		1.88	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12990	14346	27403	1.23	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
61	13260	26303	1.96	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1411	14566	27639	3.66	2.0E-38	5802097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1678	14830	27914	13.95	2.0E-38	AA437353.1	EST_HUMAN	z33d01.1 Scores ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1678	14830	27915	13.95	2.0E-38	AA437353.1	EST_HUMAN	z33d01.1 Scores ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3622	16786		0.92	2.0E-38	AF070870.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4704	17838	30824	18.99	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5252	18339	31312	0.68	2.0E-38	AA437181.1	EST_HUMAN	z61d06.1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:788129 5' similar to TR:G817857
5836	19026	32331	0.75	2.0E-38	Z26634.2	NT	G817857 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
5836	19026	32332	0.75	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankryrin B (440 kDa)
7897	20949	34457	1.47	2.0E-38	AV721103.1	EST_HUMAN	Homo sapiens mRNA for ankryrin B (440 kDa)
8680	21760		4.47	2.0E-38	BE166980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9096	22178	35719	0.49	2.0E-38	F06450.1	EST_HUMAN	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-1803
9165	22243	35786	1.26	2.0E-38	AF069755.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9422	22486		1.36	2.0E-38	BE222256.1	EST_HUMAN	hu09p02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3186130 3' similar to TR:O02710 O02710
10665	23689	37309	1.67	2.0E-38	D63479.2	NT	GAG POLYPROTEIN ;
11781	24771	38467	4.86	2.0E-38	BE712790.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11939	24925	38626	2.86	2.0E-38	AF190501.1	NT	QV2-HT0688-080800-293-a05 HT0688 Homo sapiens cDNA
11939	24925	38627	2.86	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12244	25188		6.21	2.0E-38	AV726988.1	EST_HUMAN	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12246	25187		1.26	2.0E-38	AB012723.1	NT	AV726988 HTG Homo sapiens cDNA clone HTCA107 5'
12546	25370		3.36	2.0E-38	M55630.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12559	25381	32073	4.81	2.0E-38	HS5641.1	EST_HUMAN	Human topoisomerase I pseudogene 2
12632	25426		2.87	2.0E-38	S74006.1	NT	CH220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
13174	25762		1.36	2.0E-38	11418248	NT	E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
							Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1117	14282		1.96	1.0E-38	AA401570.1	EST_HUMAN	z162602.1 Sources_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element;
2055	15196	28310	2.52	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2077	15217	28336	1.33	1.0E-38	7661989	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2564	15689	28815	1.89	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4271	17416	30405	0.93	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4439	17579	30568	0.8	1.0E-38	4506016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4444	17584	30563	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4444	17584	30564	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4719	17854	30837	1.08	1.0E-38	892543	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
5268	18387	31365	1.89	1.0E-38	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6181	19327	32672	4.59	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
6151	19327	32673	4.59	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
7563	20635	34110	2.55	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9354	22429	35987	0.58	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
9610	22865	36236	6.31	1.0E-38	BE350127.1	EST_HUMAN	h109g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
12403	25877		4.79	1.0E-38	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12116	25066	38801	1.64	9.0E-39	AA112438.1	EST_HUMAN	z12767.1 Stralagene pancreas (8937208) Homo sapiens cDNA clone IMAGE:526885 5'
55	13294	26309	4.93	8.0E-39	4502312	NT	Homo sapiens ATPase, H ⁺ -transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1426	14579	27652	1.3	8.0E-39	4758228	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1876	15020		1.8	8.0E-39	AI823404.1	EST_HUMAN	wh53f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
2160	15298	28421	7.08	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
11047	24124	37758	2.4	6.0E-39	BF331829.1	EST_HUMAN	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
13064	25967		2.24	6.0E-39	BE670394.1	EST_HUMAN	7c34c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6
1032	14201	27259	1.64	5.0E-39	AF003528.1	NT	CE00828 ; Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3050	16226	29247	9.33	5.0E-39	AI750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
12720	25479		1.53	5.0E-39	11420289	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT :contains LTR7.1 LTR7 repetitive element ; Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
564	13756	26782	4.39	4.0E-39	AB015810.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
3663	16826	29835	0.9	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5950	18136	32450	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
5950	19136	32451	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
8267	21349	34864	1.02	4.0E-39	AA682949.1	EST_HUMAN	ae92g04.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element ;
9530	22595	36165	0.46	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
9530	22595	36166	0.46	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12744	25494		6.36	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12884	25588		2.56	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0069-260800-278-c08 FN0063 Homo sapiens cDNA
48	13287	20297	11.96	3.0E-39	AA631949.1	EST_HUMAN	hmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	26298	11.96	3.0E-39	AA631949.1	EST_HUMAN	hmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	26299	11.96	3.0E-39	AA631949.1	EST_HUMAN	hmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12236	25180	38348	6.59	3.0E-39	A084557.1	EST_HUMAN	α63a10.s1 Soares, NHMPu, S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12236	25180	38349	6.59	3.0E-39	A084557.1	EST_HUMAN	α63a10.s1 Soares, NHMPu, S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12284	25212		5.72	3.0E-39	H37903.1	EST_HUMAN	yp51c08.s1 Soares, retina N2B-4HR Homo sapiens cDNA clone IMAGE:190954 3'
920	14095		7.78	2.0E-39	BE409203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
935	14110		11.55	2.0E-39	A1525119.1	EST_HUMAN	promma-7.D01 ; bvtupor Homo sapiens cDNA 5'
1057	14223		3.9	2.0E-39	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1560	14713		33.59	2.0E-39	AW372318.1	EST_HUMAN	PM0-BT0340-211289-003-d02 BT0340 Homo sapiens cDNA
2030	15171	28279	4.48	2.0E-39	AA720574.1	EST_HUMAN	mw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element ;
2692	15812	28928	1.89	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4523	17882	30849	1.74	2.0E-39	BF370207.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
5608	18803	31868	4.45	2.0E-39	AA509880.1	EST_HUMAN	ng88f03.s1 NCI_CGAP_Prd Homo sapiens cDNA clone IMAGE:941693
7528	20588	34073	2.08	2.0E-39	AA080867.1	EST_HUMAN	zn06f02.r1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
7702	20767	34251	0.88	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
7702	20767	34252	0.88	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8505	21586	36120	0.63	2.0E-39	AF078776.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8826	22866		0.79	2.0E-39	A1686660.1	EST_HUMAN	tu35e03.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2233052 3'
11716	24756	38452	2.13	2.0E-39	D86994.1	NT	Human mRNA for KIAA0205 gene, partial cds
1543	14695	27774	2.83	1.0E-39	AJ06845.1	NT	Homo sapiens KVLQ11 gene

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1543	14895	27775	2.83	1.0E-39	AJ008345.1	NT	Homo sapiens KVLQT1 gene
1661	14714	27701	5.96	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
1763	14912	28007	1.14	1.0E-39	H56224.1	EST_HUMAN	CHR220163 Chromosome 22 exon Homo sapiens cDNA clone C22_205 5'
4782	17917	30903	9.32	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4782	17917	30904	9.32	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4824	17957	30943	9.13	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
5474	18673	31686	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TIM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5474	18673	31687	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TIM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5747	18939	32239	1.2	1.0E-39	T80876.1	EST_HUMAN	y26g08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains
5781	18973	32278	4.65	1.0E-39	AJ278170.1	NT	Alu repetitive element; contains LTR1 repetitive element
5781	18973	32279	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6965	20193		1.95	1.0E-39			Mus musculus tubby like protein 3 (TULP3), mRNA
7521	20594	34069	2.15	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8762	21841	35382	1.04	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
11165	24236	37867	1.4	1.0E-39	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
659	13761	26785	2	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1263	14420	27484	16.02	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1263	14420	27485	16.02	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1480	14633	27718	15.75	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
3885	17044	30043	1.18	9.0E-40	4503784	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4081	18467	30242	3.99	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4468	17608	30594	5.63	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3106	16282	29298	1.04	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
4033	17189		3.43	8.0E-40	BE396541.1	EST_HUMAN	60128895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
7894	20948	34452	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7894	20948	34453	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11136	24208	37834	2.63	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2788	15904	29011	9.91	6.0E-40	AA381275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' and similar to zinc finger protein family
2788	15904	29012	9.91	6.0E-40	AA381276.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' and similar to zinc finger protein family
8060	19242		1.85	6.0E-40	BE504786.1	EST_HUMAN	h249g01.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3'
8275	19449		1.38	6.0E-40	7661989	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7075	20128	33544	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7075	20128	33545	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10182	23219	36811	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
10182	23219	36812	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2670	15791	28907	2.75	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1925	15098	28173	3.81	4.0E-40	AI686005.1	EST_HUMAN	h91b01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN.1
2175	15310		6.81	4.0E-40	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4508	17847	30635	7.2	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8070	21152	34672	0.64	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8181	21263	34785	6.98	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.1 NCL_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
9255	22332	35881	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
9255	22332	35882	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10855	24036	37671	1.95	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4250	17396	30385	0.9	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
4993	18122		0.83	3.0E-40	AA055118.1	EST_HUMAN	zf18i09.s1 Soares_fetal_hear1_NbHH19W Homo sapiens cDNA clone IMAGE:377163 3'
6592	19752	33137	0.66	3.0E-40	4506798	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6777	19932	33328	7.06	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8575	21656	35197	3.86	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9169	22247	35790	1.27	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9412	22466	36050	1.6	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10899	23883	37615	1.40	3.0E-40	D86064.1	NT	Human mRNA for KIAA0205 gene, partial cds
11544	24600	38276	9.12	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
335	13548		3.91	2.0E-40	AI223038.1	EST_HUMAN	qg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
817	13996		5.59	2.0E-40	AW303868.1	EST_HUMAN	xt24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2767088 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.1

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1872	15016		2.33	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1988	15130	28233	2.9	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1988	15130	28234	2.8	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2133	15269	28389	1.39	2.0E-40	AI968562.1	EST_HUMAN	w80a11.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:254716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN.
2238	15371	28500	2.21	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
2754	15871		1.66	2.0E-40	BE276932.1	EST_HUMAN	G01121597F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3198	16371	28376	5.27	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
5021	18150	31128	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5021	18150	31129	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
906	14081		1.2	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2686	15906	28922	1.82	1.0E-40	BF036881.1	EST_HUMAN	G01460375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863803 5'
2750	15867		3.88	1.0E-40	BE018348.1	EST_HUMAN	b579a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q92158 Q92158 SYNTAXIN 17.;
3370	16542		2.14	1.0E-40	4607142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4733	17688	30851	3.69	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6385	19554	32912	0.68	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6385	19554	32913	0.68	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33763	1.83	1.0E-40	AA573201.1	EST_HUMAN	nj42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7236	20320	33764	1.83	1.0E-40	AA573201.1	EST_HUMAN	nj42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7381	20459	33922	0.82	1.0E-40	P26808	SWISSPROT	POL POLYPROTEIN CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H 1
11157	24228	37858	8.41	1.0E-40	AU146045.1	EST_HUMAN	AU146345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
11983	24978	38683	1.49	1.0E-40	AA614255.1	EST_HUMAN	np08h03.s1 NCL_CGAP_P3 Homo sapiens cDNA clone IMAGE:1116861 similar to TR:G1136406
11983	24978	38684	1.49	1.0E-40	AA614255.1	EST_HUMAN	np08h03.s1 NCL_CGAP_P3 Homo sapiens cDNA clone IMAGE:1116861 similar to TR:G1136406
12079	25069		1.86	1.0E-40	AL163248.2	NT	G1136406 KIAA0173 PROTEIN.;
12687	28032		6.94	1.0E-40	BF334112.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
3906	17065	30064	0.59	9.0E-41	W01596.1	EST_HUMAN	MR2-CT0222-211099-002-e10 G10222 Homo sapiens cDNA
8106	21188	34708	1.6	8.0E-41	AL163203.2	NT	zsa36a02.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284602 5'
851	18024	27089	2.52	7.0E-41	AI934364.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
851	18024	27090	2.52	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
851	18024	27090	2.52	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5379	18581	31450	0.9	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6132	19311	32851	2.71	7.0E-41	11418208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6483	19650	33012	1.04	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7133	18559	31473	0.96	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11718	24758	38453	2.06	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
11931	24917	38620	1.41	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
13182	26028	26543	8.58	7.0E-41	11417872	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
291	13508	26543	1.13	6.0E-41	AB037163.1	NT	Homo sapiens DSCR3b mRNA, complete cds
2179	15314	28443	3.09	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
8159	21240	34760	1.31	6.0E-41	BF513783.1	EST_HUMAN	U1-HBW1-amp-b-03-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
13156	25952		1.25	6.0E-41	AW879337.1	EST_HUMAN	h04408.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains MER32.b3 MER32 repetitive element
1845	14991	28092	1.37	5.0E-41	T62828.1	EST_HUMAN	yc03e10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:79628 3'
4223	17371		1.17	5.0E-41	4885833	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6678	19837		2.34	5.0E-41	BE087042.1	EST_HUMAN	PM4-BT0341-251169-002-F11 BT0341 Homo sapiens cDNA
402	13599		1.69	4.0E-41	BE166318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1122	14287	27342	2.37	4.0E-41	AU119344.1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1442	14595	27670	14.6	4.0E-41	A1027117.1	EST_HUMAN	aw46c06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element ;
1442	14595	27671	14.6	4.0E-41	A1027117.1	EST_HUMAN	aw46c06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element ;
1454	14607	27687	3.34	4.0E-41	AB009881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1665	14817	27900	7.72	4.0E-41	A1500408.1	EST_HUMAN	htr86c04.x1 NCI_CGAP_Br25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element ;
2953	16130	29144	5.02	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2953	16130	29145	5.02	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4282	17407	30393	2.13	4.0E-41	X92585.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
8638	19797		1.8	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
9895	22935	36519	5.06	4.0E-41	BF304683.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11969	24064		7.38	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAAC007 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12900	25917		1.3	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE22 5'
13110	25725	31942	1.51	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3910059 5'
970	14143	27203	1.8	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4455	17595	30575	4.03	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5609	18804	31869	11.78	3.0E-41	X87698.1	NT	H. sapiens mRNA for putative p64 CLCP protein
6511	19676	33046	1.23	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7987	21017	34829	0.71	3.0E-41	RS4765.1	EST_HUMAN	y75008.r1 Soares breast 2NBH8st Homo sapiens cDNA clone IMAGE:154575 5'
12119	25099	36804	1.36	3.0E-41	AW994941.1	EST_HUMAN	QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA
12119	25099	36805	1.36	3.0E-41	AW994941.1	EST_HUMAN	QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA
12198	25153		1.98	3.0E-41	AA609768.1	EST_HUMAN	af17710.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'
12783	25525		1.43	3.0E-41	BF125922.1	EST_HUMAN	601762840F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:4028081 5'
1871	14744	27827	31.25	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2013	15153	28258	2.17	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2283	15425	28559	1.26	2.0E-41	D88962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2341	15472	28506	5.52	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2889	14744	27827	11.89	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3406	16576	29691	0.69	2.0E-41	AA449549.1	EST_HUMAN	z08804.r1 Soares fetal_tetus_Nb2HF8 9w Homo sapiens cDNA clone IMAGE:785839 5'
3941	17100	30097	0.69	2.0E-41	5032106	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4744	17678	30882	1.23	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4744	17678	30883	1.23	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
5656	18850	32132	0.6	2.0E-41	AA584575.1	EST_HUMAN	no12607.st NCI_GGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:X52851_rnat
6763	19919	33314	0.98	2.0E-41	4504778	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
7650	20905	34409	9.27	2.0E-41	AF038404.1	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
8259	21341	34858	1.36	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (Nedd5) mRNA, complete cds
8259	21341	34859	1.36	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8259	21370	34891	1.42	2.0E-41	AA328283.1	EST_HUMAN	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
9175	22253	35766	1.65	2.0E-41	P52742	SWISSPROT	EST31723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
9617	22672	36241	0.66	2.0E-41	11417118	NT	ZINC FINGER PROTEIN 135
9617	22672	36242	0.56	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11775	24767	38463	2.87	2.0E-41	AA372637.1	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
13148	25747		1.2	2.0E-41	11420516	NT	EST184555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3276	16450	29470	1.05	1.0E-41	BE669735.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
							601445647F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3849803 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3276	16450	29471	1.05	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4689	17824	30811	9.48	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
9818	22673	36243	1.57	1.0E-41	AL217888.1	EST_HUMAN	q775c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1758583 3'
12334	25241		1.67	1.0E-41	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8717	21797		1.19	9.0E-42	BE179191.1	EST_HUMAN	RCO-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9375	22450	36011	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9375	22450	36012	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
475	13670	28702	5.34	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2176	15311	28439	8.93	8.0E-42	AB028898.1	NT	nm07c02.x1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304
12375	26035		30.09	8.0E-42	AA493896.1	EST_HUMAN	307BP EXPRESSED SEQUENCE TAG mRNA;
							xc97a04.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2692174 3' similar to contains OFR.12
12396	25904		2.91	8.0E-42	AW088062.1	EST_HUMAN	OFR repetitive element;
955	14128		2.23	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8666	21746		0.5	7.0E-42	R10983.1	EST_HUMAN	y38g04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129174 5'
8445	23561	36124	1.32	7.0E-42	AL204359.1	EST_HUMAN	qf58g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1903	15046	28155	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1903	15046	28156	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
							xp2808.x1 NCI_CGAP_JH10 Homo sapiens cDNA clone IMAGE:2741789 3' similar to contains L1.11 L1
							repetitive element;
2363	15494		3.6	6.0E-42	AW238656.1	EST_HUMAN	Homo sapiens mRNA for KIAA1067 protein, partial cds
5684	18776	31824	1.65	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5834	18779	31824	1.5	6.0E-42	AB028990.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
138	13364		6.34	5.0E-42	AJ271735.1	NT	h31e1.1.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
451	13847	26883	1.56	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
499	13694		3.05	5.0E-42	5730038	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
500	13695		1.14	5.0E-42	5730038	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
8825	19976	33385	0.94	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6825	19978	33386	0.94	5.0E-42	11433063	NT	Homo sapiens myokubulin related protein 3 (MTMR3), mRNA
6941	20254	33691	2.57	5.0E-42	11417957	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7351	20430	33892	1.55	5.0E-42	AF071569.1	NT	

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	22057	35598	2.88	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10832	23885	37487	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10832	23865	37488	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11246	24315	37855	1.77	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
772	13953	27002	5.6	4.0E-42	AF055086.1	NT	Homo sapiens MHC class I region
772	13953	27003	5.6	4.0E-42	AF055086.1	NT	Homo sapiens MHC class I region
1091	14256	27312	1.82	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4311	17454	30442	1.39	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4343	17489	30469	1.1	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNACK mRNA, complete cds
4364	17507	30488	4.87	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4), mRNA
4706	17841	30825	17.84	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177), mRNA
5285	18404	31372	0.93	4.0E-42	7681835	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
10701	23734	37339	0.57	4.0E-42	AW371201.1	EST_HUMAN	GMV-BT0282-171299-127403 BT0282 Homo sapiens cDNA
10884	23966	37597	2.32	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
10884	23968	37598	2.32	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11240	24309	37946	1.43	4.0E-42	AI435225.1	EST_HUMAN	UT1602.x1 NCL CGAP_Par1 Homo sapiens cDNA clone IMAGE:2130147 3'
11698	24695	38387	1.69	4.0E-42	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882086 5'
1812	14695	27760	3.79	2.0E-42	BF376834.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0078 Homo sapiens cDNA
2466	15593	28718	1.6	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKGCBB08 5'
2483	15610		4.24	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2496	19523	28742	3.6	2.0E-42	AW250059.1	EST_HUMAN	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283 3'
5875	19085	32372	11.82	2.0E-42	AW855368.1	EST_HUMAN	EST367438 MAGE resequencer, MAGE Homo sapiens cDNA
5875	19085	32373	11.82	2.0E-42	AW855368.1	EST_HUMAN	EST367438 MAGE resequencer, MAGE Homo sapiens cDNA
6892	20044	33452	0.9	2.0E-42	AI052586.1	EST_HUMAN	aw83005.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1663417 3'
10046	23084	36685	1.28	2.0E-42	BE538918.1	EST_HUMAN	801061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10260	23295	36892	0.64	2.0E-42	P81949	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
10260	23295	36893	0.64	2.0E-42	P81949	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
12037	25019	38723	1.53	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
752	13932	26977	1.75	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1067	14233	27292	2.2	1.0E-42	AW296809.1	EST_HUMAN	UH-B11-afn-e-04-0-UI.st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1125	14280	27345	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1125	14280	27346	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1271	16033	27498	11.99	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1271	16033	27499	11.99	1.0E-42	AF087186.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1735	14884	27977	1.15	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2087	15227	28349	1.18	1.0E-42	AF110296.1	NT	Homo sapiens PDNP1 gene, exon 17
2609	15733	28849	1.42	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
3029	16205	29228	9.15	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3789	16960	29964	3.31	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3895	17054	30054	1.11	1.0E-42	5031670	NT	Homo sapiens Gdgl vesicular membrane trafficking protein p18 (BE11) mRNA
4036	17192	30202	0.99	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4361	17504	30486	3.47	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4716	17851	30834	0.61	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161089-012-a03 ST0197 Homo sapiens cDNA
4867	18000	30984	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4877	18000	30985	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4901	18031	31020	6.13	1.0E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
11440	24501	38169	1.39	1.0E-42	BE408611.1	EST_HUMAN	607304125F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638310 5'
10291	23326	36929	6.16	9.0E-43	4757969	NT	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
669	13855	26863	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
669	13855	26864	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
718	13900	26938	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26939	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26940	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5816	19006	32312	0.72	8.0E-43	H13952.1	EST_HUMAN	y08e11.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3731	16892	29895	7.48	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822251 5'
8968	22047		3.98	7.0E-43	A1936748.1	EST_HUMAN	wp69601.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O16475 UNNAMED HERV-H PROTEIN, contains LTR7 b1 LTR7 repetitive element 1
1374	14529		11.82	6.0E-43	AA491890.1	EST_HUMAN	ne72608.st NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:309803 similar to gb:U05095 60S
2657	15780		4.03	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
4963	18092	31068	252.27	6.0E-43	AI421540.1	EST_HUMAN	AV708201 ADG Homo sapiens cDNA clone ADCACC10 5'
6441	19508	32871	2.53	6.0E-43	9956973	NT	#26c04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097318 3' similar to SW:BRR2_YEAST P32839 PRE-MRNA SPLICING HELICASE BRR2 ; Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7048	20101	33518	1.8	6.0E-43	AW488997.1	EST_HUMAN	h30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810891 3' similar to contains MER1.13 MER1.MER1 repetitive element;
10056	23094	36898	1.77	6.0E-43	AA195154.1	EST_HUMAN	z35603.r1 Soares_NHMPJ_S1 Homo sapiens cDNA clone IMAGE:065410 5' similar to TR:G528641 G528641 DB1, COMPLETE CDS; contains element PTR7 repetitive element;
11363	24424		2.45	0.0E-43	AL119158.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761L1712 5'
145	13370		1.82	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
515	13709	28738	3.4	5.0E-43	AA382780.1	EST_HUMAN	EST196033 Testis 1 Homo sapiens cDNA 5' and
2908	16086	29100	1.69	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANG06 5'
6435	20098	33812	0.9	5.0E-43	AG13509.1	EST_HUMAN	tw22607.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2280452 3'
7043	20096	33512	0.69	5.0E-43	AG13509.1	EST_HUMAN	tw22607.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2280452 3'
8381	21462	34985	0.84	5.0E-43	AA442271.1	EST_HUMAN	z35603.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
8381	21462	34985	0.84	5.0E-43	AA442271.1	EST_HUMAN	z35603.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9080	22169		0.73	5.0E-43	H74277.1	EST_HUMAN	y448912.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:229610 5'
9584	22708	38272	4.09	5.0E-43	AA465288.1	EST_HUMAN	aa33008.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:315055 5'
10609	23643	37251	2.6	5.0E-43	AF733244.1	EST_HUMAN	co52c10.x8 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591 PV14 GENE.;
10651	23885	37295	1.02	5.0E-43	AL049110.1	EST_HUMAN	DKFZp434D0119_r1 494 (synonym: htae3) Homo sapiens cDNA clone DKFZp434D0119
11001	24080	37715	4.53	5.0E-43	AW863007.1	EST_HUMAN	MR2-SN0007-200403-004-c02 SN0007 Homo sapiens cDNA
11213	24282	37921	2.24	5.0E-43	W29011.1	EST_HUMAN	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
995	16997	27227	4.4	4.0E-43	AF003528.1	NT	gy47h03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1685013 3'
5373	18576	31444	1.09	4.0E-43	AI056338.1	EST_HUMAN	Homo sapiens glycyl-tRNA synthetase (GARS), mRNA
6469	18665	33028	0.68	4.0E-43	6896009	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
7280	20363		1.6	4.0E-43	11418783	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
8371	21482	34976	5.18	4.0E-43	AI244341.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1885354 3' similar to contains MER10.13 MER10 repetitive element;
8371	21482	34976	5.18	4.0E-43	AI244341.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1885354 3' similar to contains MER10.13 MER10 repetitive element;
10521	23556	37164	1.02	4.0E-43	6005967	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
12311	25227		2.7	4.0E-43	R20950.1	EST_HUMAN	yq08b05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element;
13030	25698		1.33	4.0E-43	AI436093.1	EST_HUMAN	th92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:O02710 O02710 GAG POLYPROTEIN.;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	14399		3.46	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1730	14080	27871	2.62	3.0E-43	X97869.1	NT	H. sapiens gene encoding La subunit
2120	16055	28377	1.1	3.0E-43	R83422.1	EST_HUMAN	yp8201.r1 Soares fetal liver spleen 'NFLS Homo sapiens cDNA clone IMAGE:193945 5' similar to contains MSK1 repetitive element
3662	16825	28834	1.22	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemia cell line SKH1, mRNA Mutant, 5938 nt]
4405	17548	30532	0.9	3.0E-43	AA548154.1	EST_HUMAN	nk56d08.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
6014	18198	32515	0.94	3.0E-43	D34613.1	NT	Human TBXAS1 gene for (thromboxane synthase, promoter region and exon 1
6487	19654	33016	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6487	19654	33017	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6887	20019	33428	5.09	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8357	21438		4.39	3.0E-43	AA458824.1	EST_HUMAN	aa8811.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element
9020	22099	35639	1	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
10088	23106	36709	0.68	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC63648), mRNA
12026	25010	38712	1.42	3.0E-43	5730038	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
189	13410		7.24	2.0E-43	AI190764.1	EST_HUMAN	qd61c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733568 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element
6604	19764	33152	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element
6604	19764	33153	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element
7426	20603	33973	1.29	2.0E-43	AW207900.1	EST_HUMAN	UHH-B1-af-a-09-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8503	21584		3.16	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11476	24635		4.75	2.0E-43	T03007.1	EST_HUMAN	FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1681	14833	27817	2.95	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1681	14833	27818	2.86	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1742	14891	27885	4.12	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2786	15902	26000	4.73	1.0E-43	BF348283.1	EST_HUMAN	602022313F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157666 5'
5526	18723	31740	0.88	1.0E-43	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8744	19800	33291	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
8744	19800	33292	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7106	18533	31488	1.19	1.0E-43	R19751.1	EST_HUMAN	yg40a01.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP-BD38_MOUSE P28858 BRAIN PROTEIN DN38:
8117	21169	34720	0.6	1.0E-43	AF175285.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8258	21338		2.17	1.0E-43	AF199490.1	NT	Homo sapiens 8q22.1 region and MTGB (CBFA2T1) gene, partial cds
9037	22116	35659	28.54	1.0E-43	AW903676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
10498	23533	37143	0.66	1.0E-43	AW953229.1	EST_HUMAN	EST385299 MAGE resequences, MAGB Homo sapiens cDNA
11206	24275	37912	5.81	1.0E-43	A1084981.1	EST_HUMAN	wf87h01.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2484705 3'
11647	24726	38418	3.05	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CAGNA1E), mRNA
12248	25189		2.29	1.0E-43	AL137964.1	EST_HUMAN	DKFZp761D1015_r1 761 (synonym: hemy2) Homo sapiens cDNA clone IMAGE:2313775 3'
12550	25373	32071	3.16	1.0E-43	AI675416.1	EST_HUMAN	w69b04.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:1845552 3'
12805	25538	32013	3.21	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (GELSR1), mRNA
913	14088	27163	5.32	8.0E-44	A1222085.1	EST_HUMAN	q723g01.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
913	14088	27154	5.32	8.0E-44	A1222085.1	EST_HUMAN	q723g01.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8736	21815	35350	2.83	8.0E-44	X94364.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10545	23580	37189	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
10545	23580	37180	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11436	24497	38164	2.87	8.0E-44	Y10486.2	NT	Homo sapiens mRNA for thymidine kinase, partial
11987	24972	38877	1.78	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
12501	25345	32065	2.89	8.0E-44	11527389	NT	Homo sapiens polyoma (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12544	25735	31946	2.17	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12945	25938	31760	1.85	8.0E-44	11418086	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
13126	25735	31046	2.29	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
676	13902		1.13	7.0E-44	R06035.1	EST_HUMAN	ye89e01.r1 Scores fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124920 5'
2307	15439	28573	1.19	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3031	16207	29229	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3031	16207	29230	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3965	17123	30126	2.71	7.0E-44	AF103284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4366	17499	30479	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4366	17499	30480	0.86	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8379	21480	34983	2.39	7.0E-44	AU159839.1	EST_HUMAN	AUT59839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
6229	19404	32754	0.67	6.0E-44	Z20946.1	EST_HUMAN	HSAAADEYU.P. Human foetal Brain Whole tissue Homo sapiens cDNA
314	13530		4.25	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0831 gene (partial), XT3 gene and LZTFL1 gene
342	13593		2.42	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0831 gene (partial), XT3 gene and LZTFL1 gene

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8072	21154	34673	4.12	5.0E-44	A1568523.1	EST_HUMAN	in40d02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9584	22726		1.39	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element:
3301	10588	29678	4.27	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5128	15253		0.89	4.0E-44	A1495225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7639	20708	34187	0.87	4.0E-44	BE883178.1	EST_HUMAN	U114602.X1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8466	21547	35077	0.86	4.0E-44	L21948.1	NT	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
8079	22158		0.71	4.0E-44	BE178618.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11513	24570	38247	5.64	4.0E-44	U90878.1	NT	RC3-HT0585-010400-023-d08 HT0585 Homo sapiens cDNA
1827	14975		1.5	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
3167	16342	29350	5.11	3.0E-44	AA169851.1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (Importin alpha 7) (KPNA6) mRNA
7970	21020	34533	0.65	3.0E-44	BE884820.1	EST_HUMAN	zpt18505.1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:608777 5'
9719	22784	36355	0.63	3.0E-44	AF003273.1	NT	601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
1074	14240	27286	1.43	2.0E-44	4826885	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1074	14240	27287	1.43	2.0E-44	4826885	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1234	14383	27455	3.61	2.0E-44	5803200	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1234	14383	27456	3.61	2.0E-44	5803200	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1340	14486	27588	6.82	2.0E-44	AF133588.1	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1400	14554	27628	1.5	2.0E-44	BE465325.1	EST_HUMAN	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2219	15353	28484	3.07	2.0E-44	AF070651.1	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2605	15728		1.26	2.0E-44	4507582	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2642	15765	28879	0.94	2.0E-44	D25303.1	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2676	15786		2.3	2.0E-44	5901693	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
3558	18724	28740	1.34	2.0E-44	D87675.1	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
4892	17827	30813	1.75	2.0E-44	AW884378.1	EST_HUMAN	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6220	18385	32744	1.75	2.0E-44	11448901	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6998	18515	31507	2.18	2.0E-44	AF038968.1	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
7572	20644	34121	3.8	2.0E-44	11418228	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
7572	20644	34122	3.8	2.0E-44	11418228	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
8623	21703	35238	0.7	2.0E-44	7706370	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
8623	21703	35239	0.7	2.0E-44	7706370	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
8819	21898	35437	1.8	2.0E-44	BE388058.1	EST_HUMAN	601288914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613586 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12152	25122		4.59	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Bay/or-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12730	26094		1.56	2.0E-44	4826893	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
53	13292	26306	5.24	1.0E-44	7657334	NT	Homo sapiens Misschaps/NIK-related kinase (MINK), mRNA
53	13292	26307	5.24	1.0E-44	7657334	NT	Homo sapiens Misschaps/NIK-related kinase (MINK), mRNA
584	13784	26504	1.63	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-03030-026-M12 CT0249 Homo sapiens cDNA
1224	14384		1.98	1.0E-44	AW694803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1605	14758		8.08	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
							contains THRF3 THR repetitive element
2299	15431	28563	6.17	1.0E-44	AA434554.1	EST_HUMAN	zws3d02.1f Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THRF3 THR repetitive element
2299	15431	28564	6.17	1.0E-44	AA434554.1	EST_HUMAN	zws3d02.1f Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THRF3 THR repetitive element
							Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
2818	15932	29043	1.74	1.0E-44	AF196779.1	NT	aa01c06.s1 Soares_NhIMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
3819	16978		3	1.0E-44	AA455869.1	EST_HUMAN	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31314	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31316	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8460	21541	35070	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8460	21541	35071	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8848	21927	35466	0.96	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9227	22305	35848	0.56	1.0E-44	AIS37183.1	EST_HUMAN	ox88g07.x1 NCI CGAP G03 Homo sapiens cDNA clone IMAGE:200628 3'
11264	24333		4.13	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYED3 5'
11820	24809	38505	3.47	1.0E-44	10092664	NT	Homo sapiens Sush1 domain (SCR repeat) containing (BK65A6.2), mRNA
11890	24878	38574	3.21	1.0E-44	AW946987.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11890	24878	38575	3.21	1.0E-44	AW946987.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4701	17836	30821	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4701	17836	30822	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6787	19942	33340	1.41	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2591	15716	28834	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5193	18315	31263	8.63	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8298	21380	34902	1.03	8.0E-45	AA377985.1	EST_HUMAN	EST190893 Synovial sarcoma Homo sapiens cDNA 5' end
							wb88c06.x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.1 L1 repetitive element
1583	14735		2.36	6.0E-45	AI075425.1	EST_HUMAN	

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Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4087	17242		3.77	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
12911	26164		1.89	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
915	14080		1.71	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2058	15199	28313	4.42	5.0E-45	BF333627.1	EST_HUMAN	CNA-CN0044-180200-515-01 CN0044 Homo sapiens cDNA
3281	18455	29477	2.87	5.0E-45	AI523766.1	EST_HUMAN	tg94f07.x1 NCI_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1 ;
5629	19823	31897	8.95	5.0E-45	AA397781.1	EST_HUMAN	z72403.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
6143	19321	32864	1.09	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6143	19321	32865	1.09	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6190	19368	32714	0.92	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6190	18366	32715	0.92	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6318	19490	32847	0.87	5.0E-45	11495268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6318	19490	32848	0.87	5.0E-45	11495268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8471	21552	35082	1.12	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9241	22318	35861	1.45	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11997	24982	38688	2.5	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1167	14330	27385	6.3	4.0E-45	X95826.1	NT	H. sapiens ART14 gene
2365	15498	28622	2.15	4.0E-45	BE285622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
9157	22235		0.81	4.0E-45	AA228220.1	EST_HUMAN	nc26c07.at NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element ;
12168	26089	31659	1.36	4.0E-45	11433847	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
3411	16580		0.93	3.0E-45	T71480.1	EST_HUMAN	y435f07.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:110245 5'
4199	16580		1.03	3.0E-45	T71480.1	EST_HUMAN	y435f07.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:110245 5'
6366	19338	32895	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
6366	18536	32895	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
8845	21725		1.78	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
8891	22070	35610	4.31	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10515	23550	37169	7.52	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10515	23550	37160	7.52	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
13040	26078		3.45	3.0E-45	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2572	15597		3.12	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3097	16273	29287	0.92	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6651	19810	33198	5.45	2.0E-45	U01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7786	20842	34334	1.1	2.0E-45	BE782184.1	EST_HUMAN	601467783F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870938 5'
8610	21690	35228	0.91	2.0E-45	AW534834.1	EST_HUMAN	RCO-LT0001-150200-032-411 LT0001 Homo sapiens cDNA
9784	22824	36402	0.51	2.0E-45	AI036786.1	EST_HUMAN	ss56a01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232552 3'
11042	25887	37754	12.66	2.0E-45	BE934350.1	EST_HUMAN	MRO-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
11450	24510	38177	2.71	2.0E-45	AA458770.1	EST_HUMAN	aa87712.1 Stratiagone fetal telina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11784	24784	38481	3.35	2.0E-45	AW270280.1	EST_HUMAN	TR:G1144569 G1144669 R-SLY1.
11794	24784	38482	3.35	2.0E-45	AW270280.1	EST_HUMAN	XP72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
13087	25710		2.73	2.0E-45	11418157	NT	XP72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
128	13617		1.22	1.0E-45	BE389855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
422	13617		1.99	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
485	13679	26714	1.02	1.0E-45	4506412	NT	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
1201	14363	27423	1.66	1.0E-45	7657290	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3172	16347	29364	10.41	1.0E-45	U32166.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3581	16746	29764	0.85	1.0E-45	8659558	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3684	16827	29836	0.89	1.0E-45	AB046811.1	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4599	17736	30716	6.4	1.0E-45	BE396633.1	EST_HUMAN	Homo sapiens mRNA for KIAA1591 protein, partial cds
4848	17961		1.05	1.0E-45	HE7443.1	EST_HUMAN	601289116F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3619803 5'
5081	18209	31181	1.56	1.0E-45	11545768	NT	Y00502.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5'
8220	21302	34822	0.7	1.0E-45	11422236	NT	Homo sapiens ribon protein (NIBAN), mRNA
8220	21302	34823	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8808	21685	35425	0.8	1.0E-45	D87675.1	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
9321	22397	35950	3.92	1.0E-45	BE887843.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9722	22787	36356	0.96	1.0E-45	AB002297.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
12369	25263	32117	3.5	1.0E-45	11418099	NT	601511228F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912635 5'
12562	25384		19.43	1.0E-45	11418099	NT	Human mRNA for KIAA0299 gene, partial cds
12568	25387		6.42	1.0E-45	11526291	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
13047	25086	31663	4.02	1.0E-45	11418177	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8423	21504	35037	2.71	9.0E-46	11418157	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8835	21814		6.82	9.0E-46	AL163209.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
10607	23730	37335	6.89	9.0E-46	AW246964.1	EST_HUMAN	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
							Homo sapiens chromosome 21 segment HS21C009
							2822449 5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2513	15639	28760	7.67	8.0E-46	AI433261.1	EST_HUMAN	U32008.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);
2513	15639	28761	7.67	8.0E-46	AI433261.1	EST_HUMAN	U32008.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);
8244	21328		2.72	8.0E-46	BE167244.1	EST_HUMAN	RC5-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
4703	17838		4.79	7.0E-46	BE386163.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4928	18058		1.33	7.0E-46	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
6167	19343	32689	4	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
6623	19783	33171	1.8	7.0E-46	BF105845.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
12708	25469		2.6	7.0E-46	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2812	15826	29037	6.87	6.0E-46	AI884381.1	EST_HUMAN	Wm31108.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 MER19 repetitive element;
2812	15826	29038	6.87	6.0E-46	AI884381.1	EST_HUMAN	Wm31108.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 MER19 repetitive element;
8257	19431	32778	11.57	6.0E-46	AI635448.1	EST_HUMAN	ts58h10.x1 NCL_CGAP_K1d8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE.;
7368	20445	33907	0.99	6.0E-46	AW513244.1	EST_HUMAN	Xc42604.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706854 3' similar to gb:L08069 DNAL PROTEIN HOMOLOG 2 (HUMAN);
7541	20614	34091	0.67	6.0E-46	BF509740.1	EST_HUMAN	U11-B14-afp-b-06-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
11673	23901		2.14	6.0E-46	BE784971.1	EST_HUMAN	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880895 6'
209	13432		5.31	6.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3617	16781	29786	1.17	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupsid_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279403 3'
3617	16781	29797	1.17	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupsid_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279403 3'
6874	20026	33436	1.52	5.0E-46	BF590442.1	EST_HUMAN	naa3807.x1 NCL_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202 O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
7080	20174	33596	3.69	5.0E-46	BF347229.1	EST_HUMAN	802021164F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156670 5'
7244	20327	33772	0.75	6.0E-46	AW592253.1	EST_HUMAN	QV4-ST0212-120100-075-09 ST0212 Homo sapiens cDNA
7544	20518	34093	0.59	5.0E-46	BE549744.1	EST_HUMAN	7b38505.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
658	13844		3.95	4.0E-46	AA601143.1	EST_HUMAN	ncs4e09.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1740	14889	27981	2.89	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1740	14889	27982	2.99	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008936 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
2739	15913	29021	7.4	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
5563	18750	31786	2.1	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5553	18750	31787	2.1	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12851	25565	31989	1.38	4.0E-46	AB002059.1	NT	Human sapiens DNA for Human P2XM, complete cds
2359	15400	28620	0.94	3.0E-46	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
4513	17632	30640	1.21	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4898	18028	31015	1.11	3.0E-46	Z73660.1	NT	H sapiens Ig lambda light chain variable region gene (7c.11.2) germline; g-Light-Lambda; VLambda
4898	18028	31016	1.11	3.0E-46	Z73660.1	NT	H sapiens Ig lambda light chain variable region gene (7c.11.2) germline; g-Light-Lambda; VLambda
8949	22028	35569	12.45	3.0E-46	A1831462.1	EST_HUMAN	W49C04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
9206	22284	35824	0.81	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
9206	22284	35825	0.81	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
11873	24861	38556	1.78	3.0E-46	D31765.1	NT	Human mRNA for KIAA0061 gene, partial cds
860	14037	27099	12.65	2.0E-46	AA468646.1	EST_HUMAN	neo6a03.x1 NCL_CGAP_C63 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
1593	14749		3.78	2.0E-46	AA678246.1	EST_HUMAN	z127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'
1671	14823	27806	5.63	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
5089	18217	31188	1.26	2.0E-46	AA399286.1	EST_HUMAN	z159a02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE C01730 RSP-1 PROTEIN;
7653	20721	34187	7.1	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
8280	21342		1.29	2.0E-46	BE889161.1	EST_HUMAN	901445137F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3949297 5'
11524	24580		1.82	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE:45052), mRNA
12294	26040		1.4	2.0E-46	BF028854.1	EST_HUMAN	601785225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3987326 5'
12555	25031		1.57	2.0E-46	H48391.1	EST_HUMAN	y32a01.r1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:208677 5'
12596	25401		3.31	2.0E-46	AA001786.1	EST_HUMAN	z184f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
12934	25923	31884	4.26	2.0E-46	AW277214.1	EST_HUMAN	xq78i03.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2766789 3'
1261	14418	27483	4.31	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2356	15487	28619	4.88	1.0E-46	AW978516.1	EST_HUMAN	EST350625 IMAGE resequences, MAGP Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2473	15600	28725	3.53	1.0E-46	H97330.1	EST_HUMAN	EST480695 WATM1 Homo sapiens cDNA clone 480695
3321	16494	28511	2.12	1.0E-46	AA631912.1	EST_HUMAN	np78502.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X78717 H. sapiens
4995	18124		3.13	1.0E-46	AB023107.1	NT	MT-11 mRNA. (HUMAN);
5917	19007	32313	5.89	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
6098	25818	32609	5.34	1.0E-46	8923762	NT	7-62b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
6098	25818	32610	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6746	19602	33295	0.64	1.0E-46	BF196247.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
11102	19007	32313	3.72	1.0E-46	BF194707.1	EST_HUMAN	7n48607.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element
11410	24471	38136	1.81	1.0E-46	AJ245621.1	NT	MER22 repetitive element ;
12323	26233	32105	1.39	1.0E-46	BF531102.1	EST_HUMAN	7e82b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
12323	26233	32106	1.39	1.0E-46	BF531102.1	EST_HUMAN	Homo sapiens CTL2 gene
13176	25784		1.99	1.0E-46	AV715377.1	EST_HUMAN	802072294.F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
787	13066		3.7	9.0E-47	AJ271735.1	NT	802072294.F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
5047	18175	31152	3.05	9.0E-47	AW770928.1	EST_HUMAN	AV715377.DCB Homo sapiens cDNA clone DCBAIE03 5'
6506	19672	33039	0.86	9.0E-47	11425439	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11388	24449	38110	1.4	9.0E-47	11432208	NT	h93604.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
12874	26027	31675	1.64	9.0E-47	11417990	NT	HYPOTHETICAL 12.4 KD PROTEIN. ;
1851	14997	28100	32.2	8.0E-47	Y18536.1	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
1851	14997	28101	32.2	8.0E-47	Y18536.1	NT	Homo sapiens similar to aldo-keto reductase family 1, member B1 (aldose reductase) (H. sapiens)
2781	15897	28007	1.5	8.0E-47	5453955	NT	(LOC63093), mRNA
3089	18265	29283	2.04	8.0E-47	AJ228043.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3715	18878	28881	0.77	8.0E-47	AB041926.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
3716	16876	28882	0.77	8.0E-47	AB041926.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
12862	25922		1.89	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
2613	16737	20051	3.04	6.0E-47	AL163246.2	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
8890	21969	35505	0.52	6.0E-47	U77054.1	EST_HUMAN	AV683284 GKC Homo sapiens cDNA clone GKCA5H11 5'
9476	22533	36097	6.83	6.0E-47	AI695189.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9913	22953	36538	0.69	6.0E-47	AB042824.1	NT	HSU77054 Human Homo sapiens cDNA clone N7
9913	22953	36539	0.69	6.0E-47	AB042824.1	NT	hs9802.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266659 3'
							Homo sapiens RECOL5 beta mRNA for DNA helicase recQ5 beta, complete cds
							Homo sapiens RECOL5 beta mRNA for DNA helicase recQ5 beta, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6707	10865	33255	5.73	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11036	24114		5.58	5.0E-47	M78590.1	EST_HUMAN	EST007938 Fetal brain, Stratiotes (cd9836208) Homo sapiens cDNA clone HFBCF07
1432	14585	27660	7.03	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300), mRNA
6971	20189	33625	0.82	4.0E-47	BE938898.1	EST_HUMAN	MR4-TN0108-280800-201-014 TN0108 Homo sapiens cDNA
8677	21757	35292	2.22	4.0E-47	BE916483.1	EST_HUMAN	601280466F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8677	21757	35293	2.22	4.0E-47	BE916483.1	EST_HUMAN	601280466F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8818	21897	35436	0.83	4.0E-47	AW893777.1	EST_HUMAN	RC3-BN0034-220300-015-05 BN0034 Homo sapiens cDNA
11636	24922		1.98	4.0E-47	AW515509.1	EST_HUMAN	xx68507.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT8_MOUSE
558	13751	26778	2.09	3.0E-47	BE907634.1	EST_HUMAN	Q94252 VIRAL INTEGRATION SITE PROTEIN INT-6, [?];
558	13751	26779	2.09	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
841	14019	27076	3.99	3.0E-47	NE57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
969	14141	27202	10.04	3.0E-47	AL163284.2	NT	Y54604.s1 Scores_multiple_colicis_2NHIMSP Homo sapiens cDNA clone IMAGE:277327 3'
3378	16348	29562	0.97	3.0E-47	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4073	17229		6.61	3.0E-47	U83181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SDF1), mRNA, partial cds
4482	17822	30803	1.14	3.0E-47	M12969.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6138	19316	32654	4.68	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6138	19316	32655	4.68	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6894	19832		1.71	3.0E-47	A1222413.1	EST_HUMAN	Q104407.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843718 3'
7940	20513	34089	0.88	3.0E-47	AB19755.1	EST_HUMAN	W11108.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
7540	20513	34090	0.88	3.0E-47	AB19755.1	EST_HUMAN	W11108.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9033	22112	35654	0.77	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGI resequences, MAGI Homo sapiens cDNA
9033	22112	35655	0.77	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGI resequences, MAGI Homo sapiens cDNA
152	13377	26409	1.21	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
990	14162	27221	2.45	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
990	14162	27222	2.45	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1598	14751		0.95	2.0E-47	A1969279.1	EST_HUMAN	W496502.x1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:2478851 3'
1023	14775	27859	1.61	2.0E-47	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1712	14863	27952	4.48	2.0E-47	AA524514.1	EST_HUMAN	ing43h12.s1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:937607 3'
4467	17007	30585	1.61	2.0E-47	4504866	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4503	17643	30628	1.67	2.0E-47	AA569592.1	EST_HUMAN	N123g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4503	17643	30629	1.67	2.0E-47	AA569592.1	EST_HUMAN	N123g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4628	17764	30746	2.14	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R), mRNA
4833	18063	31046	1.25	2.0E-47	AW965166.1	EST_HUMAN	EST377239 MAGI resequences, MAGI Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5245	18366		0.71	2.0E-47	AI041128.1	EST_HUMAN	061h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
5804	19093	32407	0.8	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6097	19278	32607	1.32	2.0E-47	BE778476.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6097	19278	32608	1.32	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7878	25864		1.34	2.0E-47	U09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8151	21233	34753	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8151	21233	34754	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8915	21894	35533	1.76	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
8990	22739	36308	1.27	2.0E-47	11526136	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
12357	28073	31653	3.36	2.0E-47	R42423.1	EST_HUMAN	Y92a08.x1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28966 3' similar to contains OFR repetitive element ;
12894	28076		1.87	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1437	14590	27663	5.42	1.0E-47	AI333420.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1631189 3'
3928	17085	30080	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3928	17085	30081	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5187	18309	31275	2.4	1.0E-47	AW813908.1	EST_HUMAN	RC3-ST0197-130400-017-H02-ST0197 Homo sapiens cDNA
7189	20054	33484	10.76	1.0E-47	AI880886.1	EST_HUMAN	at19e08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995
9069	22148		4.24	1.0E-47	AW684648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10564	23599	37205	2.26	1.0E-47	L30115.1	NT	h184811.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978072 3' similar to gb:M26326
1643	14795	27879	3.84	9.0E-48	AF223391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3646	16809	29823	0.73	9.0E-48	BF359847.1	EST_HUMAN	Papilloharedyias alcohol dehydrogenase class I (ADH) gene, 5' region
5797	18987	32290	1.1	9.0E-48	BE888196.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5797	18987	32291	1.1	9.0E-48	BE888196.1	EST_HUMAN	h184811.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3913106 5'
6226	19401	32751	0.57	9.0E-48	AI833188.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
6355	19525	32882	0.71	9.0E-48	AI123240.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
11378	24439	38093	3.06	9.0E-48	BE393813.1	EST_HUMAN	at75h09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844
1278	14436		1.75	8.0E-48	4501900	NT	Q60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN ;
1280	14436		1.65	8.0E-48	4501900	NT	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM100078 5'
1280	14436		1.65	8.0E-48	4501900	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632063 5'
3205	16380	26990	5.72	8.0E-48	AW788477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
							h61b03.x1 NCL GAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
							BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3205	16380	29391	5.72	8.0E-48	AW768477.1	EST_HUMAN	h161503.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:364707
4041	17197	30208	0.66	8.0E-48	4504116	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
503	13998		2.58	7.0E-48	AB033035.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
504	13998		18.89	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1527	14680	27761	1.96	7.0E-48	6912719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1667	14919	27902	5.39	7.0E-48	5730038	NT	Homo sapiens taurine-like kinase 1 (TLK1), mRNA
6685	19843	33233	24.01	7.0E-48	11418831	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
12125	25105	38809	2.98	7.0E-48	R19623.1	EST_HUMAN	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
3687	19880	29858	0.88	6.0E-48	A176111.1	EST_HUMAN	W37502.1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:34747 5'
6183	19359	32707	0.84	6.0E-48	AB006955.1	NT	W69h03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:239861 3'
6024	20239	33674	0.93	6.0E-48	11420995	NT	Homo sapiens mRNA for AIE-75, complete cds
7628	25849	34172	0.78	6.0E-48	AB046844.1	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7628	25849	34173	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9323	22398	35953	1.57	6.0E-48	AF026816.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9741	22806	36382	1.87	6.0E-48	11427428	NT	Homo sapiens putative oncogene protein mRNA, partial cds
							Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
							Homo sapiens hypopharyngeal protein FLJ11006 (FLJ11006), mRNA
							z445005.s1 Striatum hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to
							contains Alu repetitive element;
9890	22630	36514	2.84	6.0E-48	AA189080.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
3384	19485	29589	1.48	5.0E-48	4826891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
8774	21853	35395	1.04	5.0E-48	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2829	19343	29053	1.02	4.0E-48	R45715.1	EST_HUMAN	Hs140-f Adult heart, Clontech Homo sapiens cDNA clone a140-f
11200	24268	37005	3.11	4.0E-48	AB20420.1	EST_HUMAN	h47a02.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2254154 3'
12050	25031	38737	1.75	4.0E-48	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
1416	14570	27643	1.91	3.0E-48	4885170	NT	AV690984 GKc Homo sapiens cDNA clone GKCDRE12 5'
2032	15173	28282	31.81	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2032	15173	28283	31.81	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
3505	16672	29682	0.93	3.0E-48	AF172453.1	NT	Homo sapiens opid growth factor receptor mRNA, complete cds
							h14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN
3721	16882	29888	0.9	3.0E-48	AW664331.1	EST_HUMAN	P59555 DOWN SYNDROME CRITICAL REGION PROTEIN B.1
4362	17505		0.63	3.0E-48	AA039541.1	EST_HUMAN	204q03.r1 Soares fetal liver spleen, 1N1FS_S1 Homo sapiens cDNA clone IMAGE:429844 5'
6015	19189	32516	2.08	3.0E-48	BE084571.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
7159	20382	33735	1.07	3.0E-48	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
							nv0305.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
8585	21668		3.73	3.0E-48	AA659930.1	EST_HUMAN	PTR5 repetitive element ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11114	24188	37818	8.1	3.0E-48	BF514170.1	EST_HUMAN	UHHBW1-ant-e-10-UJ.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
5	13244	26245	0.66	2.0E-48	AA465007.1	EST_HUMAN	zx60c03.1 Scores ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:810062 5'
46	13285	26294	1.7	2.0E-48	AA631040.1	EST_HUMAN	Imf27 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-28
4654	17790	30774	0.99	2.0E-48	BE246065.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
5935	19121	32433	0.84	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
5935	19121	32434	0.84	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
7688	20753	34236	3.99	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7688	20753	34237	3.99	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7703	20768	34253	3.94	2.0E-48	11496238	NT	Homo sapiens v-rat avian reiculoendothelials viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8550	21631	35168	1.13	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
12109	25089		1.36	2.0E-48	AW291799.1	EST_HUMAN	UI-HB12-agi-b-11-UJ.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724463 3'
12320	13244	26245	2.98	2.0E-48	AA465007.1	EST_HUMAN	zx60c03.1 Scores ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:810052 5'
12674	25990	31771	1.25	2.0E-48	BE737154.1	EST_HUMAN	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
57	13295	26311	2.33	1.0E-48	7708534	NT	Homo sapiens displatein resistance-associated overexpressed protein (LOC51747), mRNA
896	14072	27137	4.67	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1101	14266	27323	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1101	14266	27324	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1324	14481	27548	4.01	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
1968	15111	28212	13.8	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3577	16742	29759	0.94	1.0E-48	AL163245.2	NT	Homo sapiens chromosome 21 segment HS21C046
6240	16362	31330	1.1	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6417	16586	32948	1.24	1.0E-48	A1880077.1	EST_HUMAN	td17g01.x1 NCI CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588
6417	16586	32949	1.24	1.0E-48	A1880077.1	EST_HUMAN	td17g01.x1 NCI CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588
6628	16788		0.87	1.0E-48	Y18000.1	NT	SIMILARITY TO U73941 ;
6727	19883	33274	0.59	1.0E-48	AB028994.1	NT	Homo sapiens NF2 gene
6727	19883	33275	0.59	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7407	20485	33954	2.21	1.0E-48	4755137	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
8031	22110	35651	0.65	1.0E-48	4758695	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
8031	22110	35652	0.65	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9031	22110	35652	0.65	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA

Single Exon Probes Expressed in Placenta

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9414	22488	36053	0.99	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9468	22526	36089	6.79	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9781	22821	36396	4.74	1.0E-48	BF304683.1	EST_HUMAN	60188099F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10581	23616	37221	4.23	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10581	23616	37222	4.23	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
12282	28014		1.41	1.0E-48	W26785.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
2064	15204	28320	0.97	8.0E-49	AB026497.1	NT	Mus musculus MyoPD2 mRNA for myosin containing PDZ domain, complete cds
6178	19354	32701	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6178	19354	32702	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8491	21572	35109	3.09	8.0E-49	U23860.1	NT	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10194	23231	36822	0.83	8.0E-49	AB008681.1	NT	Homo sapiens gene for actinW receptor type IIb, complete cds
11096	24109	37804	3.65	8.0E-49	AI623722.1	EST_HUMAN	is38d12.x1 NC1_CGAP_U14 Homo sapiens cDNA clone IMAGE:2308871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element;
12097	25077	38785	2.08	8.0E-49	AA872183.1	EST_HUMAN	cb78e08.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337482 3'
142	13602	26637	1.21	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
142	13602	26638	1.21	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26637	1.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26638	1.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
406	13602	26637	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
406	13602	26638	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
408	13602	26638	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1248	14407	27459	4.37	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4772	17807	30880	0.9	7.0E-49	O60811	SWISSPROT	HYPOPHETICAL PROTEIN D.B45Q24.3
5576	18771	31815	2.33	7.0E-49	AI807191.1	EST_HUMAN	wf28h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
5586	18781	31826	1.3	7.0E-49	AL120937.1	EST_HUMAN	O54923 RSEC15.1
5928	18771	31815	0.79	7.0E-49	AI807191.1	EST_HUMAN	DKFZD762C033.s1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762C033 3'
							wf28h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
							O54923 RSEC15.1
202	13425	26456	20.33	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
4231	17378	30367	0.64	6.0E-49	AL162061.1	EST_HUMAN	DKFZD761A138.s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'
5954	19140	32456	0.64	6.0E-49	AW511225.1	EST_HUMAN	td44a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O56636
5572	19734	33113	1.27	6.0E-49	AU140742.1	EST_HUMAN	O56636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II. ; AU140742 PLAGE4 Homo sapiens cDNA clone PLAGE4000148 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11557	24612	38291	3.39	6.0E-49	AW452218.1	EST_HUMAN	UI-H-B13-alc-a-05-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11981	24946	38650	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST77625 Pancreas tumor III Homo sapiens cDNA 5' end
11981	24946	38651	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST77625 Pancreas tumor III Homo sapiens cDNA 5' end
12870	25897		10.54	6.0E-49	AA707567.1	EST_HUMAN	z129c08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451894 3'
730	13912	26931	5.84	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
730	13912	26932	5.84	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1838	14983	28082	10.18	5.0E-49	AA172121.1	EST_HUMAN	zp28c07.r1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to
2808	13922	29032	7.1	5.0E-49	U17714.1	NT	TR:G233226 G233226 RTV-L-H PROTEIN; contains LTR7.13 LTR7 LTR7 repetitive element;
3346	16519	28533	7.59	5.0E-49	11436355	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
538	13731	28754	28.39	4.0E-49	AW189533.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S27 (metalloprotein 1) (H. sapiens) (LOC63362), mRNA
7395	20473	33939	0.96	4.0E-49	Z26634.2	NT	X08601.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2675503 3' similar to W.P.B0350.2B
7395	20473	33940	0.96	4.0E-49	Z26634.2	NT	CE06703;
7422	20499	33970	0.68	4.0E-49	11525737	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7422	20499	33971	0.68	4.0E-49	11525737	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7992	21042	34554	0.89	4.0E-49	7662209	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
8065	22144	35590	0.47	4.0E-49	11425374	NT	(GalNAc-T6) (GALNT6), mRNA
8065	22144	35591	0.47	4.0E-49	11425374	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
12514	26145		2.74	4.0E-49	AA210788.1	EST_HUMAN	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
12815	25413		2.93	4.0E-49	AF240786.1	NT	(GalNAc-T6) (GALNT6), mRNA
574	13765	28789	0.91	3.0E-49	X68988.1	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
2713	15831		2.73	3.0E-49	AA016131.1	EST_HUMAN	Homo sapiens copine III (CPN3), mRNA
5098	18226	31198	2.88	3.0E-49	U46999.1	NT	Homo sapiens copine III (CPN3), mRNA
7577	20649	34127	8.83	3.0E-49	H39479.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11582	24638	38316	1.41	3.0E-49	AA337861.1	EST_HUMAN	H. sapiens mRNA for acetyl-CoA carboxylase
878	13864		1.93	2.0E-49	BE165980.1	EST_HUMAN	z631c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1
3294	16468	29487	1.15	2.0E-49	N26446.1	EST_HUMAN	repetitive element;
							Human type IV collagen (COL4A6) gene, exon 40
							EST729612 WATM1 Homo sapiens cDNA clone 25e12
							EST42572 Endometrial tumor Homo sapiens cDNA 5' end
							MR3-HT0487-150200-113-501 HT0487 Homo sapiens cDNA
							y233d08.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:262571 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	16822	29832	0.86	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
8875	20027	33437	1.2	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DCBALB01 5'
8291	21373		1.87	2.0E-49	M86033.1	EST_HUMAN	EST02556 Fetal brain. Stragene (cat#938206) Homo sapiens cDNA clone HFBOY60
12626	26008		2.69	2.0E-49	AF103964.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
922	14097		9.1	1.0E-49	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
1584	14736	27816	73.58	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1844	14980	28091	2.93	1.0E-49	BE255216.1	EST_HUMAN	601115789F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3356273 5'
5476	18674	31888	4.68	1.0E-49	BF131007.1	EST_HUMAN	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052062 5'
6202	19377	32728	0.65	1.0E-49	H16291.1	EST_HUMAN	yr48h04.r1 Scores adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN c08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) GAMMA-1 SUBUNIT ;
6208	19383	32733	1.09	1.0E-49	AW964640.1	EST_HUMAN	EST376713 IMAGE resequences, MAGH Homo sapiens cDNA
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7453	20530	34003	2.09	1.0E-49	N25884.1	EST_HUMAN	yw779g12.s1 Scores placenta 80c9weeks_ZN6HP80c9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7453	20530	34004	2.09	1.0E-49	N25884.1	EST_HUMAN	yw779g12.s1 Scores placenta 80c9weeks_ZN6HP80c9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
8874	21953		0.71	1.0E-49	9994184	NT	Homo sapiens RNA binding motif protein 7 (LOC81120), mRNA
9193	22271	35809	1.48	1.0E-49	BE409340.1	EST_HUMAN	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10331	23366	36975	1.23	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2423 5'
11304	24359	38010	1.32	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDAWEO4 5'
11590	24843	38326	2.91	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12148	25119		1.26	1.0E-49	BE169343.1	EST_HUMAN	MRO-HT0407-010200-006-02 HT0407 Homo sapiens cDNA
12508	25349		1.82	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
5109	18237		0.92	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
9534	26218		0.63	9.0E-50	BE295758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531688 5'
174	13398	26426	4.18	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
737	13919	26959	1.92	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
737	13919	26960	1.92	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1803	14952	28046	4.32	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2552	15677	28800	1.05	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2552	15677	28801	1.05	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2784	15879	28988	2.42	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
2891	15160		2.67	8.0E-50	D90334.1	NT	Homo sapiens hepatocyte growth factor (HGF) gene, exon 18

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
634	13819	26843	1.07	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
6923	20238	33672	0.73	7.0E-50	BF091022.1	EST_HUMAN	RC5-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
6923	20238	33673	0.73	7.0E-50	BF091022.1	EST_HUMAN	RC5-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7457	20533	34008	0.74	7.0E-50	AA627822.1	EST_HUMAN	nc69e12.s1 NCL_CGAP_C09 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X69391.60S
10993	24072	37705	23.18	7.0E-50	AI872137.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
4462	17602		0.67	6.0E-50	BE794381.1	EST_HUMAN	wn55g1.1.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
8408	21489		3.28	6.0E-50	BE044076.1	EST_HUMAN	60158956F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
11053	24130	37765	3.32	6.0E-50	AA312079.1	EST_HUMAN	nc39h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2439908 3'
11053	24130	37766	3.32	6.0E-50	AA312079.1	EST_HUMAN	MER29 repetitive element;
1835	14982	28080	1.34	5.0E-50	BF32638.1	EST_HUMAN	EST182776 Jurkat T-cells VI Homo sapiens cDNA 5' end
1835	14982	28081	1.34	5.0E-50	BF32638.1	EST_HUMAN	EST182776 Jurkat T-cells VI Homo sapiens cDNA 5' end
9294	22370		5.27	5.0E-50	AA557683.1	EST_HUMAN	CM4-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
12090	26070	38777	1.78	5.0E-50	AA403053.1	EST_HUMAN	CM4-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
940	14114		2.31	4.0E-50	AA601143.1	EST_HUMAN	nl45h10.s1 NCL_CGAP_F14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.k3 PTR5 repetitive element;
3536	16701	28712	2.06	4.0E-50	AL163248.2	NT	z62601.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 6' similar to TR:G1335769
6491	19657	33020	0.92	4.0E-50	11440983	NT	G1335769 GAG-POL POLYPEPTIDE ;
7383	20461	33924	1.02	4.0E-50	BE087536.1	EST_HUMAN	nc54609.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1
1992	15134		9.4	3.0E-50	MI18048.1	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3371	16543	29557	0.92	3.0E-50	AA746142.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
3846	17006	30008	0.9	3.0E-50	AW765254.1	EST_HUMAN	Homo sapiens cysteinyl-tRNA synthetase (CARS), mRNA
6815	19898	33374	0.89	3.0E-50	11419317	NT	QV1-BT0681-280300-127.f12 BT0681 Homo sapiens cDNA
6815	19898	33375	0.89	3.0E-50	11419317	NT	Human endogenous retrovirus RTVL-H2
6904	20219	33648	1.71	3.0E-50	11421514	NT	bb03i06.s1 NCL_CGAP_K06 Homo sapiens cDNA clone IMAGE:1322627 3'
7822	20877	34376	5	3.0E-50	AF233436.2	NT	Human endogenous retrovirus RTVL-H2
7922	20877	34377	5	3.0E-50	AF233436.2	NT	bb03i06.s1 NCL_CGAP_K06 Homo sapiens cDNA clone IMAGE:1322627 3'
							Human endogenous retrovirus RTVL-H2
							Cardiomyopathy associated gene 5
							Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
							Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
							Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8782	21861	35404	0.66	3.0E-50	6601689	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10023	23061	36657	1.08	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1688 protein, partial cds
10032	23070	36670	1.03	3.0E-50	11418514	NT	Homo sapiens l-complex 10 (a murine top homolog) (TCP10), mRNA
10737	23770	37380	1.04	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0298 gene, partial cds
11384	24425	36080	1.51	3.0E-50	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11752	23838	37564	8.19	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
13217	25792	31922	1.35	3.0E-50	AB011399.1	NT	Homo sapiens gene for AIF-4, complete cds
799	13978		7.84	2.0E-50	AF05036.1	NT	Homo sapiens MHC class 1 region
1104	14269	27327	6.16	2.0E-50	4557752	NT	Homo sapiens midline 1 (Optic/BBS syndrome) (MID1), mRNA
1474	14627	27713	33.77	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
4376	17519	30489	0.75	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
5329	18442	31412	1.37	2.0E-50	AB018319.1	NT	Homo sapiens mRNA for KIAA0776 protein, partial cds
7007	20143	33562	0.61	2.0E-50	AU124066.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001609 5'
8511	21592	35126	1.03	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8511	21592	35127	1.03	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8550	21730	35288	7.21	2.0E-50	X06986.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8550	21730	35289	7.21	2.0E-50	X06986.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10088	23126	36728	1.6	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
10088	23126	36729	1.6	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
11960	24945		1.39	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
474	13689	26701	2.17	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2438	15566		10.11	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
10396	23431	37038	1.65	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6104	18284	32817	1.04	9.0E-51	AW611225.1	EST_HUMAN	h444602.X1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
6354	19524	32881	0.58	9.0E-51	AA744837.1	EST_HUMAN	O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II. ;
8872	21951	35487	0.7	9.0E-51	A1791154.1	EST_HUMAN	ny67803.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1283381 3'
9325	23500	36161	1.29	9.0E-51	AA043738.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#37210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
							SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
							ab23g04.x5 Stratagene lung (#37210) Homo sapiens cDNA clone IMAGE:486352 5'
							SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9700	22749	36317	0.68	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#37210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
							SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9700	22749	36318	0.58	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#37210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
11764	23950	37579	1.97	9.0E-51	H89078.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
							yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:283210 5'

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11764	23950	37580	1.97	9.0E-51	H89076.1	EST_HUMAN	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
12059	25050	38768	1.84	9.0E-51	AA885514.1	EST_HUMAN	am10h02.s1 Soares NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1466451 3' similar to SW:CAYP_CANFA P10463 CALCIYPHOSINE ;
4539	17697	30677	1.11	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4559	17697	30678	1.11	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4690	17825	30812	5.38	8.0E-51	AA610842.1	EST_HUMAN	np88e06.s1 NCL_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12571_ma1
7321	20403	33865	0.71	8.0E-51	AF064254.1	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7830	20885	34387	2.11	8.0E-51	11439587	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
9654	22526		1.06	8.0E-51	AU138590.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
3354	16328	29541	1.27	7.0E-51	AW89219.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone PLACE103887 5'
3447	16315	29633	0.82	7.0E-51	AW274720.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
4282	17427	30416	1.37	7.0E-51	AL079628.1	EST_HUMAN	an34e03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q92340
4282	17427	30417	1.37	7.0E-51	AL079628.1	EST_HUMAN	Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
4376	17618	30498	1.18	7.0E-51	11421595	NT	DKFZp434B2229_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229 5'
4471	17611	30589	1.44	7.0E-51	AW285603.1	EST_HUMAN	DKFZp434B2229_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229 5'
11985	24970	38674	1.36	7.0E-51	AF161449.1	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
1557	14710	27790	0.94	6.0E-51	6678763	NT	UHL-BW0-alp-B-05-0-UJ.at NCL_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2729817 3'
							Homo sapiens HSPC331 mRNA, partial cds
							Homo sapiens putative DNA binding protein (M66), mRNA
2036	15177	28287	5.83	6.0E-51	7657266	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3582	16727	29743	14.65	6.0E-51	7657266	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4426	17666	30547	0.66	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4426	17668	30548	0.66	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6113	19293	32628	1.48	6.0E-51	X01768.1	NT	Human hemoglobin related (Hpr) gene exon 3
6124	19303	32642	8.16	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6124	19303	32643	8.16	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6900	20215	33845	0.93	6.0E-51	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7032	20168	33560	0.82	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
7104	18531	31486	2.15	6.0E-51	11429665	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
8337	22413	35965	0.69	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9337	22413	35966	0.69	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9885	22925	36506	2.05	6.0E-51	7661535	NT	Homo sapiens B9 protein (B9), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9084	23003	36598	0.79	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11534	24590	38265	1.84	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
814	13893	27047	6.22	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
826	14004	27061	1.71	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1016	18028	27247	2.99	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1638	14790	27875	1.14	5.0E-51	5031980	NT	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA
2658	15781	28894	10.38	5.0E-51	AJ007568.1	NT	Homo sapiens mRNA for nucleoprotein 155
4055	17211	30221	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4055	17211	30222	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5183	18305	31289	1.04	5.0E-51	AB037832.1	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
11558	24613	38292	3.8	5.0E-51	5803138	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
137	13363	26397	14.26	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1203	14366	27425	48.14	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1976	15119	28220	1.38	3.0E-51	AA211298.1	EST_HUMAN	zq87g01.s1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326
4448	17586	30567	1.85	3.0E-51	AL169142.1	NT	Novel human gene mapping to chromosome 22
7753	20813	34304	2.3	3.0E-51	R15914.1	EST_HUMAN	y447c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4
9040	22119		3.85	3.0E-51	M28083.1	NT	RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR3 repetitive element;
9268	28227		0.61	3.0E-51	AW58377.1	EST_HUMAN	Human hnRNP C2 protein mRNA
12667	25578		6.56	3.0E-51	AF003528.1	NT	iso4d06.y1 Human Pancreatic Islets Homo sapiens cDNA 5'
377	13585	26819	1.98	2.0E-51	4507798	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
706	13889	26921	0.89	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
706	13889	26922	0.89	2.0E-51	BE391063.1	EST_HUMAN	6012856804F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1723	14873	27965	16.76	2.0E-51	AA233352.1	EST_HUMAN	6012856804F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
3827	16987	29990	3.05	2.0E-51	AI492415.1	EST_HUMAN	z308c03.r1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTVL-H PROTEIN, ; contains LTR7.3 LTR7 repetitive element;
4616	17753	30734	1.21	2.0E-51	AW137826.1	EST_HUMAN	UJ-H-B11-adj-d-02-o-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2131732 3'
5328	18439	31408	0.66	2.0E-51	AI381520.1	EST_HUMAN	UJ-H-B11-adj-d-02-o-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2092622 3' similar to TR:P93107 P93107 PF20;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6139	19317	32658	3.54	2.0E-51	BE782013.1	EST_HUMAN	601470446F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3873563 5'
7462	20537		0.73	2.0E-51	AF219927.1	NT	Homo sapiens diacylglycerol kinase α (DGK1) gene, exon 23
7816	20685	34161	1.20	2.0E-51	7662349	NT	Homo sapiens cell recognition molecule Casp2 (KIAA0868), mRNA
8890	21975	35512	1.61	2.0E-51	BE901994.1	EST_HUMAN	801676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8896	21875	35513	1.61	2.0E-51	BE901994.1	EST_HUMAN	801676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9236	22312	35854	1.03	2.0E-51	11037064	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9712	22777	36347	1.76	2.0E-51	A1917078.1	EST_HUMAN	ts74607.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
9803	22843	36420	4.86	2.0E-51	BE165960.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
9818	22858	36438	0.69	2.0E-51	AB007925.1	NT	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10648	23682	37293	1.58	2.0E-51	AV682474.1	EST_HUMAN	Homo sapiens mRNA for KIAA0457 protein, partial cds
10690	23723	37329	1.07	2.0E-51	AA378559.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
11610	18752	31789	5.82	2.0E-51	A1732851.1	EST_HUMAN	EST91296 Synovial sarcoma Homo sapiens cDNA 5' end
11610	18752	31790	5.82	2.0E-51	A1732851.1	EST_HUMAN	ab3409.x5 NCL_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
12860	25571	31992	1.62	2.0E-51	11418159	NT	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
117	13348	26375	10.94	1.0E-51	4503528	NT	ab3409.x5 NCL_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
1523	14876	31036	37.16	1.0E-51	AV742248.1	EST_HUMAN	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
4918	18048	31036	0.82	1.0E-51	AF111169.2	NT	ab3409.x5 NCL_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
6506	18704	31720	3.7	1.0E-51	T18862.1	EST_HUMAN	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
7827	20882	34384	1.03	1.0E-51	A1672532.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) (Drosophila) homolog); translocated to, 4 (MILLT4), mRNA
8087	21169	34684	0.51	1.0E-51	BF434359.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
12076	26232		1.97	1.0E-51	AV760590.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone GBFBCC12 5'
12810	25409		9.43	9.0E-52	AA777621.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
156	13381	26412	11.42	8.0E-52	AA720574.1	EST_HUMAN	p12058l Testis 1 Homo sapiens cDNA clone b12056
1526	14876	27760	2.39	8.0E-52	X84900.1	NT	tc39g02.x1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
1686	14838	27922	2.85	8.0E-52	11968028	NT	tc39g02.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644091 3' similar to TR:P87892 P87892
							PROTEASE ;
							AV760590 MDS Homo sapiens cDNA clone MDS08B02 5'
							z85607.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to
							contains THR13 THR repetitive element ;
							hw21902.x1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
							THR repetitive element ;
							H. sapiens mRNA for laminin-5, alpha3b chain
							Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1686	14838	27923	2.85	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27922	6.75	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27923	6.75	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7886	20751	34232	0.76	8.0E-52	11416595	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7886	20751	34233	0.76	8.0E-52	11416595	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9216	22993	35836	1.86	7.0E-52	W56471.1	EST_HUMAN	z659d08.1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element
1214	14375		0.63	8.0E-52	BE072409.1	EST_HUMAN	Q13-B T0537-271209-049-d07 BT0537 Homo sapiens cDNA
1729	14879	27970	7.1	6.0E-52	AF109907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5845	18035	32341	1.05	6.0E-52	AI208794.1	EST_HUMAN	tg44f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11484	24543	38214	2.36	6.0E-52	BE048172.1	EST_HUMAN	tz48h04.y1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE Q05783 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE
4562	17700	30682	2.27	6.0E-52	Z78898.1	NT	PROTEOGLYCAN CORE PROTEIN PRECURSOR ;
9582	22647	36218	0.48	5.0E-52	11437365	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
1695	14847	27931	1.66	4.0E-52	AF257318.1	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1829	14877	28072	1.63	4.0E-52	4758843	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
4037	17193	30203	0.77	4.0E-52	4507500	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
4862	17995	30980	0.81	4.0E-52	AI766814.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
6401	18603	31574	1.3	4.0E-52	4506132	NT	w88f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
5401	18603	31575	1.3	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
8228	21310	34830	1.19	4.0E-52	BE622032.1	EST_HUMAN	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
8731	21811	35347	5.5	4.0E-52	11417035	NT	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915636 5'
12429	25304		3.44	4.0E-52	11418177	NT	Homo sapiens hydroxyacid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12887	25642		12.76	4.0E-52	AB002056.1	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
13141	25741		1.3	4.0E-52	AB011399.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4204	17563		11.41	3.0E-52	11437042	NT	Homo sapiens gene for AF-6, complete cds
576	13768	26780	1.82	2.0E-52	M10976.1	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
576	13768	26781	1.82	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2071	15211	28328	1.18	2.0E-52	AB033076.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
							Homo sapiens mRNA for KIAA1249 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2588	15903	28818	1.5	2.0E-52	BE207575.1	EST_HUMAN	bb66b07.y1 Nih_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:K16483 M.musculus mRNA for Zp1.1 zinc finger protein (MOUSE);
2798	15911		11.48	2.0E-52	BF677892.1	EST_HUMAN	802084710F1 Nih_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5092	18220	31160	3.41	2.0E-52	AL137183.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5126	18251	31216	1.4	2.0E-52	AI141802.1	EST_HUMAN	ga56e05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690764 3'
5128	18251	31217	1.4	2.0E-52	AI141802.1	EST_HUMAN	ga56e05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690764 3'
5821	19011	32317	3.24	2.0E-52	AW848041.1	EST_HUMAN	L3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA
6407	19683	33026	1.98	2.0E-52	11141868	NT	Homo sapiens Interleukin 21 receptor (IL21R), mRNA
6853	20008	33415	0.96	2.0E-52	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7081	20175	33597	0.76	2.0E-52	AI792146.1	EST_HUMAN	os45d12.y5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
7996	21046	34558	0.69	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8854	21933		8.71	2.0E-52	AF147680.1	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
9138	22215	35759	0.96	2.0E-52	AA778765.1	EST_HUMAN	Macaca mulatta beta-tubulin mRNA, complete cds
							245905.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
							Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
9880	22842		1	2.0E-52	4758789	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10321	23356	36965	4.6	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10321	23356	36966	4.6	2.0E-52	5730038	NT	wf48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11481	24540	38209	3.14	2.0E-52	AI831462.1	EST_HUMAN	wf48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11481	24540	38210	3.14	2.0E-52	AI831462.1	EST_HUMAN	THR repetitive element;
11491	24550	38225	2.52	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
11634	24714		1.46	2.0E-52	W70260.1	EST_HUMAN	z449g12.r1 Soares_fetal_heart_NHHP19W Homo sapiens cDNA clone IMAGE:344038 5'
11918	24804		3.25	2.0E-52	11417980	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
							xt72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element;
12234	26194	31541	5.9	2.0E-52	AW236297.1	EST_HUMAN	wf67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859
12658	25437		5.72	2.0E-52	AI808985.1	EST_HUMAN	Q16859 CARBOXYLESTERASE;
546	13739	26764	1.89	1.0E-52	AA834445.1	EST_HUMAN	z475h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1402	14556	27630	18.76	1.0E-52	4504026	NT	Homo sapiens glutamate-aminon ligase (glutamine synthase) (GLUL) mRNA
2600	15724		1.86	1.0E-52	4302238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
							pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
3126	16302	29315	2.6	1.0E-52	S81070.1	NT	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	18648	31626	4.43	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6523	18688	33062	2.33	1.0E-52	U38964.1	NT	Human PMS2 related (HPMSR2) gene, complete cds
7588	20859	34155	2.07	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8014	21084	34576	0.59	1.0E-52	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
8560	21740		1.18	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9390	22465	36029	0.77	1.0E-52	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10804	23637		0.68	1.0E-52	AW020370.1	EST_HUMAN	d10805.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10814	23847		1.08	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11004	24083	37720	2.12	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAX1 (hPTPCAX1) mRNA, complete cds
11076	24150		1.72	1.0E-52	11425321	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
12135	25115	38819	1.31	1.0E-52	11421401	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
12135	25115	38820	1.31	1.0E-52	11421401	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3391	17050	30049	0.09	9.0E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4511	17650	30638	3.3	9.0E-53	AF001448.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12490	25332		6.65	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4132793 5'
12958	26046		7.06	7.0E-53	AI421782.1	EST_HUMAN	t144107.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2098077 3' similar to contains THR.t1 THR repetitive element;
4214	17363	30351	4.46	5.0E-53	4758543	NT	Homo sapiens heterogenous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
5283	16411	31377	0.82	5.0E-53	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12528	25360		1.93	5.0E-53	AW813563.1	EST_HUMAN	RC3-ST0197-161089-011-g10 ST0197 Homo sapiens cDNA
50	13289	26301	2.07	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
50	13289	26302	2.07	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9816	22671		0.67	4.0E-53	AI613037.1	EST_HUMAN	U06604.x1 NCI_CGAP_UJ3 Homo sapiens cDNA clone IMAGE:2278327 3'
9958	22997		0.94	4.0E-53	F13080.1	EST_HUMAN	HSC3ID041 normalized infant brain cDNA Homo sapiens cDNA clone c-3id04
11469	24548	38221	2.99	4.0E-53	BF128701.1	EST_HUMAN	601810989F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
11489	24548	38222	2.99	4.0E-53	BF128701.1	EST_HUMAN	601810989F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2726	15844	28956	2.34	3.0E-53	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3825	18985	29898	1.16	3.0E-53	AW060336.1	EST_HUMAN	wz22c07.x1 Soares_Diackgraefe_coton_NHQC Homo sapiens cDNA clone IMAGE:2558796 3'
4713	17848	30831	0.75	3.0E-53	AW803863.1	EST_HUMAN	112LM0081-240300-055-003 UM0081 Homo sapiens cDNA
5541	18738	31755	0.97	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5743	18938	32236	1.01	3.0E-53	11526297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6323	19495	32851	1.46	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7247	20330	33776	0.76	3.0E-53	Y10388.3	NT	H.sapiens grat gene
7247	20330	33777	0.76	3.0E-53	Y10388.3	NT	H.sapiens grat gene
8499	21580	35116	10.97	3.0E-53	S72043.1	NT	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
8060	22139	35683	0.85	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9257	22334		9.77	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
12361	25259		1.18	3.0E-53	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
470	13695		11.25	2.0E-53	AA36656.1	EST_HUMAN	EST17525 Pancreas tumor III Homo sapiens cDNA 5' end
2068	15209	28325	3.29	2.0E-53	7705394	NT	Homo sapiens hyaluronic acid receptor (HAR), mRNA
2404	16535	28662	6.26	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2601	15725		12.88	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
3280	16484	28483	0.79	2.0E-53	7705867	NT	Homo sapiens leucine aminopeptidase (LOC51055), mRNA
3317	16490	29508	1.29	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4170	17320	30313	2.59	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5542	18739	31756	2.46	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
5542	18739	31757	2.46	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
8055	21138	34658	1.01	2.0E-53	AW975598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
8166	21278		0.48	2.0E-53	AA095652.1	EST_HUMAN	15429.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9008	22663		3.47	2.0E-53	AW246676.1	EST_HUMAN	2822865.fprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822665 5'
10862	23895	37517	0.89	2.0E-53	BE550195.1	EST_HUMAN	7650502.X1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231627 3' similar to TR:Q04009 Q04009 MYOSIN HEAVY CHAIN.1
1477	14630	27715	2.2	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3498	16663	28675	2.99	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5078	18206	31178	1.06	1.0E-53	BE296386.1	EST_HUMAN	601176725F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3631919 5'
6631	18884	33392	1.5	1.0E-53	BF364201.1	EST_HUMAN	CM4-NN1029-150800-543-e02 NN1029 Homo sapiens cDNA
7397	20475	33942	0.87	1.0E-53	BE012071.1	EST_HUMAN	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
8120	21202	34723	0.6	1.0E-53	AA249072.1	EST_HUMAN	19571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9280	22366	35915	4.73	1.0E-53	X785536.1	NT	H.sapiens mRNA for hnRNPcore protein A1
12228	26176	38345	1.47	1.0E-53	AW245422.1	EST_HUMAN	2822943.3.fprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822943 3'
3324	16497	29515	0.61	9.0E-54	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5417	25803	31593	5.86	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
212	13435	28465	1.29	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3614031 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
1882	15026	28133	2.08	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6057	19239	32564	23.39	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
395	13632	26969	1.35	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;
1877	15021	28128	2.23	7.0E-54	Y16845.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2278	15410	28541	7.63	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:257369 3' similar to contains LTR7.b3 LTR7 repetitive element;
10333	23368	36978	2.1	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC65182), mRNA
11365	24426	38081	1.4	7.0E-54	89233698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11365	24426	38082	1.4	7.0E-54	89233698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11570	24625		3.42	7.0E-54	AH160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
25	13263	26265	0.84	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MCB, exon 4, 5 and partial cds
398	13633	26870	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
396	13633	26871	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3365	16527	29542	0.72	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4111	17266	30265	22.75	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4884	17721	30704	1.09	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPCAAC10 5'
4968	18097	31073	2.15	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4986	18126		2.04	6.0E-54	Y09846.1	NT	H. sapiens ehc pseudogene, p66 isoform
5115	18126		3.31	6.0E-54	Y09846.1	NT	H. sapiens ehc pseudogene, p66 isoform
11741	28927	37552	1.52	6.0E-54	AW813587.1	EST_HUMAN	RC3-ST0197-151099-011-008 ST0197 Homo sapiens cDNA
2218	13352	28483	1.94	6.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84(ZINC FINGER PROTEIN HPF2)
187	13409		56.19	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
978	14151	27211	14.58	4.0E-54	AA308784.1	EST_HUMAN	EST1177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1848	14594	28096	3.28	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1848	14594	28097	3.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3274	18448		1.85	4.0E-54	A935098.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN;
96	13331	26358	8.12	3.0E-54	AA313487.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:002711
1604	14757		0.96	3.0E-54	AW515742.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2635	15758	26872	1.19	3.0E-54	AL110383.1	EST_HUMAN	h87g08.x1 NCI_OGAP_G08 Homo sapiens cDNA clone IMAGE:2916542 3'
							DKFZp434E0731_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731 6'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6024	16207	32527	1.38	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7548	20620	34096	1.34	3.0E-54	AA844081.1	EST_HUMAN	ab92c08.s1 Soares_papillary_thyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1388270 3'
7548	20620	34097	1.34	3.0E-54	AA844081.1	EST_HUMAN	ab92c08.s1 Soares_papillary_thyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1388270 3'
11277	24344		1.77	3.0E-54	11434808	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA
11341	24404	38053	4.01	3.0E-54	BF345600.1	EST_HUMAN	602019408.F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121 5'
11650	24729	38421	2.88	3.0E-54	AA393362.1	EST_HUMAN	z70f12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
12336	26243	32110	1.32	3.0E-54	AW954559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
12378	26149		3.16	3.0E-54	AW748965.1	EST_HUMAN	EST366629 MAGC resequences: MAGC Homo sapiens cDNA
659	13845	26871	17.87	2.0E-54	5031900	NT	RC1-BT0313-131189-071-509 BT0313 Homo sapiens cDNA
1396	14550	27625	1.54	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
2604	15727	28846	1.25	2.0E-54	AW163175.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2666	15787	28803	2.25	2.0E-54	AL163210.2	NT	SW:CU1.1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2960	16137	28155	1.95	2.0E-54	AW087824.1	EST_HUMAN	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to
3392	16562	29577	0.6	2.0E-54	AJ278314.1	NT	SW:CU1.1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
3638	16802		6.1	2.0E-54	AA332925.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to
4321	17484		1.74	2.0E-54	4502642	NT	TR:Q62084 Q62084 PHOSPHOLIPASE C-beta-1b (PLOCB1) gene
4563	17701		7.1	2.0E-54	AF208161.1	NT	Homo sapiens mRNA for phospholipase C-beta-1b (PLOCB1) gene
5591	18786	31833	2.66	2.0E-54	4758069	NT	Homo sapiens mRNA for phospholipase C-beta-1b (PLOCB1) gene
5720	18913	32209	1.21	2.0E-54	BE047864.1	EST_HUMAN	145g08.s1 NCI_CGAP_P78 Homo sapiens cDNA clone IMAGE:896488 similar to gb:X63777 60S
5882	19071	32379	3.99	2.0E-54	11426837	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
5982	19167	32487	11.29	2.0E-54	AB046811.1	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
5982	19167	32488	11.29	2.0E-54	AB046811.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
6796	19551	33351	1.63	2.0E-54	AF008915.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
6950	20263	33701	0.68	2.0E-54	AB023212.1	NT	145g08.s1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
6950	20263	33702	0.68	2.0E-54	AB023212.1	NT	145g08.s1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
7273	20356	33810	8.33	2.0E-54	11426544	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
8828	22869	38461	3.96	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
10213	23249	38838	1.14	2.0E-54	11420127	NT	Homo sapiens EVI5 homolog mRNA, complete cds
10326	23361	38971	0.76	2.0E-54	11416762	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
							Homo sapiens mRNA for KIAA0995 protein, partial cds
							Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
							Homo sapiens mRNA for brain natriuretic receptor, complete cds
							Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
							Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10328	23361	36972	0.76	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10841	23874	37494	0.46	2.0E-54	AB007831.1	NT	Homo sapiens mRNA for KIAA0482 protein, partial cds
11276	19951	33351	1.46	2.0E-54	AF008016.1	NT	Homo sapiens EVI8 homolog mRNA, complete cds
12027	25011		1.72	2.0E-54	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
12893	25691	31970	4.38	2.0E-54	8667387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4587	17724		1.65	1.0E-54	BF316418.1	EST_HUMAN	BC11899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8927	22006	35546	0.5	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
10459	23494	37105	0.52	1.0E-54	AA412409.1	EST_HUMAN	z110e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
10459	23494	37106	0.62	1.0E-54	AA412409.1	EST_HUMAN	z110e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
13086	25709		2.33	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugeno cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-gliumyl transpeptidase mRNA, 5 end
10588	23603	37208	1.02	9.0E-55	BE081489.1	EST_HUMAN	QV2-BT0635-160400-143-h12 BT0635 Homo sapiens cDNA
1344	14500		1.59	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1348	14503		2.77	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11471	24530		1.83	8.0E-55	AW409714.1	EST_HUMAN	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2809097 5'
9004	22053		0.48	7.0E-55	AW103839.1	EST_HUMAN	xd76c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2803522 3' similar to TR:060365
9383	22458	36021	1.28	7.0E-55	AA889581.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
9416	22490	36055	1.71	7.0E-55	AU139509.1	EST_HUMAN	AU139509 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'
11485	24544	38215	8.08	7.0E-55	AI561056.1	EST_HUMAN	iq29f09.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2210249 3'
11485	24544	38216	8.08	7.0E-55	AI661056.1	EST_HUMAN	iq29f09.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2210249 3'
12726	25911	31860	1.18	7.0E-55	BE670608.1	EST_HUMAN	7637c01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284640 3'
13050	26063		6.37	7.0E-55	H23396.1	EST_HUMAN	ym57g07.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:62444 5'
11804	24794	38492	1.86	6.0E-55	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1810	14959	28051	1.21	5.0E-55	AA704971.1	EST_HUMAN	2195b09.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
1810	14959	28052	1.21	5.0E-55	AA704971.1	EST_HUMAN	2195b09.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
4894	18024	31010	1.61	5.0E-55	AW206021.1	EST_HUMAN	UI-H-B11-efy-g-09-Q-U1 at NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723538 3'
6670	19829	33217	1.49	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6670	19829	33218	1.49	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6805	25833	33360	1.08	5.0E-55	4505952	NT	Homo sapiens paroxonase 2 (PON2) mRNA, and translated products
6805	25833	33361	1.08	5.0E-55	4505952	NT	Homo sapiens paroxonase 2 (PON2) mRNA, and translated products
7182	20314	33757	1.03	5.0E-55	7382477	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA
7448	20523	33996	0.72	5.0E-55	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9244	22321	35985	2.3	5.0E-55	4909302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
9240	22585		0.91	5.0E-55	BE004396.1	EST_HUMAN	RCA-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
10243	23278	36872	1.53	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10243	23278	36873	1.53	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10427	23462	37069	1.13	5.0E-55	5453765	NT	Homo sapiens nel (chicken)-like 2 (NEL2), mRNA
11502	24560	38238	1.3	5.0E-55	11421649	NT	Homo sapiens SKAP55 homolog (SKAP-HOM), mRNA
11502	24560	38237	1.3	5.0E-55	11421649	NT	Homo sapiens SKAP55 homolog (SKAP-HOM), mRNA
12421	25298		1.73	5.0E-55	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
58	16004	26310	2.24	4.0E-55	AW957894.1	EST_HUMAN	EST370084 MAGe sequences, MAGe Homo sapiens cDNA
689	13873	26906	32.17	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1472	14626	27710	2.15	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1472	14626	27711	2.15	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1544	14696		1.72	4.0E-55	BF061411.1	EST_HUMAN	7152b10.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3300043 3' similar to contains L1 L1 repetitive element
2081	15221	28341	2.19	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2081	15221	28342	2.19	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2151	15287	28412	8.38	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2151	15287	28413	8.38	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2384	15515	28844	3.02	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
8639	21620		9.85	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11605	24563		2.31	4.0E-55	W28189.1	EST_HUMAN	43c56 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12337	25244		1.82	4.0E-55	BF030941.1	EST_HUMAN	601866575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
8731	19887	33279	0.68	3.0E-55	AA077156.1	EST_HUMAN	7B09A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B09A09
12273	25205		4.18	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
13103	25718		3.53	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
388	13594	26630	1.69	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
565	13757		1.08	2.0E-55	M10976.1	NT	Human endogenous retrovirus DNA (4-1), complete retroviral segment
666	13852	26880	3.98	2.0E-55	4507298	NT	Human endogenous retrovirus protein 1 (STXBPT1) mRNA, and translated products
3023	16199	29222	0.89	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4897	18027	31014	3.51	2.0E-55	BE19886.1	EST_HUMAN	GM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7673	25851	34217	0.85	2.0E-55	AW501988.1	EST_HUMAN	UHF-BN0-ake-f-06-0-UJ1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
9285	22342	35892	0.48	2.0E-55	BF224452.1	EST_HUMAN	h76h08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
8265	22342	35893	0.48	2.0E-55	BF224452.1	EST_HUMAN	h76h08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9361	22436		4.33	2.0E-55	AI002836.1	EST_HUMAN	am88h05.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.52 THR repetitive element;
9442	22518		0.67	2.0E-55	BE007969.1	EST_HUMAN	GVO-RN0747-280400-213-g6 BNO147 Homo sapiens cDNA
11192	24261	37697	2.33	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005983 5'
							Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
13177	16199	29222	1.94	2.0E-55	4507798	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
99	13334	26361	1.62	1.0E-55	4506080	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabeta2) mRNA, complete cds
194	13417	26448	40.5	1.0E-55	U09823.1	NT	ov65g09.x1 Scarses testis NHT Homo sapiens cDNA clone IMAGE:1844760 3'
598	13779	26788	1.38	1.0E-55	AI026718.1	EST_HUMAN	Homo sapiens mRNA for KIAA0903 protein, partial cds
1173	14336	27392	3.92	1.0E-55	AB020710.1	NT	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2006	15148	28261	2.33	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2006	15148	28262	2.33	1.0E-55	BE277861.1	EST_HUMAN	Homo sapiens SMA3 (SMA3), mRNA
2401	15532		4.65	1.0E-55	5603174	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2415	15697	28673	1.44	1.0E-55	AF000990.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2596	15711	28629	19.68	1.0E-55	X13111.1	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2620	16743	28857	5.51	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2620	16743	28858	5.51	1.0E-55	AE007866.2	NT	Homo sapiens CLP mRNA, partial cds
2677	15737	28914	3.37	1.0E-55	L54057.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
2850	15864	29073	1.22	1.0E-55	AB033046.1	NT	49c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
3495	16662	29674	1.16	1.0E-55	W28169.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C067
4087	17252	30253	4.28	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C010
4409	17551	30536	1.1	1.0E-55	AL163210.2	NT	Y44g03.f1 Scarses fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:245620 5'
4853	17986		0.94	1.0E-55	N77291.1	EST_HUMAN	Homo sapiens DSCR5b mRNA, complete cds
4949	18079	31034	1.15	1.0E-55	AB037183.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4949	18079	31055	1.16	1.0E-55	AB037183.1	NT	Homo sapiens PRO1851 mRNA, complete cds
5614	18808	31876	0.65	1.0E-55	AF119856.1	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6401	19570	32932	7.26	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6401	19570	32933	7.26	1.0E-55	11433048	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8178	21260	34782	1.7	1.0E-55	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8178	21260	34783	1.7	1.0E-55	11432994	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
8266	21348	34863	0.49	1.0E-55	11421649	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8273	21355	34872	0.93	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8273	21355	34873	0.63	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11152	24223	37851	2.41	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11152	24223	37852	2.41	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11733	23919	37644	1.86	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11755	23941	37567	1.34	1.0E-55	T10046.1	EST_HUMAN	seq1576 b4HB3MA Cor8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F161 5' similar to similar to Chinese Hamster DHFR-coamplified protein mRNA
11789	24779	38478	2.67	1.0E-55	8922743	NT	Homo sapiens hypothetical protein FLJ10891 (FLJ10891), mRNA
11876	24864	38560	1.78	1.0E-55	10567821	NT	Homo sapiens DNA-binding protein (LOC66242), mRNA
7522	20595	34070	1.85	9.0E-58	BE379074.1	EST_HUMAN	60123702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
11545	24601	38277	1.34	8.0E-58	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2793	15909	29017	7.08	7.0E-56	H19934.1	EST_HUMAN	yr62g03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element
7818	20873	34371	1.93	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231059-013-b07 CT0252 Homo sapiens cDNA
7818	20873	34372	1.93	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231059-013-b07 CT0252 Homo sapiens cDNA
1727	14877	27868	2.7	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-A01 BN0053 Homo sapiens cDNA
9362	22437	35095	0.71	5.0E-56	AW015507.1	EST_HUMAN	UIH-B10p-asu-e-05-0-U1.91 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10599	23634		1.35	5.0E-56	W28180.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12513	26137	31550	2.47	5.0E-56	H59099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
28	13266	26268	8.64	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
28	13266	26269	8.64	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2773	15888	28998	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773	15888	28999	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2873	13732	26756	9.22	4.0E-56	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6387	19556	32915	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6387	19556	32916	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10724	23757	37384	1.89	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
11163	24234	37863	7.73	4.0E-56	AI498096.1	EST_HUMAN	trf55g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2183046 3'
11163	24234	37864	7.73	4.0E-56	AI498096.1	EST_HUMAN	trf55g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2183046 3'
1372	14527	27601	2.69	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1804	14953	28047	1.84	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
2217	15361	28482	1.6	3.0E-56	6912697	NT	Homo sapiens oncogene TFC21 (TFC21), mRNA
3185	16370	29376	1.67	3.0E-56	AA325926.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3185	16370	29377	1.67	3.0E-56	AA325926.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3939	17088		2.81	3.0E-56	AF055066.1	NT	Homo sapiens MHC class I region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4507	17648	30634	0.67	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
4544	17682	30684	4.42	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4695	17830	30816	2.4	3.0E-56	5902085	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKIVL2), mRNA
5801	18991	32283	1.5	3.0E-56	4759163	NT	Homo sapiens sparc/osteoneclin, ovex and kazal-like domains proteoglycan (testican) (SPOCK), mRNA
5801	18991	32284	1.5	3.0E-56	4759163	NT	Homo sapiens sparc/osteoneclin, ovex and kazal-like domains proteoglycan (testican) (SPOCK), mRNA
7014	20150	33571	5.5	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7476	20551	34023	2.07	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2), mRNA
7476	20551	34024	2.07	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2), mRNA
9016	22055	35635	6.11	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10018	23056	36552	0.9	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10688	23731	37336	1.39	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10980	24059	37693	2.62	3.0E-56	AB042558.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
11594	24647	38330	4.64	3.0E-56	5802013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11594	24647	38331	4.64	3.0E-56	5802013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
12377	25268	32076	1.62	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12377	25268	32078	1.62	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
537	13730		11.95	2.0E-56	AA199318.1	EST_HUMAN	zq52a08.s1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:545206 3'
761	16021	26975	1.18	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-f10 BT0310 Homo sapiens cDNA
761	16021	26976	1.18	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-f10 BT0310 Homo sapiens cDNA
3053	16229	29249	0.94	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3391	16561		0.84	2.0E-56	AB008981.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3624	16788	29805	1.26	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
7239	20323	33767	1.39	2.0E-56	5730038	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR), mRNA
1003	14174		3.01	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3765	16926	29928	1.84	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI CGAP CG6 Homo sapiens cDNA clone IMAGE:2946452 3'
3765	16926	29929	1.84	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI CGAP CG6 Homo sapiens cDNA clone IMAGE:2946452 3'
5145	18268	31236	1.42	1.0E-56	AI906162.1	EST_HUMAN	QV-BT077-130189-079 BT077 Homo sapiens cDNA
10161	23198		0.69	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10254	23269	36986	1.52	1.0E-56	AW845987.1	EST_HUMAN	RC2-OT0163-220898-001-E02 OT0163 Homo sapiens cDNA
642	13827		1.39	9.0E-57	AW880885.1	EST_HUMAN	QV6-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
11494	24552	38227	1.72	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11494	24552	38228	1.72	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11811	24801	38500	2.2	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
14	13262	26252	1.02	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
308	13524	26558	2.93	8.0E-57	AW818405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
907	14082	27147	7.49	8.0E-57	AW264599.1	EST_HUMAN	xr05d10.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1869	15005	28112	1.45	8.0E-57	AA496109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
5355	26034	31679	1.92	8.0E-57	11418185	NT	z561b12.1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:757151 5'
6529	19653	33066	0.51	8.0E-57	AB020705.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6593	19753	33138	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
6593	19753	33139	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7607	20677	34152	0.82	8.0E-57	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7627	20977	34486	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
7927	20977	34487	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11768	13252	26252	3.51	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12041	25022	38726	1.74	8.0E-57	11433356	NT	Homo sapiens nRin (LOC51199), mRNA
12102	25082	38769	1.53	8.0E-57	11431250	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
12791	25528	32007	1.87	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12808	25528	32007	1.94	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1246	14405	27467	0.88	7.0E-57	AJ003100.1	NT	Homo sapiens GYS2 gene, exon 14
2698	15817	28932	0.97	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2698	15817	28933	0.97	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3344	16517	29532	0.81	7.0E-57	6003979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3982	17139	30143	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik4230) mRNA, complete cds
3982	17139	30144	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik4230) mRNA, complete cds
13185	26071		3.99	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3849	17009	30010	6.03	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
827	14005	27062	0.64	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3a (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1362	14516		12.47	3.0E-57	AA250279.1	EST_HUMAN	nc1307.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2464	15591	28716	1.12	3.0E-57	AA348335.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10 ;
2768	15883	28992	1.03	3.0E-57	BE676622.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' and 783b10.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H8C.2 CE20263 ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2768	15883	28993	1.03	3.0E-57	BE576622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CLL.1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP.Y4749C.2
3652	16816	29827	1	3.0E-57	AF232708.1	NT	CE20283 ; Homo sapiens cell-line IaA201a chloride ion current inducer protein (Chn) gene, complete cds
3786	16946		51.29	3.0E-57	AW859684.1	EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
6163	19329	32675	1.25	3.0E-57	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6261	19425	32771	3.25	3.0E-57	BE796637.1	EST_HUMAN	60158986F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8336	21419	34845	3.92	3.0E-57	W28130.1	EST_HUMAN	4216 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8363	21444	34966	1.89	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8363	21444	34967	1.99	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8476	21557	35080	0.78	3.0E-57	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8624	21704	35240	0.62	3.0E-57	J05262.1	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
8059	22138	35682	5.14	3.0E-57	AU117699.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9451	22567	38132	0.69	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9451	22567	38133	0.69	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
11148	24220	37847	2.34	3.0E-57	AW248374.1	EST_HUMAN	2820473.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
12384	26167	31854	6.37	3.0E-57	W23871.1	EST_HUMAN	2b45611.1 Soares fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12982	26840	31884	1.17	3.0E-57	AJ003649.1	EST_HUMAN	AJ003649 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPI10-1L1
1530	14683	27762	2.89	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1530	14683	27763	2.89	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2780	15908	29014	5.5	2.0E-57	AA845419.1	EST_HUMAN	ak02b02.e1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
3525	16690		1.4	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3641	16805	29818	0.72	2.0E-57	R07702.1	EST_HUMAN	ye98h01.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:125809 5'
3641	16805	29819	0.72	2.0E-57	R07702.1	EST_HUMAN	ye98h01.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:125809 5'
4304	17447	30433	0.71	2.0E-57	AA018289.1	EST_HUMAN	ze40q06.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4304	17447	30434	0.71	2.0E-57	AA018289.1	EST_HUMAN	ze40q06.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4632	17768	30749	7.42	2.0E-57	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C083
5786	18977		1.48	2.0E-57	AA016131.1	EST_HUMAN	ze31c05.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
6158	19334		31.41	2.0E-57	BF115286.1	EST_HUMAN	7n80f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.11 MER22 repetitive element ;
8288	19461	32813	6.34	2.0E-57	11431281	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
8832	21811	35449	1.03	2.0E-57	AF045482.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
10051	23089	36691	1.06	2.0E-57	AF057722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11548	24604	38281	1.55	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11548	24604	38282	1.55	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11592	24645	38327	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX6 related protein
11592	24645	38328	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX6 related protein
13214	26097	31664	2.69	2.0E-57	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
2305	15437	28569	1.89	1.0E-57	AW503208.1	EST_HUMAN	UHF-BN0-akt-g-07-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
8891	21970		1.87	1.0E-57	BE043031.1	EST_HUMAN	HYPOTHETICAL 9.3 KD PROTEIN ; hs32a08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039092 3' similar to TR:O00246 O00246
12545	25369		11.29	1.0E-57	AW470791.1	EST_HUMAN	THR repetitive element ; hs33408.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
5794	18895	32288	0.93	9.0E-58	AA297847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
12654	25597	31990	1.94	9.0E-58	BE395061.1	EST_HUMAN	607309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
602	13791		1.68	8.0E-58	BE68715.1	EST_HUMAN	607445948F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3650211 5'
871	13857	26886	4.24	8.0E-58	AI798375.1	EST_HUMAN	ts34507.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
871	13857	26887	4.24	8.0E-58	AI798375.1	EST_HUMAN	ts34507.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1904	15047	28157	2.4	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1904	15047	28158	2.4	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
3040	16216		2.76	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
7387	20465	33930	0.93	7.0E-58	BE561971.1	EST_HUMAN	607348704F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687577 5'
11095	24168		4.54	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
11170	24241	37873	2.61	7.0E-58	AW504109.1	EST_HUMAN	UHF-BN0-ali-g-10-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078867 5'
11170	24241	37874	2.61	7.0E-58	AW504109.1	EST_HUMAN	UHF-BN0-ali-g-10-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078867 5'
2328	15460	28593	1.53	6.0E-58	BE395051.1	EST_HUMAN	607309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2448	15576	28706	5.25	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2969	18142	29160	1.01	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) BAYOR-HQSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2968	18142	29161	1.01	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) BAYOR-HQSC project=TCAA Homo sapiens cDNA clone TCAAP1219
6289	19472	32827	0.98	6.0E-58	AF106911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10817	23552	37163	1.27	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12654	25434		1.22	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
311	13527	26560	3.06	5.0E-58	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
728	13910	26950	6.98	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-180600-016-505 NT0057 Homo sapiens cDNA
1221	14382	27442	2.9	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1221	14382	27443	2.9	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1222	14382	27442	2	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1222	14382	27443	2	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3400	16570	28585	4.09	5.0E-58	AA688183.1	EST_HUMAN	cx38e07.st NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4373	17616	30466	0.93	5.0E-58	AI838745.1	EST_HUMAN	ts89e07.st NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2238408 3' similar to SW:PRO2_ACACA
5746	18938	32834	1.91	5.0E-58	11496282	NT	P19984 PROFILIN II;
6307	19479	32834	0.55	5.0E-58	H23072.1	EST_HUMAN	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6524	19689	33063	0.70	5.0E-58	AL163285.2	NT	ym51h07.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:52071 5'
6600	19760	33148	1.03	5.0E-58	11421330	NT	Homo sapiens chromosome 21 segment HS21C085
6917	20232	33665	0.6	5.0E-58	AF051334.1	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6917	20232	33668	0.8	5.0E-58	AF051334.1	NT	Homo sapiens nibrin (NBS) mRNA, complete cds
7255	20338	33788	0.71	5.0E-58	4885400	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCCS) mRNA
8156	21238	34759	9.08	5.0E-58	8922693	NT	Homo sapiens hypodermal protein FLJ10826 (FLJ10826), mRNA
8548	21629	35167	0.68	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
10061	23059	36701	0.96	5.0E-58	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Ptp18 (PRP18), mRNA
10328	23363	36973	1.8	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10512	23646	37254	0.65	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10612	23646	37255	0.66	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
12362	26066		4.5	5.0E-58	11626293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12850	26102		1.47	5.0E-58	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
384	13592	26827	1.71	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP6O) mRNA
819	13998	27052	1.87	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1496	14649	27731	1.24	4.0E-58	4503548	NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9) mRNA
2696	15816	28930	2.12	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3402	16572	29587	1.41	4.0E-58	D16470.1	NT	Human mRNA, 3' terminal portion
3634	16994	29956	1	4.0E-58	5031660	NT	Human mRNA, EGF-like repeats and discoidin-like domains 3 (EDL3), mRNA
7885	21045	34557	0.68	4.0E-58	BE463857.1	EST_HUMAN	hy18a02.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:3197642 3'
11624	24675	38366	7.44	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 6 (E1B-AP6), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
345	13558		0.96	3.0E-58	R17878.1	EST_HUMAN	ygl0c02.f1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31893 5'
1420	14574	27647	2.6	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3246	16420	29435	3.07	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3248	16420	28436	3.07	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6390	19559	32918	0.61	3.0E-58	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-109 BT0702 Homo sapiens cDNA
6574	19736	33115	1.1	3.0E-58	F07056.1	EST_HUMAN	HSC1TG081 normalized infant brain cDNA Homo sapiens cDNA clone c-11g08
6778	19933	33329	2.49	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 5'
963	14136	27197	12.47	2.0E-58	AF086624.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
							ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb-X69391 60S
							RIBOSOMAL PROTEIN L6 (HUMAN); gb-X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
1318	14474		7.98	2.0E-58	BE208532.1	EST_HUMAN	xa08a09.x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2567704 3'
6451	18851	31630	0.94	2.0E-58	AW074831.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5473	25805	31632	2.63	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5473	25805	31685	2.63	2.0E-58	BE907186.1	EST_HUMAN	UI-H-BW1-ams-g-11-q-U1-17 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
6182	18358	32706	1.7	2.0E-58	BF513488.1	EST_HUMAN	em57602.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP-ZK328.1
							CE05065 UBIQUITIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6249	19423	32768	2.16	2.0E-58	AI124874.1	EST_HUMAN	Y08H08.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:186379 5'
6283	19456	32806	0.83	2.0E-58	R92587.1	EST_HUMAN	qm84c01.x1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896424 3'
7066	20119	33633	0.83	2.0E-58	AI291407.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7307	20389	33848	2.79	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7307	20389	33949	2.79	2.0E-58	AF134838.1	NT	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
10979	24058	37692	16.01	2.0E-58	BF307745.1	EST_HUMAN	hm2508.x1 NC1_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
11207	24276	37813	1.58	2.0E-58	AW872841.1	EST_HUMAN	Human complement component C3 mRNA, 3' end
740	13922	28962	1.06	1.0E-58	M65134.1	NT	
							Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22KD: B22) (NDUFB9), mRNA
1093	14258	27314	1.33	1.0E-58	6274549	NT	EST369252 IMAGE sequences, MAGD Homo sapiens cDNA
1358	14513	27596	1.12	1.0E-58	AW857182.1	EST_HUMAN	EST369252 IMAGE sequences, MAGD Homo sapiens cDNA
1358	14513	27687	1.12	1.0E-58	AW957182.1	EST_HUMAN	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1427	14581	27654	2.8	1.0E-58	AJ238093.1	NT	hy10f08.x1 NC1_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3196935 3'
1697	14949	27935	1.28	1.0E-58	BE466132.1	EST_HUMAN	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds
2719	15837	28047	1.01	1.0E-58	AF217514.1	NT	Homo sapiens elcrl regulatory element binding transcription factor 2 (SREBF2) mRNA
2863	15977	29087	1.14	1.0E-58	4759169	NT	
2892	16206	28322	1.01	1.0E-58	5174444	NT	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3627	16791	28808	0.93	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3627	16791	28810	0.93	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3814	16974	29977	0.66	1.0E-58	4507628	NT	Homo sapiens translin protein 1 (during histone to plectamine replacement) (TNPT1) mRNA
5085	18213	31186	7.13	1.0E-58	A1141063.1	EST_HUMAN	α43n01.X1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1078129 3'
5964	19150	32466	1.37	1.0E-58	BE061860.1	EST_HUMAN	RC1-BT0254-290100-015-e01 BT0254 Homo sapiens cDNA
7002	20138	33566	0.87	1.0E-58	11422031	NT	Homo sapiens hypodermal protein (LOC51260). mRNA
8305	21397		0.49	1.0E-58	AW973537.1	EST_HUMAN	EST385637 MAGC resequences, MAGM Homo sapiens cDNA
9070	22149	35695	0.62	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2). mRNA
9182	22260	35802	0.77	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH08 5'
9282	22358	35907	0.64	1.0E-58	AA412397.1	EST_HUMAN	z89f05.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9282	22358	35908	0.64	1.0E-58	AA412397.1	EST_HUMAN	z89f05.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10389	23424	37031	0.65	1.0E-58	11432984	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2). mRNA
12074	25055		2.1	1.0E-58	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
12100	25080	38787	2.61	1.0E-58	D61405.1	NT	Human MSH3 gene, exon10
2303	15435	28567	53.38	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6879	20207	33635	0.74	8.0E-59	AA382291.1	EST_HUMAN	EST95983 Testis I Homo sapiens cDNA 5' end
6879	20207	33636	0.74	8.0E-59	AA382291.1	EST_HUMAN	EST95983 Testis I Homo sapiens cDNA clone IMAGE:2384171 3'
8374	21455	34979	1.55	8.0E-59	A1761963.1	EST_HUMAN	wh50406.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:3862086 5'
182	16005		1.97	6.0E-59	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:1553550 3' similar to TR:Q13732 Q13732
8015	21066	34579	0.82	6.0E-59	AA962431.1	EST_HUMAN	cn81.e04.s1 NCI CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1553550 3' similar to TR:Q13732 Q13732
8440	21521	35050	0.69	6.0E-59	A1750970.1	EST_HUMAN	SA GENE PRODUCT PRECURSOR. ;
3197	16372	29379	7.75	5.0E-59	A1807484.1	EST_HUMAN	cn08h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH.TBC.cn08h02 random
4780	17915	30901	9.94	5.0E-59	X83497.1	NT	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
7129	18555	31470	8.22	5.0E-59	AW162304.1	EST_HUMAN	H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat
9008	22065	35628	1.03	5.0E-59	11421778	NT	eu66c07.x1 Schnader fetal brain 00004 Homo sapiens cDNA clone IMAGE:2761228 3' similar to contains element TAR1 repetitive element ;
9906	22846	36532	1.44	5.0E-59	AV762869.1	EST_HUMAN	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39). mRNA
11146	24218	37845	4.54	5.0E-59	11434908	NT	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
816	13995	27050	1.9	4.0E-59	D80006.1	NT	Homo sapiens hypodermal protein (LOC57149). mRNA
1266	14423	27489	0.61	4.0E-59	4505818	NT	Human mRNA for KIAA0184 gene, partial cds
							Homo sapiens phosphatidylinositol 4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1266	14423	27490	0.61	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
4912	18042	31032	1.14	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4912	18042	31033	1.14	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5654	18848	32130	0.95	4.0E-59	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12498	25996		3.99	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	13248		6.74	3.0E-59	AW965624.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
234	13455	26481	3.88	3.0E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1748	14897	27992	10.81	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1748	14897	27993	10.81	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2198	15333	28456	8.54	3.0E-59	AB028035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2198	15333	28460	8.54	3.0E-59	AB028035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3104	16280	29294	0.67	3.0E-59	T18855.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3104	16280	29295	0.67	3.0E-59	T18855.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3198	16374	29384	4.27	3.0E-59	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3199	16374	29384	4.27	3.0E-59	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3930	17089	30086	1.19	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4808	17942	30929	2.79	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4865	18094	31071	2.12	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
5162	18284		1.22	3.0E-59	M85861.1	NT	Human prothormone converting enzyme (NEC2) gene, exon 2
6350	19520	32877	2.4	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7516	20589	34084	1.85	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
8116	21198	34718	1.11	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
8116	21198	34719	1.11	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
10250	23285	36880	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
10250	23285	36881	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12635	25428		11.11	3.0E-59	11417868	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTL1), mRNA
6946	20239		0.59	2.0E-59	AA470073.1	EST_HUMAN	288405.s1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:730377 3'
7216	20881	33494	0.59	2.0E-59	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
9837	22877		4.84	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10745	23778		1.34	2.0E-59	BF36554.1	EST_HUMAN	RCO-NT0036-100700-Q32-a07 NT0036 Homo sapiens cDNA
11069	24144	37780	2.19	2.0E-59	AW410698.1	EST_HUMAN	h07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11069	24144	37781	2.19	2.0E-59	AW410698.1	EST_HUMAN	fr07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2681654 5'
12373	25266	32118	4.28	2.0E-59	A631809.1	EST_HUMAN	wa36c12.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12663	26019	31669	3.87	2.0E-59	L11045.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element ;
157	13392		5.66	1.0E-59	BE286411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
1569	14722	27803	1.04	1.0E-59	T92522.1	EST_HUMAN	60117675F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3331927 5'
2693	15903		2.66	1.0E-59	AA748468.1	EST_HUMAN	ye25c09.r1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:116768 5' similar to SP:S21348
7735	20796	34285	1.14	1.0E-59	AJ130894.1	NT	S21348 HYPOTHETICAL PROTEIN 4 ;
7895	20947	34454	1.3	1.0E-59	BE256814.1	EST_HUMAN	oa56h11.a1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13637
7895	20947	34455	1.3	1.0E-59	BE256814.1	EST_HUMAN	Q13637 MER37 TRANSCRIPTIONAL ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
9585	22727	36296	0.88	1.0E-59	11419930	NT	Homo sapiens mRNA for transcription factor
9804	22844	36421	0.58	1.0E-59	11428949	NT	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9804	22844	36422	0.59	1.0E-59	11428949	NT	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
11094	20798	34285	10.98	1.0E-59	AJ130894.1	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
783	13963	27013	1.45	8.0E-60	AW977845.1	EST_HUMAN	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
1499	14652	27734	3.21	8.0E-60	4759159	NT	Homo sapiens mRNA for transcription factor
2241	15374	28502	4.76	8.0E-60	5174656	NT	EST T389849 MAGE resequences, MAGE Homo sapiens cDNA
2241	15374	28503	4.76	8.0E-60	5174656	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
6103	19283	32616	1.16	8.0E-60	AB028004.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6833	19792	33181	0.89	8.0E-60	S83182.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7874	20928	34434	0.89	8.0E-60	11420841	NT	hyaluronan-binding protein=heparocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8162	21234	34755	3	8.0E-60	X17033.1	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCT1B), mRNA
9139	22218	35762	2.93	8.0E-60	11428949	NT	Human mRNA for integrin alpha-2 subunit
9671	22633	36202	0.78	8.0E-60	11417118	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
9671	22633	36203	0.78	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10799	23832	37455	0.62	8.0E-60	5453997	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11071	24146	37783	4.17	8.0E-60	AL163204.2	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11071	24146	37784	4.17	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
773	13954	27004	11.11	7.0E-60	AF050566.1	NT	Homo sapiens chromosome 21 segment HS21C004
774	13954	27004	25.11	7.0E-60	AF050566.1	NT	Homo sapiens MHC class 1 region
838	14016	27071	1.47	7.0E-60	4504634	NT	Homo sapiens MHC class 1 region
							Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2197	15332	28458	1.82	7.0E-60	AF07188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2845	15969	29068	0.98	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4295	17438	30425	2.4	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4638	17833	30818	0.91	7.0E-60	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
9607	22662	36235	4.21	7.0E-60	H58041.1	EST_HUMAN	y1204.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
11646	24725	38417	1.73	7.0E-60	H58041.1	EST_HUMAN	y1204.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
2248	15381	28509	1.16	6.0E-60	BE964974.2	EST_HUMAN	60168751R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3886069 3'
8632	21712		8.04	6.0E-60	H52456.1	EST_HUMAN	y478h09.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains ORF repetitive element;
86	13321	26348	1.08	5.0E-60	AB07817.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
86	13321	26349	1.06	5.0E-60	AB07817.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2308	15440	28574	1.83	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2308	15440	28575	1.83	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
3037	16213		1.45	4.0E-60	AA290037.1	EST_HUMAN	EST11498 Ulenus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7508	20582	34055	0.78	4.0E-60	BF196058.1	EST_HUMAN	tr81b05.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
8926	22402		0.85	4.0E-60	AL163278.2	NT	Q61085 GTP-RHO BINDING PROTEIN 1;
1907	15050	28161	4.88	3.0E-60	BE682811.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1907	15050	28162	4.98	3.0E-60	BE682811.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1918	15061		2.81	3.0E-60	6031190	NT	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
4579	17116	30689	2.75	3.0E-60	AJ271735.1	NT	Homo sapiens prohibitin (PHB) mRNA
5494	18693	31709	0.69	3.0E-60	BF365143.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
5757	18949	32261	2.21	3.0E-60	AW836196.1	EST_HUMAN	QV44NN1149-250900-423-f01 NN1149 Homo sapiens cDNA
7093	18520	31513	1.07	3.0E-60	AI792814.1	EST_HUMAN	RC3-LT0023-200700-012-g01 LT0023 Homo sapiens cDNA
8597	21678	35215	4.59	3.0E-60	5174844	NT	d60h11.y5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE
8597	21678	35216	4.58	3.0E-60	5174844	NT	P52624 URIDINE PHOSPHORYLASE;
8783	21862	35405	0.6	3.0E-60	AI040235.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8940	22019	35560	3.84	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
13053	25058		1.55	3.0E-60	AA485286.1	EST_HUMAN	SW:FORM_MOUSE Q05960 FORMIN;
							ab07b04.r1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:840161 5' similar to contains LTR10.1 LTR10 repetitive element;

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
31	13269	26273	1.7	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1455	14608	27688	3.99	2.0E-60	Z11694.1	NT	H sapiens 41kDa protein kinase related to rat ERK2
1759	14908	28001	2.2	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
3659	16832	29843	0.78	2.0E-60	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4025	17181	30180	0.73	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6430	19598	32964	0.85	2.0E-60	A1791952.1	EST_HUMAN	nm011212 NCL CGAP_Cc9 Homo sapiens cDNA IMAGE:1076495 5' similar to contains THR.L1 THR repetitive element;
6621	19781	33169	1.26	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6855	20008	33418	1.08	2.0E-60	AF167476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
6989	18508	31524	2.15	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6989	18508	31525	2.15	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7259	20342	33793	8.18	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prolactin, alpha
7259	20342	33794	8.18	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prolactin, alpha
7810	20865	34799	0.9	2.0E-60	BF512808.1	EST_HUMAN	U-H-BW1-arnu-c-02-0-U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
8194	21276	34799	1.33	2.0E-60	X85937.1	EST_HUMAN	HS198EST human adult testis Homo sapiens cDNA clone CAM, TEST15
9068	22147	36894	3.12	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
10183	23220	36813	1.83	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
10183	23220	36814	1.83	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
11769	23945	37572	1.7	2.0E-60	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5), mRNA
12872	25448		2.36	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12829	25985		1.47	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12848	25664		1.5	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
535	13728	26762	1.02	1.0E-60	BE178686.1	EST_HUMAN	PNX3-HT0605-270200-001-608 HT0605 Homo sapiens cDNA
4011	17168	30176	1.08	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y76AA1 Homo sapiens cDNA clone Y76AA1001854 5'
5070	18198	31172	2.57	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8134	21216	34737	1.39	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
							nc04e12.r1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element;
8955	22034		2.84	1.0E-60	AA244041.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
8982	22051	36601	1.35	1.0E-60	AV754081.1	EST_HUMAN	Homo sapiens genomic hybrid Rhesus box
12606	26079		1.49	1.0E-60	AJ262313.1	NT	Homo sapiens genomic hybrid Rhesus box
1123	14288	27343	8.4	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005593 5'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8908	21987	35526	0.63	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8908	21987	35527	0.63	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2735	15852	28865	1.41	8.0E-61	AW006478.1	EST_HUMAN	w05510.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2735	15852	28866	1.41	8.0E-61	AW006478.1	EST_HUMAN	w05510.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
3018	16182		2.63	8.0E-61	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV8)
8079	21181	34679	1.03	8.0E-61	AA583988.1	EST_HUMAN	m59006.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
130	13357	26389	0.79	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
130	13357	26390	0.79	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
278	13484	26524	3.06	6.0E-61	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
834	14012	27068	6.49	6.0E-61	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1352	14507	27579	12.72	6.0E-61	AF110880.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1659	14831	27896	1.04	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1678	14831	27916	2.91	6.0E-61	AA590033.1	EST_HUMAN	m56109.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3381	16553	29667	8.16	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
6155	19331	32877	2.98	6.0E-61	S79248.1	NT	lg-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7497	20572	34045	1.49	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7795	20851	34343	1.85	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-I (GTF2) mRNA, complete cds
12564	14012	27068	1.06	6.0E-61	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
13157	26792	31923	1.42	6.0E-61	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
226	13448	26476	2.54	5.0E-61	8922890	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
226	13448	26477	2.54	5.0E-61	8922890	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
370	13579	26612	0.7	6.0E-61	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1713	14884	27853	2.84	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3101	16277	29291	2.19	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3268	16442	29462	1.82	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4050	17245		2.22	5.0E-61	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5118	13579	26612	0.75	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1798	14947	28039	1.94	4.0E-61	AU140307.1	EST_HUMAN	AU140307 PLAGE2 Homo sapiens cDNA clone PLACE2000302 5'
5836	10122	32435	0.71	4.0E-61	7661637	NT	Homo sapiens DKFZP566B023 protein (DKFZP566B023), mRNA
12349	25252		9.47	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
8816	21696	35234	0.7	3.0E-61	AF150190.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CDBAGB04
511	13705	26733	1.8	2.0E-61	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1239	14398	27460	5.33	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1239	14398	27461	5.33	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1699	14851	27938	1.36	2.0E-61	N53039.1	EST_HUMAN	y63d11.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to g5:L26444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
2706	15824		1.72	2.0E-61	N39397.1	EST_HUMAN	y403f11.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270169 5' Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116KD) (ATP6N1A), mRNA
6595	19718	33094	0.88	2.0E-61	11426166	NT	AV694317 GK Homo sapiens cDNA clone GKCELG06 5'
9217	22295	35839	1.67	2.0E-61	AV694317.1	EST_HUMAN	Homo sapiens mRNA for KIAA0535 protein, partial cds
9762	22700		0.98	2.0E-61	AB011108.1	NT	U1-HF-BNO-akd4-12-Q-U1.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076774 5'
10126	23164	36763	1.34	2.0E-61	AW500256.1	EST_HUMAN	Homo sapiens polymerase (RNA) III (DNA directed) (39KD) (RPC39), mRNA
10456	23481	37101	2.84	2.0E-61	11421778	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
11123	24195		4	2.0E-61	11419728	NT	QV0-BN0042-170300-162-F10 BN0042 Homo sapiens cDNA
13144	25744	31960	1.45	2.0E-61	AW995326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
448	13644		1.37	1.0E-61	AL163203.2	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog) like (ORC2L) mRNA
794	13973	27026	1.26	1.0E-61	6453828	NT	Homo sapiens chromosome 21 segment HS21C003
1430	14584	27658	1.07	1.0E-61	AL163203.2	NT	Human polymorphic thiodactile repeat in X-linked retinitis pigmentosa (RP3) gene region
1809	14958		1.02	1.0E-61	U32857.1	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
1906	15049	28160	4.43	1.0E-61	6005983	NT	xr11b09.y1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element MSR1 repetitive element;
2270	15403	28531	1.54	1.0E-61	AW827281.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
2896	16075	29093	0.98	1.0E-61	BE395363.1	EST_HUMAN	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3463	16630	29650	0.85	1.0E-61	7662319	NT	QV2-HT0577-140300-077-g06 HT0577 Homo sapiens cDNA
3826	16986	29989	1.16	1.0E-61	BE174455.1	EST_HUMAN	Human monamine oxidase A (MAOA) mRNA, complete cds
4374	17517	30497	1.05	1.0E-61	M68840.1	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4561	17699	30881	0.95	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4661	17699	30881	0.95	1.0E-61	4759249	NT	U1-H-BW0-ajl-b-08-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
4981	18110	31096	9.55	1.0E-61	AW298181.1	EST_HUMAN	U1-H-BW0-ajl-b-08-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
4981	18110	31087	9.55	1.0E-61	AW298181.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
5075	18203	31175	0.62	1.0E-61	AL183210.2	NT	H sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5509	18708	31723	0.71	1.0E-61	MT6423.1	NT	H sapiens KIAA0783 gene product (KIAA0783), mRNA
5805	18986	32301	1.07	1.0E-61	7662303	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
6004	19188	32608	1.32	1.0E-61	11416891	NT	Human P40 T-cell and mast cell growth factor (HP40) gene, complete cds
7041	20094	33510	8.92	1.0E-61	M30135.1	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
7240	20324	33768	0.77	1.0E-61	4759171	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7341	20421	33883	1.39	1.0E-61	6923130	NT	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7341	20421	33884	1.39	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8328	21408	34935	2.69	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8608	21588	35123	3.34	1.0E-61	AF224669.1	NT	Homo sapiens mannose-6-phosphate isomerase (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9482	22539		2.78	1.0E-61	AW889726.1	EST_HUMAN	MR0-BN0070-040400-010-K01 BN0070 Homo sapiens cDNA
9557	22822	36193	0.58	1.0E-61	11418280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
10235	23270	36861	4.8	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10871	23956	37585	6.81	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11178	24247	37680	1.72	1.0E-61	AB044550.1	NT	Homo sapiens P/OXG1.19 mRNA for ubiquitin-conjugating enzyme E2, complete cds
11325	24398	38033	1.44	1.0E-61	AB007830.1	NT	Homo sapiens mRNA for CSR2, complete cds
12242	26043		21.57	1.0E-61	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12288	26031	31677	4	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12868	26031	31678	4	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13028	26676	31959	10.94	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10865	23600	37206	1.08	8.0E-62	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
4673	17608	30798	0.85	8.0E-62	AAB30420.1	EST_HUMAN	cc66h11.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVK
1131	14296	27351	1.12	7.0E-62	AV714334.1	EST_HUMAN	P31795 POL POLYPROTEIN ;
3695	16759	28775	0.84	7.0E-62	P17480	SWISSPROT	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'
6038	19221	32544	0.97	7.0E-62	11427965	NT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
11632	24712	38403	4.05	7.0E-62	AJ208681.1	EST_HUMAN	(AUTOANTIGEN NOR-90)
3063	16239		1.55	6.0E-62	U09410.1	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
3471	16638		5.37	6.0E-62	11418255	NT	cg56a04.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103
7803	20859	34351	3.47	6.0E-62	AJ762801.1	EST_HUMAN	O15103 HYPOTHETICAL 27.3 KD PROTEIN ;
7803	20859	34352	3.47	6.0E-62	AJ762801.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
8277	21359		0.66	6.0E-62	AW501124.1	EST_HUMAN	Homo sapiens CGI-58 protein (CGI-58), mRNA
8452	21533	36063	1.52	6.0E-62	11431139	NT	w04402.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
9554	22619	36189	3.67	6.0E-62	AW814393.1	EST_HUMAN	w04402.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
429	13624	26664	1.46	5.0E-62	AJ950526.1	EST_HUMAN	UHF-BP0p-alkd-09-0-UI.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
2478	15605	28729	5.18	5.0E-62	AJ271735.1	NT	Homo sapiens ST0203-130100-025-609 ST0203 Homo sapiens cDNA
2478	15605	28730	5.18	5.0E-62	AJ271735.1	NT	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
							Q08379 GOLGIN-95, contains element MER22 repetitive element;
							Homo sapiens Xq pseudautosomal region; segment 1/2
							Homo sapiens Xq pseudautosomal region; segment 1/2

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3506	18673	28683	2.55	5.0E-62	4506758	NT	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
4447	17987	30568	1.75	5.0E-62	AA431093.1	EST_HUMAN	zw78e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SWJNRDC_RAT
8746	21825	35362	0.74	5.0E-62	4506758	NT	P47245 NARDILYSIN;
9717	22782	38353	12.91	5.0E-62	AW410687.1	EST_HUMAN	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
11543	24559	38274	2.38	5.0E-62	11425574	NT	fl07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961616 5'
11543	24559	38275	2.38	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
863	14040	27102	2.17	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens muscle specific gene (M9), mRNA
863	14040	27103	2.17	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
864	14040	27102	1.32	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
864	14040	27103	1.32	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2529	15654	28778	1.9	4.0E-62	AB279000.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
3486	16654	28779	9.09	4.0E-62	4557887	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6046	19229	32553	1.71	4.0E-62	4506978	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
8426	18594	32960	2.81	4.0E-62	11420654	NT	W12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
7322	20404	33866	1.75	4.0E-62	11421041	NT	gb:X57138_rna1 HISTONE H2B.2 (HUMAN);
7812	20867	34361	2.21	4.0E-62	7657057	NT	W12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
7812	20867	34362	2.21	4.0E-62	7657057	NT	gb:X57138_rna1 HISTONE H2B.2 (HUMAN);
8364	21445	34968	1.12	4.0E-62	11429973	NT	Homo sapiens keratin 18 (KRT18) mRNA
9047	22128	35670	6.42	4.0E-62	AB033089.1	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11263	24332	37973	2.62	4.0E-62	Z78766.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
11263	24332	37974	2.62	4.0E-62	Z78766.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
11500	24558	38233	63.7	4.0E-62	S70564.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
12269	25202	38360	1.18	4.0E-62	11418086	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA16D3
12497	25989		1.65	4.0E-62	11418192	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA16D3
							(thyroid-stimulating hormone alpha subunit [human, Genomic, 268 nt, segment 3 of 4])
							Homo sapiens putative nuclear protein (HNP2L1), mRNA
							Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12946	25667	31955	1.66	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
13004	25663	31952	6.86	4.0E-62	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13004	25663	31953	6.86	4.0E-62	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13060	25693	31965	2.16	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
76	13312	26338	0.69	3.0E-62	4557784	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2), mRNA
3111	16287	29301	1.13	3.0E-62	AB040908.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3111	16287	29302	1.13	3.0E-62	AB040908.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3789	16950	29956	4.19	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
8737	21816	35351	3.74	3.0E-62	AI632733.1	EST_HUMAN	wa3304.x1 NCI CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2299903 3' similar to contains THR.12
1259	14417	27482	2.71	2.0E-62	AL163284.2	NT	THR repetitive element;
8974	22053	35595	5.59	2.0E-62	BF328911.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
8974	22053	35596	5.59	2.0E-62	BF328911.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10376	23411		3.71	2.0E-62	AF224669.1	NT	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
11888	24973		8.83	2.0E-62	BF330676.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1089	14235	27294	1.14	1.0E-62	AF248540.1	NT	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
1575	14728	27809	18.41	1.0E-62	L78810.1	NT	Homo sapiens intersein 2 (SH3D1B) mRNA, complete cds
1842	14988	28038	1.64	1.0E-62	AA025207.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
2981	16157	29176	1.22	1.0E-62	AL035044.1	EST_HUMAN	af70e11.1 Soares_NhHMPU_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
4648	17784	30767	1.84	1.0E-62	8923201	NT	CE03453 ;
							DKFZp566F104.r1 366 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566F104 5'
6418	19587	32950	2.02	1.0E-62	U52111.2	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
7284	20367	33820	1.07	1.0E-62	AA490050.1	EST_HUMAN	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein >
7295	20377	33834	2.89	1.0E-62	AA722878.1	EST_HUMAN	ab05c02.st Stratigene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839906 3'
7295	20377	33835	2.89	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
8997	22038	35577	0.54	1.0E-62	AA280050.1	EST_HUMAN	zg89f10.s1 Soares_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
9258	22335	35885	1.65	1.0E-62	7562289	NT	zs93e07.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705060 5'
9258	22335	35886	1.65	1.0E-62	7562289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9302	22378	35928	1.92	1.0E-62	X15533.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9302	22378	35929	1.92	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9757	22695	36263	3.03	1.0E-62	AA465170.1	EST_HUMAN	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11848	24727	38419	2.26	1.0E-62	Z78698.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA14D8
12809	25540		4.83	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
13042	25684	31082	3.16	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
348	13559	26587	2.27	9.0E-63	AW16405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2421	15550		2.17	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFujihara) Homo sapiens cDNA clone GEN-558C10 5'
4152	17304	30287	8.77	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4152	17304	30298	8.77	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5368	18484	38824	4.69	9.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5582	18777	31822	1.44	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PRK kinase
7332	20413	33875	3.78	9.0E-63	11426985	NT	Homo sapiens nucleoporin 88kd (NUP88), mRNA
8009	21059	34571	1.77	9.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8521	21602	35139	1.18	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
11296	24362	38003	1.3	9.0E-63	BF203406.1	EST_HUMAN	601855628F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4086487 5'
2420	15549	28877	3.05	8.0E-63	4537734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2446	15574	28703	2.86	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3550	18715	28727	4.26	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3550	18715	28728	4.26	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4381	17524	30505	4.38	8.0E-63	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
952	14125		3.38	7.0E-63	AB72137.1	EST_HUMAN	vm55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
5455	18555		70.59	6.0E-63	AA428803.1	EST_HUMAN	nc63f02.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
9075	22154	35688	0.62	5.0E-63	11526454	NT	RIK102.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
3398	18568	28584	0.88	4.0E-63	AL163278.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3910	17069	30066	1.06	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3910	17069	30087	1.06	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6575	19737	33118	2.6	4.0E-63	AW1750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6575	19737	33117	2.8	4.0E-63	AW1750372.1	EST_HUMAN	CM3-BT0595-190100-072-a08 BT0595 Homo sapiens cDNA
11397	24458	38121	2.02	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11397	24458	38122	2.02	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-e-02-Q-U1 st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1989	15131	28235	15.19	3.0E-63	AB018260.1	NT	UI-H-B11-abq-e-02-Q-U1 st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
2840	15954	29061	1.49	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2882	14425	27493	11.84	3.0E-63	6005963	NT	Human Mel-RNA-1 gene 1
6803	19763	33151	33.93	3.0E-63	11545810	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
							Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9907	22947	36533	0.83	3.0E-63	BE376158.1	EST_HUMAN	601485659F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
9907	22947	36534	0.83	3.0E-63	BE376158.1	EST_HUMAN	601485659F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
198	13419	26449	1.69	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
203	13426	26457	1.65	2.0E-63	4885228	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
510	13704		1.19	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
849	14027	27087	3.07	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1597	14760	27834	1.54	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1597	14760	27835	1.54	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1806	14955	28049	2.02	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3883103 5'
2146	15282	28407	1.05	2.0E-63	AI863861.1	EST_HUMAN	wj54602.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406603 3' similar to gbM57609 GLI3 PROTEIN (HUMAN);
3225	16389	28411	1.94	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3357	16529	28544	2.4	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
4014	17171	30179	3.19	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4988	18117	31096	1.28	2.0E-63	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5376	25802	31447	0.95	2.0E-63	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
6005	19190	32509	2.41	2.0E-63	BF373641.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6005	19190	32510	2.41	2.0E-63	BF373641.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6315	19487	32842	1.07	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6315	19487	32843	1.07	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germ-line T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6841	19994	33403	1.43	2.0E-63	U86059.1	NT	Homo sapiens MIST mRNA, partial cds
6887	20039	33448	0.72	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6887	20039	33449	0.72	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7222	20086	33502	1.72	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC66934), mRNA
7222	20086	33503	1.72	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC66934), mRNA
7957	21007	34517	0.98	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8730	21810	35346	4.29	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9254	22331	35570	0.94	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9254	22331	35580	0.94	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
10143	23181	38778	1.2	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10985	24084	37699	10.73	2.0E-63	N78945.1	EST_HUMAN	zb18b05.s1 Soares_fetal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gbX17208 40S RIBOSOMAL PROTEIN S4 (HUMAN);
11012	24091	37728	2.89	2.0E-63	AF099810.1	NT	Homo sapiens neurabin III-alpha gene, partial cds
11012	24091	37728	2.89	2.0E-63	AF099810.1	NT	Homo sapiens neurabin III-alpha gene, partial cds
12380	25829	31769	3.64	2.0E-63	11418185	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), mRNA
13101	25717	31940	1.19	2.0E-63	11418187	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
13172	25760	31930	1.37	2.0E-63	AB011389.1	NT	Homo sapiens gene for AF-8, complete cds
786	13985	27018	1.55	1.0E-63	7106448	NT	Mus musculus wingless-related MMTV integration site 3A (Wnt3a), mRNA
786	13985	27017	1.55	1.0E-63	7106448	NT	Mus musculus wingless-related MMTV integration site 3A (Wnt3a), mRNA
4461	17601	30579	3.31	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4461	17601	30580	3.31	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5468	18698	31647	1.73	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
6890	19078	32388	1.38	1.0E-63	AW582266.1	EST_HUMAN	QV0-ST0215-060100-083-109 ST0215 Homo sapiens cDNA
6521	19886	33088	0.68	1.0E-63	AW451950.1	EST_HUMAN	UIH-B13-alk-h-02-Q-UI.s1 NCL CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
6521	19886	33089	0.68	1.0E-63	AW451950.1	EST_HUMAN	UIH-B13-alk-h-02-Q-UI.s1 NCL CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
8688	21748		2.97	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
13121	26047		8.88	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6089	19270	32598	0.81	9.0E-64	AW401433.1	EST_HUMAN	UIH-F-BKO-aad-b-09-Q-UI.r1 NIH_MGC 38 Homo sapiens cDNA clone IMAGE:3053153 5'
8051	21134	34654	5.57	9.0E-64	AJ478186.1	EST_HUMAN	Im50507.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2161626 3'
1071	14237		3.45	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3139038 5'
6266	19442	32791	3.51	8.0E-64	BE865755.1	EST_HUMAN	601508958F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3910338 5'
12187	25148		2.79	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12243	25185		3.68	8.0E-64	T60851.1	EST_HUMAN	y98802.r1 Stragano Lung (8937210) Homo sapiens cDNA clone IMAGE:79176 5'
3618	16782		0.74	7.0E-64	BE394321.1	EST_HUMAN	601311459F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3633204 5'
4854	17937	30974	5.34	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4854	17987	30975	5.34	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
10239	23274	36855	2.62	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
1760	14908	28002	5.73	6.0E-64	A1651992.1	EST_HUMAN	wb51e07.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gbM15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1760	14908	28003	5.73	6.0E-64	A1651992.1	EST_HUMAN	wb51e07.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gbM15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3192	16367	29372	3.91	6.0E-64	AW026446.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529438 3'
3192	16387	29373	3.91	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529438 3'
5739	18932	32230	2.95	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5739	18932	32231	2.05	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5758	18950	32252	5.32	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5767	18959	32260	0.88	6.0E-64	6912461	NT	Homo sapiens atrophin-1 Interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
5951	19137	32452	0.74	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
5951	19137	32453	0.74	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
7384	20492	33925	2.54	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7384	20492	33926	2.54	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9528	22593	36164	7.39	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
9708	22785	36329	1.75	6.0E-64	AF274733.1	NT	Homo sapiens progressive ankylosis-like protein (ANK), mRNA, complete cds
9919	22959	36546	2.16	6.0E-64	S76475.1	NT	trkC [human, brain, mRNA, 2715 nt]
11008	24087	37724	4.68	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11008	24087	37725	4.68	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11269	16367	29373	1.73	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529438 3'
11269	16367	29373	1.73	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529438 3'
12400	25280	32081	2.98	6.0E-64	11526198	NT	Homo sapiens interleukin 10 receptor, beta (L1TORB), mRNA
843	14021	27078	4.18	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
843	14021	27079	4.18	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1369	14524	27598	1.02	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1453	14608	27685	1.15	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1453	14608	27686	1.15	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1749	14898	27694	1.54	5.0E-64	U89358.1	NT	Human [3]mb1 protein homolog mRNA, complete cds
2887	14653	27746	4.43	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2887	14653	27747	4.43	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4068	17224	30231	7.26	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
8000	21050	34563	0.71	4.0E-64	BE794607.1	EST_HUMAN	601590382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3844397 5'
11051	24128	37763	2.34	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-e03 S10197 Homo sapiens cDNA
11051	24128	37764	2.34	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-e03 S10197 Homo sapiens cDNA
2271	15404	28532	8.77	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (Tfujilwara) Homo sapiens cDNA clone GEN-569E02 5'
3327	16900	29518	0.82	3.0E-64	BE794381.1	EST_HUMAN	601590565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3528	16694	29704	1.83	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3529	16694	29705	1.83	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6206	19391	32731	1.31	3.0E-64	Z26273.1	NT	H sapiens isoform 1 gene for L-type calcium channel, exon 28
6471	19338	32997	0.88	3.0E-64	AW500861.1	EST_HUMAN	UI-HF-BP0p-ak-c-05-Q.U1.1 NIH_MGC 51 Homo sapiens cDNA clone IMAGE:3073161 5'
6622	19782	33170	3.2	3.0E-64	BF370000.1	EST_HUMAN	RC6-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
8661	21741	35281	1.86	3.0E-64	AF249933.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8661	21741	35282	1.86	3.0E-64	AF249933.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8662	21772	35303	1.48	3.0E-64	BE206521.1	EST_HUMAN	b572h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:U08069 DNAJ
8662	21772	35304	1.48	3.0E-64	BE206521.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
8627	22682	36251	1.12	3.0E-64	AL163246.2	NT	b572h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:U08069 DNAJ
8627	22682	36252	1.12	3.0E-64	AL163246.2	NT	PROTEIN HOMOLOG 2 (HUMAN);
9714	22779	36349	0.86	3.0E-64	AW977384.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9714	22779	36350	0.86	3.0E-64	AW977384.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
11514	24571	36248	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11814	24571	36249	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11890	24975	36679	2.16	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1112	14277	27334	1.1	2.0E-64	AA609940.1	EST_HUMAN	af09d08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1428	14582	27655	3.2	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2592	15717		1.28	2.0E-64	AI627030.1	EST_HUMAN	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element
2597	15721	28840	2.4	2.0E-64	AL163246.2	NT	L1 repetitive element;
2597	15721	28841	2.4	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3887	17048	30046	0.98	2.0E-64	AW968145.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
3887	17048	30046	0.98	2.0E-64	AW968145.1	EST_HUMAN	EST370215 MAGe resequences, MAGe Homo sapiens cDNA
6129	19308	32848	2.28	2.0E-64	AU124397.1	EST_HUMAN	EST370215 MAGe resequences, MAGe Homo sapiens cDNA
6372	19541	32900	1.23	2.0E-64	AF113708.1	NT	AU124397 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6614	19774	33165	5.04	2.0E-64	BF668537.1	EST_HUMAN	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6724	19881	33272	1.3	2.0E-64	A078387.1	EST_HUMAN	602123474F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4280395 5'
6840	19993	33402	2.98	2.0E-64	M77185.1	NT	alpha2B603.x1 Soares testis_Nb2HFB_gw Homo sapiens cDNA clone IMAGE:1678717 3'
7990	21040	34552	0.67	2.0E-64	11431054	NT	H sapiens dopamine receptor D6 pseudogene 1, partial cds
8868	21947	35480	1.08	2.0E-64	11434008	NT	Homo sapiens atadn 2-binding protein 1 (A2BP1), mRNA
8868	21947	35481	1.08	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-lystn) (LCP1), mRNA
9431	22505	36071	1.09	2.0E-64	AU132570.1	EST_HUMAN	Homo sapiens lymphocyte cytosolic protein 1 (L-lystn) (LCP1), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10184	23221	36815	0.5	2.0E-64	T06397.1	EST_HUMAN	EST04288 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDS88
10184	23221	36816	0.5	2.0E-64	T06397.1	EST_HUMAN	EST04288 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDS88
11000	24079	37714	2.21	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180556 5'
11306	24371	38012	4.28	2.0E-64	A1922911.1	EST_HUMAN	wn81b08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11306	24371	38013	4.28	2.0E-64	A1922911.1	EST_HUMAN	wn81b08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11509	24667	38244	1.46	2.0E-64	AW664773.1	EST_HUMAN	PM2-SN0018-220300-002-ef2 SN0018 Homo sapiens cDNA
12804	25537		3.59	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone G22_132 5'
268	13487	26517	1.39	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1820	14969	28061	24.22	1.0E-64	A1929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2619136 3' similar to gbl.21698_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element ;
3076	18252	29274	0.8	1.0E-64	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3601	16765	29781	5.47	1.0E-64	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a
3675	16838	29848	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3675	16838	29849	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
4008	17165	30173	0.98	1.0E-64	8922829	NT	Homo sapiens TRIAD3 mRNA, partial cds
10269	23304	36901	1.17	1.0E-64	AA042975.1	EST_HUMAN	Homo sapiens hypochloral protein FLJ11026 (FLJ11026), mRNA
12291	25216		4.56	1.0E-64	AL163246.2	NT	Z65308.s1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:486567 3'
2350	15481	28613	1.87	9.0E-65	X89211.1	NT	Homo sapiens chromosome 21 segment HS21C046
2350	15481	28614	1.87	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
11826	24815		19.08	9.0E-65	BF330876.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
11798	24789	38486	7.24	8.0E-65	A1929244.1	EST_HUMAN	QV4-BT0257-081189-017-e03 B T0257 Homo sapiens cDNA
10358	23393	37004	2.16	7.0E-65	BE081853.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW_RL21_HUMAN P48778 60S RIBOSOMAL PROTEIN L21. ;
12095	26075	38782	2.88	7.0E-65	Z21378.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
1081	14247	27304	0.81	6.0E-65	AV721898.1	EST_HUMAN	HSAAAEAWO TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test346 (b)
1974	15117		20.04	6.0E-65	AA560929.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
6899	19557	33247	0.8	6.0E-65	AA503892.1	EST_HUMAN	h86d10.s1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:989379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
8945	22024	35564	2.45	6.0E-65	AW083252.1	EST_HUMAN	h837b07.s1 NCI_CGAP_P15 Homo sapiens cDNA clone IMAGE:964517
9213	22291	35633	4.63	6.0E-65	AA427878.1	EST_HUMAN	xc07b09.x1 NCI_CGAP_Ccd21 Homo sapiens cDNA clone IMAGE:2683545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFS. ; contains L1.b2 L1 repetitive element ; zw63b06.s1 Soares_total_Tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9213	22291	35834	4.63	6.0E-65	AA427878.1	EST_HUMAN	z55306.s1 Soares_tetal_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9275	22351	35802	0.62	6.0E-65	AI085314.1	EST_HUMAN	qf18h05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750425 3'
9276	22351	36903	0.62	6.0E-65	AI085314.1	EST_HUMAN	qf18h05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750425 3'
11113	24185	37817	3.58	6.0E-65	BE667816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
11294	24360	38001	4.18	6.0E-65	BF3-0825.1	EST_HUMAN	602037721F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185677 5'
11788	24778	38475	1.80	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
648	13833	26859	1.89	5.0E-65	AF064604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1384	14539	27613	1.82	5.0E-65	7661651	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1384	14539	27614	1.92	5.0E-65	7661651	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2223	15357	28487	1.07	5.0E-65	AB033788.1	NT	Homo sapiens hPAD-cdny10 mRNA for peptidylarginine deaminase type I, complete cds
3328	16501	29519	1.79	6.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3328	16501	29520	1.79	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7008	20144	33593	1.39	5.0E-65	4504606	NT	Homo sapiens Interferon-related developmental regulator 1 (IFRD1), mRNA
10684	23718	37324	1.36	5.0E-65	AF006686.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
198	13421	26452	1.3	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
764	13945	26891	1.23	4.0E-65	AI266468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:1891800 3'
764	13945	26892	1.23	4.0E-65	AI266468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:1891800 3'
1103	14268	27326	1.44	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1515	14668	27761	24.91	4.0E-65	4506686	NT	Homo sapiens ribosomal protein L34 (RPL34), mRNA
2413	15543	28670	1.02	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2413	15543	28671	1.02	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
6284	19457	32807	4.96	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6284	19457	32808	4.96	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7233	20317	33760	0.66	4.0E-65	AY008372.1	NT	Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds
7286	20349	33801	6.04	4.0E-65	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7368	20447	33910	2.3	4.0E-65	11545780	NT	Homo sapiens hypophthal protein FLJ22087 (FLJ22087), mRNA
7721	20785	34273	0.65	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7721	20785	34274	0.65	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7893	21043	34555	0.67	4.0E-65	U36656.1	NT	Human MAP kinase kinase 5 (MKK5) mRNA, complete cds
8025	21108	34624	0.83	4.0E-65	5453765	NT	Homo sapiens nd (chicken)-like 2 (NELL2), mRNA
8025	21108	34625	0.83	4.0E-65	5453765	NT	Homo sapiens nd (chicken)-like 2 (NELL2), mRNA
9346	22422	35875	0.88	4.0E-65	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10808	23841		2.12	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11360	24422	38078	1.92	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12926	14268	27326	2.03	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
13201	13421	26452	1.26	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
100	13336	26364	0.65	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
1260	15990		18.37	3.0E-65	X76932.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1689	14741	27822	4.52	3.0E-65	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1688	16014	28122	1.31	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.31 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
3350	16322	28538	1.24	3.0E-65	4504950	NT	MSR1 repetitive element:
3815	16975	28078	1.08	3.0E-65	AI000692.1	EST_HUMAN	Homo sapiens testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
4773	17908	30891	1.38	3.0E-65	6912385	NT	MSR1 repetitive element:
10274	23309	36905	1.61	3.0E-65	BE787366.1	EST_HUMAN	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
11872	23900	37523	8.41	3.0E-65	AA430006.1	EST_HUMAN	801479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
3490	16957	29670	7.53	2.0E-65	BF680294.1	EST_HUMAN	zw65a06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
6688	19825		3.73	2.0E-65	BE263373.1	EST_HUMAN	802156082F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4265066 5'
7282	20365	33818	20.62	2.0E-65	BF576922.1	EST_HUMAN	801190893F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3334741 5'
9046	22125	35668	1.2	2.0E-65	AK024463.1	NT	802134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
8046	22125	35669	1.2	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
10892	23976	37608	1.46	2.0E-65	11419247	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
12241	25184		6.27	2.0E-65	AA307904.1	EST_HUMAN	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
12748	25906		3.99	2.0E-65	BF248086.1	EST_HUMAN	EST178755 Odon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus
93	13328		0.69	1.0E-65	BF125544.1	EST_HUMAN	801854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
552	13745	26770	1.43	1.0E-65	7657465	NT	801763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
1889	15033	28141	3.31	1.0E-65	AB028998.1	NT	Homo sapiens putative Rab5 GTP/GTP exchange factor homologue (RABEX5), mRNA
2098	15238	28360	1.48	1.0E-65	AB040946.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3488	16825	29645	0.8	1.0E-65	BE486881.1	EST_HUMAN	Homo sapiens mRNA for KIAA1513 protein, partial cds
4105	17259	30259	2.07	1.0E-65	4504082	NT	h224e09.x1 NCJ CGAP_G08 Homo sapiens cDNA clone IMAGE:3208898 3'
							Homo sapiens glypican 4 (GPC4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4103	17259	30260	2.07	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4323	17466	30451	2.63	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4323	17466	30462	2.53	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5143	18266	31235	1.57	1.0E-65	AW238282.1	EST_HUMAN	xp20cd01.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740866 3'
5143	18266	31236	1.57	1.0E-65	AW238282.1	EST_HUMAN	xp20cd01.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740866 3'
5400	18602	31672	0.86	1.0E-65	BE089508.1	EST_HUMAN	QV6-BT0702-170400-194-f09 BT0702 Homo sapiens cDNA
5400	18602	31673	0.86	1.0E-65	BE089508.1	EST_HUMAN	QV6-BT0702-170400-194-f09 BT0702 Homo sapiens cDNA
5594	18766	31837	0.58	1.0E-65	AI243738.1	EST_HUMAN	q186h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR:Q07823
8448	21528	35057	1.5	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8448	21528	35058	1.5	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8475	21566	35088	0.66	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8475	21566	35089	0.66	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8514	21595	35129	2.04	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYR01 Homo sapiens cDNA clone THYR01000356 5'
8514	21595	35130	2.04	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYR01 Homo sapiens cDNA clone THYR01000356 5'
9041	22120	35682	1.01	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
9222	22300	35843	1.33	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9222	22300	35844	1.33	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9231	22309		2.79	1.0E-65	11431984	NT	Homo sapiens Insitol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9309	22385	35937	0.55	1.0E-65	7692227	NT	Homo sapiens KIAA0656 gene product (KIAA0656), mRNA
9678	22640	36210	5.5	1.0E-65	AI191716.1	EST_HUMAN	q58602.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29881 ZINC
10089	23127	36730	1.32	1.0E-65	AU153793.1	EST_HUMAN	FINGER PROTEIN 8 (HUMAN); contains MER19.11 MER19 repetitive element;
10509	23544	37155	0.65	1.0E-65	AA089569.1	EST_HUMAN	z175a04.11 Soares_pined_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'
10796	23829	37453	1.23	1.0E-65	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10885	23969	37599	1.91	1.0E-65	M26187.1	NT	Homo sapiens platelet factor 4 variation 1 (PF4var1) gene, complete cds
11016	24095	37734	9.39	1.0E-65	4506860	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11395	24456	38118	1.9	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
11485	24545	38217	2.58	1.0E-65	AI621017.1	EST_HUMAN	ts76a06.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L16533_ma1
12292	26217		2.38	1.0E-65	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
12391	26276	32078	3.77	1.0E-65	11418322	NT	Homo sapiens TNF-inducible protein GG12-1 (CG12-1), mRNA
73	13310	26334	0.9	9.0E-66	AI160311.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
73	13310	26335	0.9	9.0E-66	AI160311.1	NT	Novel human gene mapping to chromosome 22

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1385	14540	27615	1.53	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1385	14540	27616	1.53	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1513	14666		5.93	9.0E-66	M87299.1	NT	Human transposon-like element, partial
4007	17164	30171	0.66	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4007	17164	30172	0.66	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
11628	24708		1.6	7.0E-66	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
4485	17625	30605	1.16	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595
4485	17625	30606	1.16	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595
4485	17625	30607	1.16	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595
8629	21709		0.46	6.0E-66	BE178663.1	EST_HUMAN	PM2-HT0604-030300-001-h06 HT0604 Homo sapiens cDNA
11427	24488	38152	3.22	6.0E-66	X69181.1	NT	H sapiens mRNA for ribosomal protein L31
1388	14552	27627	2.45	5.0E-66	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
9494	22551	36113	8.4	6.0E-66	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
813	13992	27046	1.8	4.0E-66	6679818	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1775	14924	28018	0.97	4.0E-66	AW897798.1	EST_HUMAN	RC1-NN0063-100500-022-602 NN0063 Homo sapiens cDNA
2355	15486	28618	6.3	4.0E-66	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
2543	15668		3.15	4.0E-66	A1233364.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4903	18035		5.02	4.0E-66	96355487	NT	Human endogenous retrovirus, complete genome
5688	18862	32147	3.57	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5881	19051	32358	0.87	4.0E-66	AW593919.1	EST_HUMAN	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA
6995	18514	31508	4.91	4.0E-66	AW865473.1	EST_HUMAN	EST377546 MAGI resequences, MAGI Homo sapiens cDNA
7281	20364	33817	7.88	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
7807	18862	32147	0.83	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase (MTHFD2), mRNA
8280	21351	34867	6.14	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
8327	21409	34936	0.7	4.0E-66	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
10896	23680	37612	1.49	4.0E-66	BF507493.1	EST_HUMAN	U1-H-BW1-ami-e-10-0-UJ.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
11660	24739	38430	1.63	4.0E-66	AB023215.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1458	14611	27692	14.93	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1458	14611	27693	14.93	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
2039	15180	28290	1.04	3.0E-66	N55323.1	EST_HUMAN	SW:H2B1_TIGCA P35063 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
2039	15180	28291	1.04	3.0E-66	N55323.1	EST_HUMAN	yz27g12.1 Soares multiple sclerosis 2/NBHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to
2039	15180	28292	1.04	3.0E-66	N55323.1	EST_HUMAN	SW:H2B1_TIGCA P35063 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
2772	15887	28987	3.44	3.0E-66	111417890	NT	yz27g12.1 Soares multiple sclerosis 2/NBHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to
3186	16361	29367	7.29	3.0E-66	7662223	NT	SW:H2B1_TIGCA P35063 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
5583	17778	31823	0.85	3.0E-66	AB020699.1	NT	yz27g12.1 Soares multiple sclerosis 2/NBHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to
5685	18889	32180	0.65	3.0E-66	M13975.1	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5683	19081	32391	1.72	3.0E-66	11417946	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5683	19081	32392	1.72	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
7585	20657	34134	1.74	3.0E-66	X92211.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8725	22780	36361	0.59	3.0E-66	AK024453.1	NT	H. sapiens germline immunoglobulin heavy chain, variable region, (15-1)
9920	22660	36547	0.52	3.0E-66	11417118	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
10278	23313	36911	0.86	3.0E-66	7019480	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10741	23774	37389	0.95	3.0E-66	AF155639.1	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
11800	24790	38487	4.55	3.0E-66	5453949	NT	Homo sapiens molybdenum cofactor biosynthesis protein E (MCOBPE) mRNA, complete cds
52	13291	26304	1.48	2.0E-66	7657334	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
52	13291	26305	1.48	2.0E-66	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
435	13235	26235	0.87	2.0E-66	4505524	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
435	13235	26236	0.87	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products
1873	15017	28126	2.02	2.0E-66	AL163301.2	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products
3039	16216	29236	1.07	2.0E-66	X66855.1	NT	Homo sapiens chromosome 21 segment H521C101
3009	16773	29788	0.85	2.0E-66	8923290	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3861	17021	30019	0.78	2.0E-66	AL117233.1	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
4176	17326	30317	0.89	2.0E-66	AF109389.1	NT	Novel human gene mapping to chromosome 1
							Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4778	17913	30898	13.88	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4778	17913	30899	13.88	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
5937	19123	32436	0.82	2.0E-66	AW988854.1	EST_HUMAN	EST380930 IMAGE ressequencing, MAGJ Homo sapiens cDNA
5937	19123	32437	0.82	2.0E-66	AW988854.1	EST_HUMAN	EST380930 IMAGE ressequencing, MAGJ Homo sapiens cDNA
9048	22127	35671	3.57	2.0E-66	N45480.1	EST_HUMAN	W59602.1 Soares, multiple sclerosis, 2NcHMSF Homo sapiens cDNA clone IMAGE:277826 5'
12637	26147		2.84	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
1717	14867		1.14	1.0E-66	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3609931 5'
2959	16136	29153	1.47	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2959	16136	29154	1.47	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4504	16136	29153	4.18	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4504	16136	29154	4.18	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5497	18696	31712	5.97	1.0E-66	BE673088.1	EST_HUMAN	602152396F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
5900	19089	32402	0.67	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
5900	19089	32403	0.67	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
7078	20131	33548	1.53	1.0E-66	BF328623.1	EST_HUMAN	RCB-BN0193-019000-034-G06 BN0193 Homo sapiens cDNA
8652	21732	35271	1.2	1.0E-66	AA668868.1	EST_HUMAN	aa60e04.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827262 3'
9628	22881	36250	0.84	1.0E-66	AA018828.1	EST_HUMAN	ze67e12.1 Soares, retina N2B4HR Homo sapiens cDNA clone IMAGE:363118 5'
10682	23617	37223	0.93	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10582	23617	37224	0.93	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
11185	24254	37889	2.24	1.0E-66	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
12398	25278		1.82	8.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
6034	18162		0.91	8.0E-67	M78158.1	EST_HUMAN	EST101750 Subtracted Hippocampus, Stragene (cat. #336205) Homo sapiens cDNA clone HHCPN31 similar to L1 repetitive element
391	13828	26665	1.63	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
1413	14567	27641	2.68	7.0E-67	AA383416.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1585	14737	27817	1.39	7.0E-67	W85947.1	EST_HUMAN	EST98812 Testis 1 Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, ccsmid ZK353
1585	14737	27818	1.39	7.0E-67	W85947.1	EST_HUMAN	zh56b05.1 Soares, fetal liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2089	15229	28350	1.94	7.0E-67	7657243	NT	zh56b05.1 Soares, fetal liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2089	15229	28351	1.84	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2089	15229	28351	1.84	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2871	13628	26665	1.36	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6205	19380	32730	0.98	7.0E-67	10190695	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6400	19569	32830	1.87	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6400	19569	32831	1.87	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6863	20015	33425	1.12	7.0E-67	4885034	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
7809	20884	34358	0.99	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
7809	20884	34359	0.99	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8268	21340	34857	0.52	7.0E-67	4826895	NT	Homo sapiens phosphodiesterase 1/nucleotide pyrophosphatase 3 (PDN3), mRNA
8518	21599	35134	0.7	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
9132	22211	35766	0.86	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11565	24620		2.42	7.0E-67	11434579	NT	Homo sapiens fucosyltransferase 8 (alpha 1,6) fucoseyltransferase (FUT8), mRNA
11973	24958	38680	2.02	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit I (COX8A1P) pseudogene, complete cds
12168	25131	38829	4.05	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12168	25131	38830	4.05	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12864	26441	32053	1.92	7.0E-67	AB011396.1	NT	Homo sapiens gene for AF-6, complete cds
13106	26721		1.74	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA
573	13765	26788	1.09	6.0E-67	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
818	13997	27051	2.4	6.0E-67	Z17272.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1302	14458	27524	1.07	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3, 4, 5, 6 & 7
3237	16411	29426	1.39	6.0E-67	4506434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1), mRNA
3524	16689	29698	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3), mRNA, and translated products
3524	16689	29699	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3), mRNA, and translated products
4243	17389	30375	0.92	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4243	17389	30376	0.92	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4827	17660	30947	2.22	6.0E-67	7687020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4827	17660	30948	2.22	6.0E-67	7687020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
13224	17665	26788	2.74	6.0E-67	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
3283	19467	29486	2.26	5.0E-67	AF009690.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11230	24299		2.17	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1359	14514	27598	1.13	4.0E-67	R90819.1	EST_HUMAN	yn02d11.1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'
8211	21293	34813	0.8	4.0E-67	AI733032.1	EST_HUMAN	928605.x5 NC1 CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1483288 3' similar to SW:Z33A_HUMAN
8576	21657		1.48	4.0E-67	BF357321.1	EST_HUMAN	Q06730 ZINC FINGER PROTEIN 33A ;
							RC0-HT0934-150900-028-c03 HT0934 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11318	24381		1.76	4.0E-67	AA714294.1	EST_HUMAN	nm00601.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385 PRO-POL-OUTPASE POLYPROTEIN;
2874	13835	28862	2.03	3.0E-67	AA333788.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' and
3542	16707	29718	2.05	3.0E-67	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-106 BT0311 Homo sapiens cDNA
4816	17949	30934	2.96	3.0E-67	AW869159.1	EST_HUMAN	MR3-SN0066-040800-008-401 SN0066 Homo sapiens cDNA
4845	17978		1.38	3.0E-67	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8376	21456	34980	1.37	3.0E-67	BF196068.1	EST_HUMAN	hr81f06.s1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
11537	24593		15.42	3.0E-67	AA927874.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1;
193	13416	28445	0.59	2.0E-67	BE348354.1	EST_HUMAN	hm18b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
868	14044	27109	5.29	2.0E-67	AW816405.1	EST_HUMAN	QV4-S10234-181189-037-405 S10234 Homo sapiens cDNA
1129	14294		2.48	2.0E-67	AF167460.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
1933	15078	28179	1.23	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2908976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN;
1933	15078	28180	1.23	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2908976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN;
2488	16685	28713	1.18	2.0E-67	AF309561.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
2502	15629	28749	1.37	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3557	16722	29737	3.76	2.0E-67	AA825755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
4109	17263	30263	3.13	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6197	16372	32723	0.83	2.0E-67	AL049784.1	NT	Novel human gene mapping to chromosome 13
6252	19428	32772	4.95	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
6425	18593	32958	1.74	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6425	18593	32959	1.74	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6779	18934	33330	0.64	2.0E-67	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A229 5'
8755	21834	35374	1.09	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8755	21834	35375	1.09	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
9187	22276	35812	1.31	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-407 BT0566 Homo sapiens cDNA
9187	22276	35813	1.31	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-407 BT0566 Homo sapiens cDNA
9786	22763	36332	0.55	2.0E-67	AV731333.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
9910	22960	36536	0.99	2.0E-67	AW293624.1	EST_HUMAN	U1-H-B12-ahn-s-10-0.U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
10848	23881	37501	0.53	2.0E-67	AA928089.1	EST_HUMAN	nm86s07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563541 3'
11141	24213	37840	1.75	2.0E-67	BF685788.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11310	26230		2.55	2.0E-67	11436448	NT	Homo sapiens KIAA0085 protein (KIAA0085), mRNA
11504	24582	38240	2.05	2.0E-67	BE265714.1	EST_HUMAN	601175782F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11743	23929	37555	2.44	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12527	25988	31770	2.47	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
263	13482	26514	2.37	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
726	13908	26948	0.93	1.0E-67	AA702794.1	EST_HUMAN	z80b04.s1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4833	17966	30954	0.73	1.0E-67	BF439247.1	EST_HUMAN	inab6108.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
11268	24337		1.47	1.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
12105	25055		3.44	9.0E-68	4506050	NT	Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA
2245	15378	28506	8.3	8.0E-68	BE970732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3973	17130	30133	5.75	8.0E-68	AA209456.1	EST_HUMAN	SW_SAV_SULAC Q07590 SAV PROTEIN. ;
3973	17130	30134	5.75	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to
8293	21375	34895	0.56	7.0E-68	A1870505.1	EST_HUMAN	SW_SAV_SULAC Q07590 SAV PROTEIN. ;
10666	23700	37310	6.43	6.0E-68	11422086	NT	wp89e03.x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:2312860 3'
11417	24478	38143	1.31	6.0E-68	AF133901.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
12668	25579		2.84	6.0E-68	BE612554.1	EST_HUMAN	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
13165	25766	31927	1.45	6.0E-68	BF310675.1	EST_HUMAN	601462067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
825	15986	27059	2	5.0E-68	AF231919.1	NT	601694635F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
825	15986	27060	2	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	14020	27076	4.93	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	14020	27077	4.93	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3216	16390	29401	2.99	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4297	17440		0.64	5.0E-68	4826987	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
2594	15719	28836	1	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2594	15719	28837	1	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5090	16218		7.11	4.0E-68	P04406	SWISSPROT	Homo sapiens transcription factor NRF (NRF), mRNA
6085	19267	32596	0.69	4.0E-68	AF157063.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6912	20227	33659	6.03	4.0E-68	11055991	NT	Homo sapiens sedlin (SEDL) gene, exon 4
6912	20227	33660	6.03	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCF1), mRNA
7899	20913	34418	0.84	4.0E-68	7661683	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCF1), mRNA
							Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9240	22317	35859	5.59	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9240	22317	35860	5.59	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9380	22455	36018	3.17	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
11251	24320	37960	1.64	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11251	24320	37961	1.64	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11434	24485	38161	1.72	4.0E-68	AB040948.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2) mRNA
12728	25485	32026	1.17	4.0E-68	11417966	NT	Homo sapiens G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
3751	16912	28916	3.54	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9656	21099		3.5	3.0E-68	AI342323.1	EST_HUMAN	THR12 THR repetitive element
10720	23763	37359	1.35	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
13111	25902		2.83	3.0E-68	AW839485.1	EST_HUMAN	QV1-DT0072-01020-056-h08 DT0072 Homo sapiens cDNA
2825	18474		28.7	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4135	17288	30283	0.79	2.0E-68	BE675766.1	EST_HUMAN	71502x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:3264747 3' similar to TR:O80828 O80828
4803	17938	30826	2.33	2.0E-68	AB008681.1	NT	HYPOTHETICAL 88.8 KD PROTEIN
7015	20151		9.21	2.0E-68	R45088.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
7209	20074	33486	3.81	2.0E-68	BF035316.1	EST_HUMAN	Y68904.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34896 3'
7527	20800	34074	0.68	2.0E-68	BF336745.1	EST_HUMAN	601458514F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862034 5'
9150	22228	35772	0.56	2.0E-68	Q03859	SWISSPROT	IL3-CT0834-180800-273-A01 CT0834 Homo sapiens cDNA
11521	24577	38255	1.49	2.0E-68	BF330594.1	EST_HUMAN	FORMIN 4 (LIMB DEFORMITY PROTEIN)
12285	26170		1.58	2.0E-68	BE867376.1	EST_HUMAN	QV0-BT0074-130999-014-g04 BT0074 Homo sapiens cDNA
13192	25775		1.32	2.0E-68	AW016803.1	EST_HUMAN	601437367F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3922192 5'
81	13316	26344	0.93	1.0E-68	AW816405.1	EST_HUMAN	U1H-B10-alam-b-05-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708824 3'
307	13523	26557	16.49	1.0E-68	AB011149.1	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
2326	15458	28590	1.24	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2326	15458	28591	1.24	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
4117	17271	30270	0.8	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3532344 5'
5140	15263	31231	0.71	1.0E-68	AA897343.1	EST_HUMAN	601177002F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:1460518 3'
5437	16637	31616	1.92	1.0E-68		NT	al47g12.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
7653	20908	34412	0.76	1.0E-68		NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
10385	23420	37027	0.45	1.0E-68		NT	Homo sapiens centrin/SUMO-specific protease (SENPF1), mRNA
11089	24163	37799	2.16	1.0E-68		NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
						NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA

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11089	24163	37800	2.16	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11142	24214	37841	2.81	1.0E-68	L78416.1	NT	Homo sapiens MIF2 suppressor (HSMIT3), mRNA, complete cds
11468	24527	38200	1.7	1.0E-68	11433277	NT	Homo sapiens myosin IC (MYO1C), mRNA
11580	24634	38313	2.83	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11580	24634	38314	2.83	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11663	24948	38553	1.81	1.0E-68	11418431	NT	Homo sapiens CGI-78 protein (LOC51632), mRNA
11663	24948	38554	1.81	1.0E-68	11418431	NT	Homo sapiens CGI-78 protein (LOC51632), mRNA
12849	13316	26344	2.53	1.0E-68	4506222	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13100	26092	31661	3.05	1.0E-68	11430480	NT	Homo sapiens meninoma (disrupted in balanced translocation) 1 (MN1), mRNA
13164	25755		1.88	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
22	13260	26280	2.42	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
22	13260	26281	2.42	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1053	14219	27275	0.99	9.0E-69	5031980	NT	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA
1053	14219	27276	0.99	9.0E-69	5031980	NT	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA
4246	17392	30380	0.6	9.0E-69	4757867	NT	Homo sapiens v-rf murine sarcoma viral oncogene homolog B1 (BRAP) mRNA
4268	17411	30397	0.89	9.0E-69	4504010	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD) (GLCLR) mRNA
11128	24200		7.86	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3473	18840		1.28	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
6482	18848	33011	4.44	7.0E-69	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
8047	21130	34649	1.85	6.0E-69	A192764.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743801 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8047	21130	34650	1.88	6.0E-69	A192764.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743801 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
9174	22552	35795	1.05	5.0E-69	A4826039.1	EST_HUMAN	cd60a03.x1 NCL_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1372800 3'
533	13726		1.18	4.0E-69	A1873630.1	EST_HUMAN	wm26h11.x1 NCL_CGAP_UK4 Homo sapiens cDNA clone IMAGE:2437125 3'
5881	28812	32378	1.53	4.0E-69	BE561063.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677641 5'
5966	19152	32467	4.62	4.0E-69	A1764973.1	EST_HUMAN	wh57506.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137
6764	19920	33315	3.17	4.0E-69	4557732	NT	O55137 ACYL-COA THIOESTERASE. ;
6764	19920	33316	3.17	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9115	22194	36739	0.55	4.0E-69	AU118634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
397	13634	26872	5.24	3.0E-69	BE288012.1	EST_HUMAN	AU118634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
627	13812	26834	2.78	3.0E-69	AF221712.1	NT	801110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3361352 5'
							Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1586	14738		1.12	3.0E-69	T80514.1	EST_HUMAN	yt08a02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48836
2449	15577		2.18	3.0E-69	6729910	NT	A48836 SPEGF III-EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN ;
5357	18483	38823	1.37	3.0E-69	11418185	NT	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
7529	20602	34078	0.76	3.0E-69	AF095703.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
7578	20650	34128	1.74	3.0E-69	U52351.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
7724	20788	34277	8.4	3.0E-69	AF268075.1	NT	encoding mitochondrial protein, complete cds
8567	21648	35190	1.33	3.0E-69	AW138846.1	EST_HUMAN	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
8967	22046		0.74	3.0E-69	AA376389.1	EST_HUMAN	U14H.B11-acv-g-01-Q.U1 s1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
8613	22686	36238	1.74	3.0E-69	X13223.1	NT	EST188807 HSC172 cells II Homo sapiens cDNA 5' and similar to similar to ribosomal protein S18
9733	22798	36372	3.15	3.0E-69	X08233.1	NT	H1.sapiens mRNA for N-acetylglucosaminide (beta 1-4)-galactosyltransferase
10034	23072	36672	0.56	3.0E-69	5730036	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
10877	23862	37590	2.74	3.0E-69	11432120	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
11080	24155		7.88	3.0E-69	AA376399.1	EST_HUMAN	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
12112	25092	38785	1.77	3.0E-69	AB011541.1	NT	EST188807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
12112	25092	38786	1.77	3.0E-69	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
12305	25223		3.1	3.0E-69	11419157	NT	Homo sapiens mRNA for MEGF8, partial cds
131	13612	26651	1.09	2.0E-69	AF160252.1	NT	Homo sapiens HGC8.2 protein (HGC8.2), mRNA
131	13612	26652	1.09	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
417	13612	26651	4.42	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
417	13612	26652	4.42	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1934	15077	28181	1.79	2.0E-69	BE257857.1	EST_HUMAN	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
2906	16084		4.14	2.0E-69	AA431157.1	EST_HUMAN	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
8761	21830	35368	0.95	2.0E-69	AA114270.1	EST_HUMAN	z717g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
1680	14632		1	1.0E-69	BF330124.1	NT	z717g01.r1 Stragelene pancreas (8937208) Homo sapiens cDNA clone IMAGE:527088 5'
1739	14888	27980	2.4	1.0E-69	AF053768.1	NT	R60-BN0305-200600-031-405 BN0305 Homo sapiens cDNA
5137	18260		0.63	1.0E-69	BE408094.1	EST_HUMAN	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
6175	18351	32697	0.83	1.0E-69	BE902501.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
6175	18351	32698	0.83	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3665532 5'
6738	19884	33285	4.36	1.0E-69	AW393969.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3665532 5'
6958	20271	33709	1.22	1.0E-69	7662263	NT	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6958	20271	33710	1.22	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIA0716), mRNA
6978	20204	33631	2.91	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6978	20204	33632	2.91	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7021	20157	33578	0.51	1.0E-69	BE531007.1	EST_HUMAN	60127832F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
7021	20157	33578	0.51	1.0E-69	BE531007.1	EST_HUMAN	60127832F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
10377	23412	37020	5.01	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10377	23412	37021	5.01	1.0E-69	BE245070.1	EST_HUMAN	cDNA clone TCBAP2678
10625	23659	37268	0.9	1.0E-69	BF528429.1	EST_HUMAN	602043762F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181325 5'
11112	24184		35.41	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
12237	25181	38352	1.95	1.0E-69	BF125987.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12673	25449		3.4	1.0E-69	AB099994.1	EST_HUMAN	wf64c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2409	16061	29887	1.56	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4493	17633	30615	1.84	8.0E-70	L77596.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1856	15002	28108	2.42	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1856	15002	28109	2.42	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1884	15127	28229	1.67	7.0E-70	AA282955.1	EST_HUMAN	215h04.1 NCI_CGAP_G0BT1 Homo sapiens cDNA clone IMAGE:713239 5'
2125	15261		5.13	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4340	17483	30465	4.29	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5600	18795	31844	5.4	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5800	18795	31845	5.4	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7064	20117	33531	1.9	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
7845	20895	34506	0.64	7.0E-70	11417308	NT	Homo sapiens titin immunoglobulin domain protein (myotilin) (TTID), mRNA
8626	21708	35242	2.55	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
8626	21708	35243	2.55	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
8919	21698	35538	3.8	7.0E-70	MT4099.1	NT	Human displacement protein (CCAAT) mRNA
8919	21698	35539	3.8	7.0E-70	MT4099.1	NT	Human displacement protein (CCAAT) mRNA
9358	22433	35991	5.59	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9358	22433	35992	5.59	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9635	21078	34590	2.88	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9660	21102	34617	1.7	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transporin (TRN2), mRNA
9660	21102	34618	1.7	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transporin (TRN2), mRNA

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9857	22897	36480	0.53	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8KD) (GLCLC) mRNA
10505	23540	37149	0.85	7.0E-70	AB036420.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10505	23540	37150	0.85	7.0E-70	AB036420.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11329	24392	38039	1.77	7.0E-70	11428685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant spastin) (SPG4), mRNA
11329	24392	38040	1.77	7.0E-70	11428685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant spastin) (SPG4), mRNA
11897	24885	38583	2.37	7.0E-70	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11897	24885	38584	2.37	7.0E-70	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
894	14070	27135	2.51	6.0E-70	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2205	15339	28466	2.29	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4629	17765	30747	0.7	6.0E-70	AF164121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
2618	18086	28854	1.78	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2618	18086	28855	1.78	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12247	25188		5	5.0E-70	BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
6894	20045	33454	1.03	4.0E-70	T06037.1	EST_HUMAN	EST03928 Fetal brain, Stratagene (cat#3636206) Homo sapiens cDNA clone HFBDN25
6833	20248	33682	1.84	4.0E-70	AW793226.1	EST_HUMAN	GM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
6833	20248	33683	1.84	4.0E-70	AW793226.1	EST_HUMAN	GM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
1619	14771	27853	1.71	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071289-011-a12 BT0522 Homo sapiens cDNA
1619	14771	27854	1.71	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071289-011-a12 BT0522 Homo sapiens cDNA
5737	18389	31357	1.11	3.0E-70	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5737	18389	32227	0.59	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5737	18389	32228	0.59	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6066	19248	32575	1	3.0E-70	A1831975.1	EST_HUMAN	wh90d03.x1 NCJ_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2388005 3'
6503	19669	33033	1.69	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302805 5'
6503	19669	33034	1.69	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302805 5'
10314	23349	36955	0.62	3.0E-70	BE502073.1	EST_HUMAN	h281h02.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
39	13277	26283	1.03	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 200 (p4K200) mRNA, complete cds
							yy07a10.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270522 5' similar to
707	13890	26923	15.24	2.0E-70	N42161.1	EST_HUMAN	SW:D3HL_RAT P28266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;

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Table 4
Number Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
						EST_HUMAN	Y07410.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P28280 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
707	13890	26924	15.24	2.0E-70	N42161.1	EST_HUMAN	qx51h01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004613 3'
723	13905	28947	1.85	2.0E-70	A1246893.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1046	14212	27269	1.36	2.0E-70	8923069	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1211	14372	27432	2.16	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1211	14372	27433	2.16	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1211	14372	27433	2.16	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1441	14594	27669	1.23	2.0E-70	BE467311.1	EST_HUMAN	h264c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:612441 5' similar to
						EST_HUMAN	TR:G1041283 G1041283 D2085.5 ;
1688	14840	27924	1.07	2.0E-70	AA180093.1	EST_HUMAN	TR:G1041283 G1041283 D2085.5 ;
1688	14840	27925	1.07	2.0E-70	AA180093.1	EST_HUMAN	TR:G1041283 G1041283 D2085.5 ;
1781	14930	28023	4.92	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21TC002
						EST_HUMAN	ZK4804.1 Soares retina N254-HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
2394	15525		9.42	2.0E-70	AA054010.1	EST_HUMAN	P03345 GAG POLYPROTEIN ;
3923	17082	30078	0.71	2.0E-70	AL133207.2	NT	Novel human gene mapping to chromosome X
4160	17311	30307	5.86	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5632	18826	31901	8.42	2.0E-70	X72662.1	NT	H sapiens gene for schwannomin (CS6)
5632	18826	31902	8.42	2.0E-70	X72662.1	NT	H sapiens gene for schwannomin (CS6)
5632	18826	31902	8.42	2.0E-70	AF310103.1	NT	H sapiens NALP1 mRNA, complete cds
6333	19504	32982	1.23	2.0E-70	D12625.1	NT	Homo sapiens NALP1 mRNA, complete cds
6771	19926	33321	2.65	2.0E-70	D12625.1	NT	Homo sapiens NALP1 mRNA, complete cds
6806	19960	33362	10.35	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6806	19960	33362	10.35	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6806	19960	33362	10.35	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7136	19562	31477	1.5	2.0E-70		NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
8103	21185	34704	2.81	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
8417	21498	35030	0.66	2.0E-70		EST_HUMAN	Homo sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA
8860	21638	36007	1.34	2.0E-70	H47869.1	EST_HUMAN	y079g02.1 Soares fetal liver spleen NFLS Homo sapiens cDNA clone IMAGE:193882 5'
9370	22446	36088	1.14	2.0E-70		NT	Homo sapiens dynactin p82 subunit (LOC51104), mRNA
10342	23377	36031	1.26	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
11324	24387	36032	3.39	2.0E-70	5923420	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
11324	24387	36032	3.39	2.0E-70	5923420	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
11324	24387	36032	3.39	2.0E-70	5923420	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
11840	24926	36028	7.78	2.0E-70		NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
12662	26438	32050	2.42	2.0E-70		NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
						NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48KD) (EIF3S6) mRNA
						NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12862	25439	32051	2.42	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3480	18647		3.72	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
8480	22637		0.84	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416024 5'
10003	23041		0.88	1.0E-70	AA442292.1	EST_HUMAN	zh54c03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
11176	24244	37877	7.61	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLB0810 5'
6065	19247	32573	6.03	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6065	19247	32574	6.03	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
7175	20308	33751	2.05	9.0E-71	AI654903.1	EST_HUMAN	wh52c05.x1 NCJ CGAP_G06 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TODD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
11813	20308	33751	3.47	9.0E-71	AI654903.1	EST_HUMAN	wh52c05.x1 NCJ CGAP_G06 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TODD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
9270	22346		2.88	8.0E-71	AA171451.1	EST_HUMAN	zp21d11.r1 Strelagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL. ;
10828	23881	37484	0.53	8.0E-71	AW273820.1	EST_HUMAN	XZ24d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR:O54730
7633	20608	34081	7.86	7.0E-71	AA442230.1	EST_HUMAN	Q84730 TRANSPLANTABILITY ASSOCIATED PROTEIN 1 ;
8877	21956	35491	1.34	7.0E-71	AA705457.1	EST_HUMAN	zh60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
11614	24605	38353	2.2	7.0E-71	AL163210.2	NT	z81a08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
2284	15416	28548	7.11	5.0E-71	AF056322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
4235	17382	30371	1.18	6.0E-71	AW816405.1	EST_HUMAN	Homo sapiens SP-100-HMG nuclear autoantigen (SP100) mRNA, complete cds
6002	19187	32506	1.59	5.0E-71	11641408	NT	GVA-ST0234-181189-037-003 ST0234 Homo sapiens cDNA
8801	18956	33356	1.4	5.0E-71	7862209	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
7060	20113	33528	0.94	5.0E-71	7862209	NT	Homo sapiens keratin, hair, acidic, 7 (KRT7A7), mRNA
7296	20378	33836	0.82	5.0E-71	11431590	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7679	20744	34225	1.78	5.0E-71	M38108.1	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7884	20936	34442	0.8	5.0E-71	11628445	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7912	20963	34471	20.85	5.0E-71	AF072810.1	NT	Homo sapiens MAGUK protein p55T; Protein Associated with Line 2 (LOC51678), mRNA
8720	21800	35335	0.96	5.0E-71	5453777	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8720	21800	35336	0.96	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
10115	23153		2.06	6.0E-71	X13487.1	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
10476	23511	37124	0.49	5.0E-71	U70968.1	NT	Human PresA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
							Human arrestin (SAG) gene exon 8

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10870	23955	37584	1.45	5.0E-71	5729900	NT	Homo sapiens [GF-I] mRNA-binding protein 3 (KOC1), mRNA
10849	24026	37660	1.53	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10843	24025	37661	1.53	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11226	24295	37936	3.85	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide II, neutrophil-activating peptide-2) (PPBP), mRNA
11487	24526	38169	2.1	5.0E-71	11436069	NT	Homo sapiens similar to hypothetical protein FLJ20763 (H. sapiens) (LOC63325), mRNA
12558	25380		1.75	5.0E-71	11418039	NT	Homo sapiens RNA binding motif protein 8 (RBM8), mRNA
106	13342	26370	1.84	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA
360	13571	26601	31.81	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
360	13571	26602	31.81	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2951	16128	29141	1.67	4.0E-71	4508890	NT	Homo sapiens plasminogen (PLG) mRNA
4548	17686	30667	1.87	4.0E-71	AF056322.1	NT	Homo sapiens SP-100-HMG nuclear autoantigen (SP-100) mRNA, complete cds
5101	18229	31200	4.68	4.0E-71	7657602	NT	Homo sapiens putative home-binding protein (SOL), mRNA
8223	21305		1.13	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACET Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element ;
10931	24013	37646	3.32	3.0E-71	AA557583.1	EST_HUMAN	Homo sapiens chromosome 21 segment RS21C006
1258	14416	27481	4.54	2.0E-71	AL76206.2	NT	Human mRNA for KIAA0272 gene, partial cds
5435	18635	31614	7.23	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5435	18635	31615	7.23	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
7107	18534	31489	0.71	2.0E-71	AL042439.1	EST_HUMAN	DKFZ434D1721.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZ434D1721.1
9207	22285	35826	0.5	2.0E-71	BF195585.1	EST_HUMAN	7n85c11.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571221 3' similar to TRQ9Z165
10813	23846	37467	2.12	2.0E-71	AF095703.1	NT	Q9Z165 PUTATIVE FOUR REPEAT ION CHANNEL ;
10813	23846	37468	2.12	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10833	24015	37647	4.37	2.0E-71	BE018477.1	EST_HUMAN	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
11860	24848	38545	1.46	2.0E-71	BF149173.1	EST_HUMAN	DB81806.Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048764 6' similar to SW_R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B ;
11860	24848	38546	1.46	2.0E-71	BF149173.1	EST_HUMAN	Tm1022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to gl 6598881
11882	24870	38567	2.05	2.0E-71	R55626.1	EST_HUMAN	Tm1022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to gl 6598881
12318	25231		4.88	2.0E-71	T05489.1	EST_HUMAN	y177c11.1 Soares breast 2N6HBst Homo sapiens cDNA clone IMAGE:154772 5'
							y043c09.1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:120520 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
655	13841	26868	1.55	1.0E-71	AI077927.1	EST_HUMAN	oy15603.s1 Soares_senescent_fibroblasts, NBHSP Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1 b2 LOR1 repetitive element;
964	14137	27198	1.39	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1124	14289	27344	13.07	1.0E-71	AF205690.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1371	14526	27600	11.13	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2147	15283	28408	1.52	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2147	15283	28409	1.52	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2757	16874	28982	6.06	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3590	18754	29769	1.66	1.0E-71	AF118665.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3685	18948	29855	6.57	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3685	18948	29856	6.57	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3738	16899	29902	0.9	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library. Upregulated Transcripts Homo sapiens cDNA clone 02_15 similar to Homo sapiens chromosome 19
3738	16899	29903	0.9	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library. Upregulated Transcripts Homo sapiens cDNA clone 02_15 similar to Homo sapiens chromosome 19
3835	16899	29997	2.2	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 19
4593	17730	30712	2.13	1.0E-71	D28478.1	NT	Human mRNA for KIAA0045 gene, complete cds
6881	20033	33443	1.48	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
7235	20318	33762	1.48	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7464	20539	34013	12.52	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8340	21421	34946	0.82	1.0E-71	AF105287.1	NT	Homo sapiens glycyl-protein-6 (GPC6) mRNA, complete cds
8302	21443	34965	2.21	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (185kd) (MYOM2), mRNA
8641	21721	35257	4.23	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
8641	21721	35258	4.23	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
9429	22503	36069	0.88	1.0E-71	S72393.1	NT	CSNK2A1-ecadherin kinase I (GKI) subunit alpha [human, Genomic, 18662 nt]
10211	23247	36837	6.22	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
10273	23308	37411	2.74	1.0E-71	AV761217.1	EST_HUMAN	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
10759	23792	37411	0.97	1.0E-71	11433142	EST	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
11024	24103	37824	2.49	1.0E-71	AV761217.1	EST_HUMAN	Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA
11121	24193	38138	3.31	1.0E-71	11418903	NT	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
11413	24474	38138	3.2	1.0E-71	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11413	24474	38139	3.2	1.0E-71	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
12708	25471		10.17	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
420	13815	26854	0.77	9.0E-72	A1897635.1	EST_HUMAN	wk85g03.x1 NCL CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN ; contains Alu repetitive element
420	13816	26855	0.77	9.0E-72	A1897635.1	EST_HUMAN	wk85g03.x1 NCL CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN ; contains Alu repetitive element
6237	19412	32780	0.86	8.0E-72	BF035782.1	EST_HUMAN	801458747F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862451 5'
4228	17375	30381	1.75	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4228	17375	30382	1.75	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4228	17375	30383	1.75	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7274	20357	33811	3	7.0E-72	S41694.1	NT	(pseudogene) PTMAP2-pyrophosphatase alpha [human, Genomic, 1192 nt, segment 2 of 3]
12857	28569		1.53	7.0E-72	F28289.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s4000051 G02
8578	21659		6.7	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
64	13302	26324	1.19	5.0E-72	BF333707.1	EST_HUMAN	QV0-GS0010-150900-398-e11 CS0010 Homo sapiens cDNA
64	13302	26325	1.19	5.0E-72	BF333707.1	EST_HUMAN	QV0-GS0010-150900-398-e11 CS0010 Homo sapiens cDNA
65	13302	26324	3.1	5.0E-72	BF333707.1	EST_HUMAN	QV0-GS0010-150900-398-e11 CS0010 Homo sapiens cDNA
65	13302	26325	3.1	5.0E-72	BF333707.1	EST_HUMAN	QV0-GS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1162	14326		2.31	5.0E-72	L11845.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7089	20183	33607	1.82	5.0E-72	AU126584.1	EST_HUMAN	AU126584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8978	22055	35698	4.16	5.0E-72	AW181274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR:Q89785 Q89785 HYPOTHETICAL 32.4 KD PROTEIN ; contains element MSR1 repetitive element ;
10168	23203	36787	0.71	5.0E-72	AV724632.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAKB01 5'
11519	24575	38252	2.96	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d03 BT0598 Homo sapiens cDNA
11519	24575	38253	2.95	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d03 BT0598 Homo sapiens cDNA
11945	24931	38633	1.55	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
11945	24931	38634	1.55	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
12390	23136		2.48	5.0E-72	BE026645.1	EST_HUMAN	QV1-BT0632-280800-342-e10 BT0632 Homo sapiens cDNA
4943	18073		0.91	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dJ1057B20.2 (DJ1057B20.2), mRNA
5581	18778	31821	0.68	4.0E-72	AF170025.1	NT	Homo sapiens zinc finger protein ZFP95 (ZFP95) mRNA, alternatively spliced, complete cds
6687	18945	33238	0.86	4.0E-72	T87947.1	EST_HUMAN	yd93a01.r1 Soares fetal liver spleen cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
7587	20639	34115	3.26	4.0E-72	5729867	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9987	23026	36618	0.87	4.0E-72	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10312	23947	36953	0.57	4.0E-72	11434344	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10604	23638	37245	0.54	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
10604	23638	37246	0.54	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
							q187c02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to TR:Q14498 Q14498 SPLICING FACTOR, [1], contains Alu repetitive element; contains element L1 repetitive element.
10634	23668	37278	1.04	4.0E-72	A1248796.1	EST_HUMAN	aa23f08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR.
11563	24618	38298	1.57	4.0E-72	AA465388.1	EST_HUMAN	aa23f09.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR.
11563	24618	38299	1.57	4.0E-72	AA465388.1	EST_HUMAN	aa23f09.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR.
11818	24807	38503	6.28	4.0E-72	H79421.1	EST_HUMAN	y128a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
11938	24924	38624	2.19	4.0E-72	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11938	24924	38625	2.19	4.0E-72	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11876	24961	38663	1.67	4.0E-72	T81910.1	EST_HUMAN	y128d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
12779	25521	32003	11.86	4.0E-72	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
21	13268	28259	0.7	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
926	14101		1.48	3.0E-72	AA723823.1	EST_HUMAN	ah63a08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310280 3'
1180	14343	27398	6.32	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1180	14343	27399	6.32	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1220	14381	27440	3.98	3.0E-72	U80228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1220	14381	27441	3.98	3.0E-72	U80228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1548	14700	27779	1.16	3.0E-72	BE242161.1	EST_HUMAN	TCAAPE1E1262 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAPE1252
3143	16319	28331	12.72	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3352	16524	28539	2.7	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3927	17086	30082	2.51	3.0E-72	S77589.1	NT	TOR V delta 2-C alpha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction) [Human, precursor B-cell line REH, mRNA Partial, 211 nt]
4867	17802	30789	3.17	3.0E-72	11416196	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4889	18019	31003	1.25	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4889	18019	31004	1.26	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5637	18831		1.12	3.0E-72	4759093	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6101	19281	32613	1.94	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6101	19281	32614	1.94	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6295	19468	32822	4.53	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6295	19468	32823	4.53	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6747	19503	33286	4.1	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
7758	20817	34307	2.01	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
8369	21450	34973	5.42	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
10646	23680	37280	1.09	3.0E-72	X98289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
12878	25453	32018	2.18	3.0E-72	AB011388.1	NT	Homo sapiens gene for AF-6, complete cds
6079	19281	32690	1.39	2.0E-72	11426971	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
8297	22373	35923	0.84	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9297	22373	35924	0.84	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
10978	24057	37691	5.46	2.0E-72	AA789277.1	EST_HUMAN	aj28609.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391809 3' similar to gb:X02067 H. sapiens mRNA for 7SL RNA pseudogene (HUMAN);
12772	25515	31999	3.39	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
2137	15273	26394	8.14	1.0E-72	AA848225.1	EST_HUMAN	aj83d02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'
5887	19075	32384	3.54	1.0E-72	7657678	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6889	19847	33237	1.22	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6889	19847	33238	1.22	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6769	25932	33319	1.29	1.0E-72	AV751818.1	EST_HUMAN	AV751818.NPD Homo sapiens cDNA clone NPDAIE11 5'
7815	20870	34386	3.5	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7815	20870	34387	3.5	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9790	22830	36408	7.37	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
9780	22830	36409	7.37	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1488	14641	27723	1.17	8.0E-73	AW374968.1	EST_HUMAN	VR0-GT0063-071099-002-h11 CT0063 Homo sapiens cDNA
6164	19340	32887	0.92	9.0E-73	11525863	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
11183	24292		24.49	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1063	14228	27265	0.73	8.0E-73	AW071755.1	EST_HUMAN	wa55c08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2501088 3' similar to TR:Q69050
5698	18892	32184	0.98	8.0E-73	4505798	NT	Q59050 HYPOTHETICAL PROTEIN MJ1656 ; Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6702	18860	33250	6.29	8.0E-73	11428469	NT	Homo sapiens lysozyme homolog (LOC57151), mRNA
8287	21369	34890	2.1	8.0E-73	AF113129.1	NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9553	22618	36188	4.35	8.0E-73	BE019900.1	EST_HUMAN	b662a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3090034 5' similar to gb:X04098_cds1 ACTIN, CYTOSOLIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9941	22980	36570	1.76	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9941	22980	36571	1.76	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10134	23172	36770	0.51	8.0E-73	X91940.1	NT	H. sapiens mRNA for WNT-88 protein
10834	23867	37490	0.47	8.0E-73	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNF1) mRNA
12001	24986	38690	1.49	8.0E-73	AF084520.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 mRNA, complete cds
12598	25403	32044	1.2	8.0E-73	AB002056.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12842	25580	31986	4.55	8.0E-73	11418169	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G2P1), mRNA
1157	14321	27378	1.61	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3373	16545	28559	0.7	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5059	18187		1.29	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
162	13387		3.04	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7323	20405	33867	3.42	6.0E-73	BE166574.1	EST_HUMAN	QV0-HT0494-020300-137-003 HT0494 Homo sapiens cDNA
5369	18571	31439	2.05	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM441), mRNA
1911	15054	28165	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1911	15054	28166	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
8837	18990	33398	0.73	3.0E-73	AA136403.1	EST_HUMAN	zn05604.e1 Stratagene field refseq 537202 Homo sapiens cDNA clone IMAGE:565950 3' similar to
8958	22037	35578	0.73	3.0E-73	AV729428.1	EST_HUMAN	gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8958	22037	35579	0.73	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAA071 5'
10927	24010		1.45	3.0E-73	X99860.1	NT	AV729428 HTC Homo sapiens cDNA clone HTCAA071 5'
11261	24330	37970	1.41	3.0E-73	BE711238.1	EST_HUMAN	H. sapiens SH3GLP2 pseudogene, 5' end
11261	24330	37971	1.41	3.0E-73	BE711238.1	EST_HUMAN	RC8-HT0678-280600-013-HT10 HT0678 Homo sapiens cDNA
11910	24897		1.82	3.0E-73	AI004040.1	EST_HUMAN	RC8-HT0678-280600-013-HT10 HT0678 Homo sapiens cDNA
13118	25730		3.04	3.0E-73	AL163246.2	NT	cd11402.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1625953 3'
13122	25732		2.05	3.0E-73	AW898081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
874	14050	27115	1.57	2.0E-73	AF139897.1	NT	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2000	15141		9.67	2.0E-73	AW898081.1	EST_HUMAN	Homo sapiens BAS1 (BAS1) mRNA, partial cds
2371	15502		1.49	2.0E-73	U01317.1	NT	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
3249	16423	29440	2.03	2.0E-73	4502582	NT	Human beta globin region on chromosome 11
							Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3840	18804	29816	0.68	2.0E-73	769539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3840	18804	29817	0.65	2.0E-73	769539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4555	17693		1.31	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6867	19729	33106	0.59	2.0E-73	AF086824.1	NT	Mus musculus rho/rao-interacting citron kinase (Crik) mRNA, complete cds
6867	19729	33107	0.59	2.0E-73	AF086824.1	NT	Mus musculus rho/rao-interacting citron kinase (Crik) mRNA, complete cds
6810	19770	33180	5.46	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6839	19892	33400	1.87	2.0E-73	AB046811.1	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6839	19892	33401	1.87	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7984	21033	34546	1.01	2.0E-73	M84048.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
9732	22797	36370	0.54	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9732	22797	36371	0.54	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10637	23671	37281	1.31	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10716	23748	37355	1.38	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10716	23748	37356	1.38	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
11308	24374	38017	2.91	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11308	24374	38018	2.91	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11339	24402	38051	1.44	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12599	15141		4.32	2.0E-73	AB028982.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0068 Homo sapiens cDNA
1824	14973	28068	3.52	1.0E-73	AW898081.1	EST_HUMAN	AU121565 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
6490	19658	33019	1.19	1.0E-73	AU121585.1	EST_HUMAN	(CM1-HT0282-111199-042-H10 HT0282 Homo sapiens cDNA
					BE151283.1	EST_HUMAN	cg61b07.r1 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:1839837 5' similar to contains element
						EST_HUMAN	MER22 repetitive element:
6699	22748	36318	1.22	1.0E-73	A1147427.1	EST_HUMAN	80127607F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
11736	23922	37547	3.74	1.0E-73	BE385477.1	EST_HUMAN	H sapiens mRNA for THIA
12045	25028	38731	1.34	9.0E-74	X77225.1	NT	H sapiens mRNA for THIA
12045	25028	38732	1.34	9.0E-74	X77225.1	NT	H sapiens mRNA for THIA
769	13940	26985	4.83	8.0E-74	4557428	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
8036	19219	32541	1.73	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3429 nt]
6036	19219	32542	1.73	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3429 nt]
2004	15144	28249	4.96	7.0E-74	AJ001869.1	NT	Homo sapiens NK2D gene, exon 10
3407	16577	29562	1.83	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8444	22560	36123	1.48	7.0E-74	BE867432.1	EST_HUMAN	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932897 5'
12841	25559	31985	4.73	7.0E-74	BE286305.1	EST_HUMAN	601181927F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3835855 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1146	14311	27368	3.65	6.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1658	14809	27893	1.03	6.0E-74	AW203177.1	EST_HUMAN	xm78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700836 3'
2390	15521	28649	15.92	6.0E-74	BE388250.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805453 5'
2390	15521	28650	15.52	6.0E-74	BE388250.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805453 5'
2927	16104	29119	0.97	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-0-U1.st NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2706965 3'
2927	16104	29120	0.97	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-0-U1.st NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2706965 3'
3805	16985	29968	1.22	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3805	16985	29969	1.22	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
6481	18680	31695	3.49	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
928	14103	27166	1.83	5.0E-74	AW020986.1	EST_HUMAN	df17c08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2767	15882		4.96	5.0E-74	AW362756.1	EST_HUMAN	PM0-CT0286-271069-001-h07 CT0286 Homo sapiens cDNA
5823	18720	31736	1.82	5.0E-74	11425477	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5910	18096	32413	12.5	5.0E-74	X69870.1	NT	Homo sapiens mRNA for TPCR16 protein
5961	19147	32462	8.1	5.0E-74	4507865	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6030	19213	32533	2.94	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6030	19213	32534	2.94	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7035	20171	33593	3.69	6.0E-74	7662263	NT	Homo sapiens KIAA0719 gene product (KIAA0719), mRNA
8226	21308	34828	2.33	5.0E-74	11345463	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10873	24053	37656	1.67	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10873	24053	37657	1.67	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
11090	24184	37801	1.36	5.0E-74	5729768	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
280	13507	26542	3.31	4.0E-74	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
875	14031	27116	10.3	4.0E-74	AB026942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
2018	15158	28262	3.07	4.0E-74	AB026938.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2018	15158	28263	3.07	4.0E-74	AB026938.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2134	15270	28390	9.98	4.0E-74	4508192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2134	15270	28391	9.98	4.0E-74	4508192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2201	15336	28463	1.32	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2498	15825	28745	1.16	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3160	16335	26346	6.22	4.0E-74	AJ009976.1	NT	Homo sapiens PLP gene
3916	16780	26795	1.1	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4174	17324	30315	1.29	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4679	17614	30802	1.89	4.0E-74	7662183	NT	Homo sapiens KIA0569 gene product (KIA0569), mRNA
4735	17870	30854	1.07	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5133	18258	31224	1.03	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
5185	18307	31271	1.12	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5185	18307	31272	1.12	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
8747	21826		3.53	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
8773	21852	36394	0.62	3.0E-74	5968912	NT	Homo sapiens actin-related protein 3-beta (ARPP3BETA), mRNA
9572	22714	36282	2.32	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #836205) Homo sapiens cDNA clone HICPF91
10546	23581	37191	2.16	3.0E-74	AA601493.1	EST_HUMAN	no17g05.st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
980	14153	27213	28.83	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
980	14153	27214	28.83	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1202	14964	27424	1.63	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1273	14430	27501	1.44	2.0E-74	AI950528.1	EST_HUMAN	wx51607.xt NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2647204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95, contains element MER22 repetitive element
1625	14777	27861	10.45	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1625	14777	27862	10.45	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2668	15789	28905	2.18	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.1.tumor2 Homo sapiens cDNA 3'
5119	18245	31210	2.52	2.0E-74	AL365092.1	NT	Novel human gene mapping to chromosome 22
5119	18245	31211	2.52	2.0E-74	AL365092.1	NT	Novel human gene mapping to chromosome 22
6919	25813	32419	1.88	2.0E-74	BE711134.1	EST_HUMAN	R05-HT0678-220600-011-C03 HT0678 Homo sapiens cDNA
6017	25816	32518	1.77	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6017	25816	32519	1.77	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6087	25816	32518	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6087	25816	32519	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7252	20335	33784	2.5	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
8126	21208	34728	1.8	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9582	22724	36294	5.27	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12526	25359		2.87	2.0E-74	AA186181.1	EST_HUMAN	z98a06.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
13169	26176		1.16	2.0E-74	BF002855.1	EST_HUMAN	7g5a08.x1 NC1_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309878 3'
54	13293	28308	1.3	1.0E-74	7857334	NT	Homo sapiens MissipenNIK-related kinase (MINK), mRNA
347	13558	26586	3.71	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA
512	13708	28734	1.8	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
519	13712	26739	2.59	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
614	13803	26823	1.28	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259), mRNA
804	13884	27036	0.86	1.0E-74	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
1024	14195	27253	2.26	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2301	15433	28566	6.03	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3209	16383	29394	2.82	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3460	16827	29646	1.29	1.0E-74	AA258549.1	EST_HUMAN	z60c01.r1 Soares_NhmMPu_S1 Homo sapiens cDNA clone IMAGE:667776 5'
3460	16827	29647	1.29	1.0E-74	AA258549.1	EST_HUMAN	z60c01.r1 Soares_NhmMPu_S1 Homo sapiens cDNA clone IMAGE:667776 5'
4031	17187	30197	0.84	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4031	17187	30198	0.84	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4075	17231	30237	5.41	1.0E-74	AL183268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4175	17325	30316	0.85	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-008 BT0642 Homo sapiens cDNA
4382	17525	30506	0.87	1.0E-74	BE467769.1	EST_HUMAN	hz73h08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:80511.12 CE:17351
6844	19597	33404	1.29	1.0E-74	M88914.1	NT	Human neurofibronin (NF1) gene, complete cds
7804	20860	34353	1.05	1.0E-74	11417877	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8248	21328	34844	1.27	1.0E-74	BE549105.1	EST_HUMAN	601070089F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456280 5'
8248	21328	34845	1.27	1.0E-74	BE549105.1	EST_HUMAN	601070089F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456280 5'
9005	22084	35627	7.81	1.0E-74	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8034	22113	35656	0.67	1.0E-74	BF331651.1	EST_HUMAN	MRO-HT0559-230500-021-003 HT0559 Homo sapiens cDNA
10445	23480	37086	0.69	1.0E-74	AJ281950.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10445	23480	37087	0.65	1.0E-74	AJ281950.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10696	23732	37337	1.77	1.0E-74	11420549	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
12154	25124	38826	1.94	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12238	25182		4.97	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12386	15433	28566	1.61	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12925	25610		1.38	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2709	15827		5.1	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12552	25375		3.07	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2395	15526	28554	1.25	6.0E-75	AB17415.1	EST_HUMAN	wk38a08.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:U141423_cds4
11780	24770	38466	1.39	6.0E-75	BE791831.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
9109	22188	35731	1.09	5.0E-75	BE272329.1	EST_HUMAN	6013586108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3640130 5'
9317	22353	35944	0.77	5.0E-75	AA132611.1	EST_HUMAN	601126068F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2989885 5'
9395	22470	36034	0.47	5.0E-75	BE591655.1	EST_HUMAN	2017608.11 Striatogene colon (#937204) Homo sapiens cDNA clone IMAGE:537174 5'
9395	22470	36035	0.47	5.0E-75	BE591655.1	EST_HUMAN	601349909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9573	22715	36283	1.1	5.0E-75	BF690254.1	EST_HUMAN	602188616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:3687458 5'
10439	23474	37078	2.64	5.0E-75	AB38623.1	EST_HUMAN	U31612.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:4298738 3'
115	13346	26373	2.1	4.0E-75	BE081333.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN;
471	13668		1.88	4.0E-75	N36757.1	EST_HUMAN	QV1-BT0632-210200-076-e02 BT0632 Homo sapiens cDNA
1805	14954	28048	1.08	4.0E-75	AW897230.1	EST_HUMAN	Y98080.1 Scars melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:269055 5'
2910	16088	29101	5.84	4.0E-75	BE409464.1	EST_HUMAN	CN0-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
5646	18840	32120	0.68	4.0E-75	11417948	NT	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
5646	18840	32121	0.68	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6399	19598	32029	5.18	4.0E-75	5579457	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6898	20048	33458	1.4	4.0E-75	11417948	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (EIF3S8), mRNA
6898	20048	33459	1.4	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10924	24007	37642	10.52	4.0E-75	7669506	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
1027	14198	27256	3.9	3.0E-75	AF157623.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1028	14198	27256	3.58	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1883	15027	28134	2.23	3.0E-75	AB011153.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2180	15315	28444	1.44	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2494	16621	28740	4.39	3.0E-75	4507334	NT	Homo sapiens synaptosomal-associated protein, 29KD (SNAP29) mRNA
3096	16362	29279	0.98	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3268	18432	29449	1.09	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3431	16599	29617	0.93	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3431	16599	29617	0.93	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3833	16993	29995	0.8	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4283	17428	30418	2.82	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
5365	18588	31434	1.15	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5365	18558	31435	1.15	3.0E-75	11420958	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6637	19796	33185	0.59	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6637	19796	33186	0.59	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6809	20224	33654	1.57	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6809	20224	33655	1.57	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7285	20368	33821	4.12	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7285	20368	33822	4.12	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7800	20896	34346	2.66	3.0E-75	485632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7800	20896	34347	2.66	3.0E-75	485632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
9185	22263	35805	1.33	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNA1), mRNA
9880	22920	36504	0.83	3.0E-75	11420222	NT	Homo sapiens Drosophila Kech like protein (DKEICH), mRNA
5790	18882		1.34	2.0E-75	AV734930.1	EST_HUMAN	AV734930 cDNA Homo sapiens cDNA clone cA8ED02 5'
8950	22029	35570	1.36	2.0E-75	AI011783.1	EST_HUMAN	q091e02.x1 NCI_CGAP_Ki45 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q66386 Q66386 POL/ENV GENE:
2377	15508	28635	10.98	1.0E-75	AW168135.1	EST_HUMAN	xg60d02.x1 NCI_CGAP_Utk Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.1f
3012	16188	29213	2.95	1.0E-75	X52221.1	NT	PTR7 repetitive element:
7762	20821	34311	0.64	1.0E-75	BE082528.1	EST_HUMAN	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
7762	20821	34312	0.64	1.0E-75	BE082528.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
9609	21889		3.12	1.0E-75	AA399270.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
9628	22883	36253	3.95	1.0E-75	BF313845.1	EST_HUMAN	z157h03.s1 Soares, tests_NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:U13932.40S
9628	22883	36254	3.95	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN):
11122	24194		6.88	1.0E-75	AA884377.1	EST_HUMAN	601800284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
11351	24413	36067	2.22	1.0E-75	AF223391.1	NT	601800284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
12440	18502	31938	1.97	1.0E-75	BE894182.1	EST_HUMAN	601800284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
45	13284	26282	0.89	9.0E-76	AI652548.1	EST_HUMAN	ac77b08.s1 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:868599 3'
45	13284	26293	0.89	9.0E-76	AI652548.1	EST_HUMAN	ac77b08.s1 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:868599 3'
2486	15613		0.94	9.0E-76	AA702415.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
							w630b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
							TRAP1:
							w630b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
							TRAP1:
							z185b07.s1 Soares, fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10105	23143	36741	5.44	9.0E-76	M12937.1	NT	Human ferritin Heavy subunit mRNA, complete cds
961	14134	27184	1.18	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
961	14134	27185	1.18	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2976	16152	29173	0.95	8.0E-76	7708724	NT	Homo sapiens mediator (Sur2), mRNA
6300	19473	32828	5.84	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7658	20725	34200	1.17	8.0E-76	11435215	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
7798	20800	34289	1.05	8.0E-76	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8492	21573	35110	0.69	8.0E-76	11418961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
10589	23624	37231	1.26	8.0E-76	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
10603	23987	37610	4.29	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 8 (BIRC8), mRNA
12824	25500		2.51	8.0E-76	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0930), mRNA
797	13976	27029	1.89	7.0E-76	6016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3366	16638	29651	3.84	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3372	16544	29658	9.08	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4491	17631	30612	5.52	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4491	17631	30613	5.52	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1282	14419		37.29	6.0E-76	BE396253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3656757 5'
11753	23939	37865	2.52	6.0E-76	BE279201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1997	15138	28243	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1997	15138	28243	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1997	15138	28245	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3278	16452	29473	0.64	4.0E-76	BE814096.1	EST_HUMAN	QV3-BN0047-270700-283-g06 BN0047 Homo sapiens cDNA
5384	18598	31455	1.13	4.0E-76	BE783412.1	EST_HUMAN	601471723F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
10230	23285	36854	5.48	4.0E-76	D81928.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujivara) Homo sapiens cDNA clone GEN-178G01 5'
10230	23285	36855	5.48	4.0E-76	D81928.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujivara) Homo sapiens cDNA clone IMAGE:3083862 3'
646	13831	26856	2.01	3.0E-76	BF516282.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
646	13831	26857	2.01	3.0E-76	BF516282.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1629	14781	27866	8.04	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1629	14781	27867	8.04	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3515	16681	28691	5.75	3.0E-76	BF376689.1	EST_HUMAN	RC5-ST0300-180700-033-A03 ST0300 Homo sapiens cDNA
3515	16681	28692	5.75	3.0E-76	BF376689.1	EST_HUMAN	RC5-ST0300-180700-033-A03 ST0300 Homo sapiens cDNA
5352	18480	38822	1.82	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zad04 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5851	19041	32347	0.92	3.0E-76	AA160611.1	EST_HUMAN	z079c07.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592524 5' similar to gb:L32976 MIXED LINEAGE KINASE 1 (HUMAN);
6110	19290	32625	0.61	3.0E-76	AW027705.1	EST_HUMAN	w75c05.x1 Soares_thymus_NHIFTh Homo sapiens cDNA clone IMAGE:2935368 3'
6498	19634	33027	8.19	3.0E-76	AF286698.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
8344	21425	34951	1.27	3.0E-76	N42671.1	EST_HUMAN	y20g10.r1 Soares_melanocyte 2NpHM Homo sapiens cDNA clone IMAGE:271842 5'
9917	22957	36544	3.03	3.0E-76	AW290353.1	EST_HUMAN	z054d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:273009 3'
9942	22981	36572	1.08	3.0E-76	AA442309.1	EST_HUMAN	z054d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
9942	22981	36573	1.08	3.0E-76	AA442309.1	EST_HUMAN	z054d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
12144	26943	31763	2.1	3.0E-76	AW967984.1	EST_HUMAN	EST360059 MAGe resequences, MAG. Homo sapiens cDNA
12251	28184	31542	6.95	3.0E-76	AW956455.1	EST_HUMAN	EST360059 MAGe resequences, MAGD Homo sapiens cDNA
292	13509	26544	1.11	2.0E-76	D84296.1	NT	Human mRNA for possible protein TPRDII, complete cds
352	13563	26590	3.21	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
362	13563	26591	3.21	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
473	13668		0.96	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
603	13792	26812	1.07	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1056	14222	27281	1.60	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1568	14719	27799	11.31	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1568	14719	27800	11.31	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1982	15126	28227	0.99	2.0E-76	AA253964.1	EST_HUMAN	z050h11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2504	16082	29097	2.13	2.0E-76	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3369	16341	29555	2.21	2.0E-76	AA445992.1	EST_HUMAN	z064e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:760986 3' similar to SW:ITB6_HUMAN
3369	16341	29556	2.21	2.0E-76	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3665	16730	29746	0.93	2.0E-76	A821149.1	EST_HUMAN	z064e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:760986 3' similar to SW:ITB6_HUMAN
4254	13509	26544	1.01	2.0E-76	D84295.1	NT	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
4683	17789	30773	0.91	2.0E-76	AL163283.2	EST_HUMAN	ac83b02.y6 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:O14591
5062	18190	31165	11.15	2.0E-76	AW875618.1	EST_HUMAN	O14591 SIMILARITY TO P22059 ;
5163	18285	31249	3.13	2.0E-76	5174568	NT	Human mRNA for possible protein TPRDII, complete cds
5424	18625		2.99	2.0E-76	AF127845.1	NT	Homo sapiens chromosome 21 segment HS21C083
5736	18929	32226	4.83	2.0E-76	AB029004.1	NT	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
7570	20842	34119	0.66	2.0E-76	11421326	NT	Human sapiens murine retrovirus integration site 1 homolog (MRV1) mRNA
7582	20863	34139	0.69	2.0E-76	11426908	NT	Gonilla gorilla olfactory receptor (GGO18) gene, partial cds
							Homo sapiens mRNA for KIAA1081 protein, partial cds
							Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
							Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7840	20895	34397	1.82	2.0E-78	11427410	NT	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA
10499	23924	37134	1.42	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63150), mRNA
11161	24232	37662	2.44	2.0E-76	7548807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA
4412	17554	30539	2.49	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4412	17554	30540	2.49	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5584	18761	31801	5.93	1.0E-76	BE766537.1	EST_HUMAN	G0158896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8374	19543	31801	0.7	1.0E-76	AA33207.1	EST_HUMAN	ES137301 Embryo, 8 week 1 Homo sapiens cDNA 5' end
7083	20116	33530	4.56	9.0E-77	BE889525.1	EST_HUMAN	G0151243F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
13003	25652		1.98	9.0E-77	BE410354.1	EST_HUMAN	G01302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
192	13414	26443	0.77	8.0E-77	R83144.1	EST_HUMAN	yp11h02.r1 Soares breast 3NHBat Homo sapiens cDNA clone IMAGE:187155 5' similar to SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1;
4844	17780	30762	1.41	8.0E-77	BF205181.1	EST_HUMAN	G01866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109803 5'
5569	18766	31807	1.37	8.0E-77	4506230	NT	(Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mow34 homolog) (PSMD7) mRNA
11669	24746	38438	1.78	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11669	24746	38439	1.78	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
12979	25637	31982	32.5	8.0E-77	R00245.1	EST_HUMAN	ye69f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MIER10 repetitive element;
1093	15126	28228	2.2	7.0E-77	AA625755.1	EST_HUMAN	z091g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2482	15609	28733	2.78	7.0E-77	4503944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2482	15609	28734	2.78	7.0E-77	4503944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
273	13491	26522	4	6.0E-77	4504600	NT	Homo sapiens Interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1165	14329	27384	1.05	6.0E-77	AW957753.1	EST_HUMAN	EST368823 MAGE resequences, MAGE Homo sapiens cDNA
1574	14727	27808	3.29	6.0E-77	AI204066.1	EST_HUMAN	qe77h12.x1 Soares_fetal_lung_NHHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1284	14421	27486	2.89	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1391	14545	27821	3.46	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2749	15866	28977	1.75	5.0E-77	AF162666.1	NT	Homo sapiens tissue-like kinase 1 (TLK1) mRNA, complete cds
2822	15836	29046	1.58	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3611	16775	29791	0.65	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4825	17958	30944	0.97	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4825	17958	30945	0.97	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
5052	18180	31156	3.57	5.0E-77	AL043963.1	EST_HUMAN	DKFZp434G1728.J1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G1728 5'
6922	20237	33871	0.65	5.0E-77	MT13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7480	20555	34027	0.59	5.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase

Table 4

Single Exon Probes Expressed in Placenta

Probe, SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7767	20555	34027	0.72	5.0E-77	X98286.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8563	21644	35183	1.21	5.0E-77	11428549	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8563	21644	35184	1.21	5.0E-77	11428549	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8769	22765	36335	2.61	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9768	22765	36336	2.61	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10708	23741	37346	0.97	5.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
10708	23741	37347	0.97	5.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
2028	15170	28277	1.39	3.0E-77	5730038	NT	Homo sapiens SET domain and mafinr transposase fusion gene (SETMAR) mRNA
2028	15170	28278	1.39	3.0E-77	5730038	NT	Homo sapiens SET domain and mafinr transposase fusion gene (SETMAR) mRNA
10496	23531	37139	0.9	3.0E-77	H65167.1	EST_HUMAN	yu64g01.1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10496	23531	37140	0.9	3.0E-77	H65167.1	EST_HUMAN	yu64g01.1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
11115	24187	37819	2.83	3.0E-77	BF35917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1383	14538	27612	1.74	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBT10 5'
1464	14618	27702	9.74	2.0E-77	AW98712.1	EST_HUMAN	RC3-BN0053-170200-011-401 BN0053 Homo sapiens cDNA
2157	15283	28419	1.1	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2170	15305	28432	2.75	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2659	16087	28895	1.89	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2659	16087	28896	1.89	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4143	17295	30287	1.98	2.0E-77	BE044316.1	EST_HUMAN	h043p05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4534	17672	30856	0.87	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL CGAP_Bms52 Homo sapiens cDNA clone IMAGE:2280466 3' similar to TR:O65245
4534	17672	30857	0.87	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL CGAP_Bms52 Homo sapiens cDNA clone IMAGE:2280466 3' similar to TR:O65245
4534	17672	30857	0.87	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL CGAP_Bms52 Homo sapiens cDNA clone IMAGE:2280466 3' similar to TR:O65245
4891	18021	31006	2.34	2.0E-77	AA653025.1	EST_HUMAN	ns88g12.s1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47814 50S RIBOSOMAL PROTEIN L29. [1] contains element MSRI repetitive element ;
6075	19257	32586	2.08	2.0E-77	BE288940.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028436 5'
6301	19474	32829	1.86	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878605 5'
7325	20407	33869	15.02	2.0E-77	AI833003.1	EST_HUMAN	ai74d09.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151. [1] ;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8726	21806	35343	0.88	2.0E-77	A1362707.1	EST_HUMAN	qy70c09.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F29D11.1
9728	22783	36366	5.83	2.0E-77	U50321.1	NT	CE05765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN;
9728	22783	36367	5.88	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10109	23236	36825	0.47	2.0E-77	BF310349.1	EST_HUMAN	601895183FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
10109	23236	36826	0.47	2.0E-77	BF310349.1	EST_HUMAN	601895183FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
44	13282	26288	2.62	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
44	13282	26289	2.62	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
283	13301	26533	1.68	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
283	13301	26534	1.68	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	16025	27140	3.4	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	16025	27141	3.4	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1969	15112	28213	1.36	1.0E-77	AW058119.1	EST_HUMAN	w83e05.x1 Soares_thymus_NHFFt Homo sapiens cDNA clone IMAGE:2536160 3'
2516	15641	28763	1.17	1.0E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3110	16286	29300	2.28	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4473	17613	30862	4.24	1.0E-77	7706289	NT	Homo sapiens CGI-50 protein (LOC51628), mRNA
4646	17782	30764	22.17	1.0E-77	AJ229041.1	NT	Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
4774	17909	30862	2.05	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4816	17948	30933	0.61	1.0E-77	A1273014.1	EST_HUMAN	qy09g04.x1 NCL CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1681110 3'
6051	19233	32557	1.48	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6051	19233	32558	1.48	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6172	19348	32694	1.72	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6577	19739	33120	1.1	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7198	20093	33473	15.97	1.0E-77	6881412	NT	Homo sapiens elastin (supraclavicular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7644	20699	34402	0.82	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
7940	20980	34500	0.71	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9465	22522	36085	0.83	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
9465	22522	36086	0.83	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10742	23775	37387	1.05	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10742	23775	37388	1.05	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10773	23806	37429	2.76	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280999-011-505 CT0254 Homo sapiens cDNA
6576	16738	33118	2.29	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-005 ET0023 Homo sapiens cDNA
6676	16738	33110	2.29	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-005 ET0023 Homo sapiens cDNA
89	13323	26351	1.66	6.0E-78	AU118788.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
88	13323	26352	1.66	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3389	16559	29574	0.9	6.0E-78	BF344101.1	EST_HUMAN	602016028F1 NC1 CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4192511 5'
6690	19848		2.54	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
224	13446	26474	6.13	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2929	15752	28987	5.71	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP.Y48B6A.6
3472	10639	29659	5.09	5.0E-78	M85986.1	NT	CE22121 ;
5528	18726	31741	2.73	5.0E-78	AF038536.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5993	18887	32177	18.13	6.0E-78	11416585	NT	Homo sapiens Beaf's macular dystrophy related protein mRNA, partial cds
7304	20386	33846	2.18	5.0E-78	AW953120.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB), mRNA
9284	22360	35910	7.02	5.0E-78	U60899.1	NT	Homo sapiens MAGS, MAGB Homo sapiens cDNA
9285	22361	35911	2.94	5.0E-78	BE960836.1	EST_HUMAN	Human lysosomal alpha-mannosidase (manib) gene, exon 7
1160	14924	27379	1.29	4.0E-78	AL043314.2	EST_HUMAN	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1547	14699	27778	1.81	4.0E-78	AL355841.1	NT	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
2392	15523	28952	5.1	4.0E-78	AF107403.1	NT	Novel human gene mapping to chromosome 22
4442	17582	30560	6.17	4.0E-78	7656876	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4896	18026	31012	1.2	4.0E-78	4503808	NT	Homo sapiens synovial (LOC30816), mRNA
4896	18026	31013	1.2	4.0E-78	4503808	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5888	19078	32385	1.25	4.0E-78	11420732	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
6302	19475	32830	0.71	4.0E-78	7662109	NT	Homo sapiens SFRS3 protein kinase 2 (SRPK2), mRNA
6302	19475	32831	0.71	4.0E-78	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
6703	19861	33251	0.74	4.0E-78	4508736	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
7690	20727	34203	0.69	4.0E-78	4508736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9054	22133	35677	1.15	4.0E-78	AF012872.1	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9054	22133	35678	1.15	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9568	22710	36278	0.61	4.0E-78	11417251	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
10650	23694	37303	1.95	4.0E-78	11560151	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10680	23694	37304	1.95	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11705	24702	38994	1.84	4.0E-78	AF169148.1	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
							Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11854	24842	38538	6.72	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12855	25568	31981	3.83	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-5, complete cds
1465	13390	28417	1.89	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
165	13390	28418	1.89	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
2488	15615	28736	1.01	3.0E-78	7705705	NT	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
3860	17020		0.81	3.0E-78	AU140804.1	EST_HUMAN	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
3918	17077	30074	0.78	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4221	17077	30074	0.82	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
10493	23528		5.44	3.0E-78	BE144758.1	EST_HUMAN	GM0-HT0180-041099-085-c07 HT0180 Homo sapiens cDNA
11227	24286	37937	2.5	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-180200-114-q09 HT0367 Homo sapiens cDNA
3191	16366		2.49	2.0E-78	U04499.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4122	17276		1.69	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
7631	20700	34177	1.09	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-seg-g-10-0-UL-1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7031	20700	34178	1.09	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-seg-g-10-0-UL-1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7908	20860	34466	3.36	2.0E-78	BF689800.1	EST_HUMAN	G02186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
8230	21312	34832	2.49	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
8948	21726	35292	1.72	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8648	21726	35293	1.72	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
11336	24399	38048	9.58	2.0E-78	AI197837.1	EST_HUMAN	q150h05.x1 NCJ CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1858861 3' similar to WP:R90.1
11358	24420		1.47	2.0E-78	BE439409.1	EST_HUMAN	CE06325 PROTEIN KINASE ;
11386	24447	38108	3.01	2.0E-78	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
8420	18621	31597	3.16	1.0E-78	11417304	NT	z44812.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
7094	18521	31514	0.82	1.0E-78	AV648699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC87306), mRNA
8553	21434		1.81	1.0E-78	U52373.1	NT	AV648699 GLC Homo sapiens cDNA clone GLOBMCD1 3'
12324	25234	32107	1.83	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
12422	25299	32086	2.44	1.0E-78	11435603	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4820	17953	30638	4.04	9.0E-79	11525391	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC83140), mRNA
4896	18115	31093	1.6	9.0E-79	BE008837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
5549	18746	31781	16.88	9.0E-79	AB028070.1	NT	RC2-BN0074-000300-014-c12 BN0074 Homo sapiens cDNA
6470	19637	32996	2.52	9.0E-79	6454145	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6752	19808	33301	0.98	9.0E-79	11430822	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
							Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7505	25848		0.99	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7748	20808	34298	0.63	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-DBA (H_GS166L15.1), mRNA
7748	20808	34299	0.63	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-DBA (H_GS166L15.1), mRNA
8541	21622	35158	0.52	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8541	21622	35159	0.52	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9263	22340	35880	4.78	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9263	22340	35891	4.78	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9580	22722	36292	0.66	9.0E-79	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10574	23609	37214	0.82	9.0E-79	11438643	NT	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA
10632	23666	37274	1.05	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216), mRNA, complete cds
10632	23666	37275	1.05	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216), mRNA, complete cds
11323	24385	38029	1.61	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated Ikk activator 1 beta Uev1A mRNA, complete cds
11802	24792	39489	2.94	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
11802	24792	39490	2.94	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
13088	26711	31967	1.4	9.0E-79	11417677	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3836	16996	28998	1.18	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3326	16498	29516	6.36	7.0E-79	BE619648.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
8844	21923		0.62	6.0E-79	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
12169	25132		5.44	6.0E-79	AA699829.1	EST_HUMAN	204604.81 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to
11786	24776	38473	3.63	5.0E-79	AL163262.2	NT	TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
323	13637	26569	1.74	3.0E-79	AF114488.1	NT	Homo sapiens chromosome 21 segment HS21C082
1001	14172	27233	1.22	3.0E-79	AF232708.1	NT	Homo sapiens interocotin short isoform (ITSN) mRNA, complete cds
3188	16343	29351	1.74	3.0E-79	U09410.1	NT	Homo sapiens cell-line tsA201 a chloride ion current inducer protein (Cln) gene, complete cds
5477	18676	31689	7.05	3.0E-79	AF110322.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5841	19031	32337	1.69	3.0E-79	AB020699.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5866	19056	32363	0.93	3.0E-79	BE789470.1	EST_HUMAN	Homo sapiens mRNA for KIAA0882 protein, partial cds
5866	19056	32364	0.93	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3894554 5'
5889	19077	32386	3.87	3.0E-79	11426770	NT	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3894554 5'
5889	19077	32387	3.87	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6894	20036	33445	0.84	3.0E-79	BE256993.1	EST_HUMAN	Homo sapiens netrin 1 (NTN1), mRNA
7206	20071	33481	2.58	3.0E-79	AB014520.1	NT	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7206	20071	33482	2.58	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8012	21062	34574	0.87	3.0E-79	6912455	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
							Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8358	21439	34961	0.78	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
9003	22658	36230	0.89	3.0E-79	10935036	NT	Homo sapiens tetrafricopeptide repeat domain 3 (TTC3), mRNA
10555	23590		0.62	3.0E-79	AY696115.1	EST_HUMAN	AV699115 GKc Homo sapiens cDNA clone GKCAHE11.5'
298	13515		1.4	2.0E-79	H63129.1	EST_HUMAN	y48003.s1 Soares fetal liver spleen 'NfLS Homo sapiens cDNA clone IMAGE:208541.3'
651	13837	26864	1.05	2.0E-79	BE379926.1	EST_HUMAN	601159415P2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107.5'
951	14124	27186	1.14	2.0E-79	475784.1	NT	Homo sapiens BCL2-like 2 (BCL2L2), mRNA
1007	14178	27239	4.97	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1007	14178	27240	4.97	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1080	14226		2.15	2.0E-79	A1623747.1	EST_HUMAN	th18107.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:2118685.3'
2215	15349	28478	8.17	2.0E-79	4585963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2216	15349	28479	6.17	2.0E-79	4585963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2266	15399	28527	1.35	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2387	15516	28648	1.1	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2780	15996	29008	1.2	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds
4023	17179	30188	0.69	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLC4 (GIC4) mRNA, complete cds
4280	17425	30414	1.25	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4813	17948	30931	0.83	2.0E-79	AJ163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
5788	18980		1.06	2.0E-79	AA312223.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
5844	19034	32340	0.9	2.0E-79	11181769	NT	EST182928 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
6373	19542	32901	1.19	2.0E-79	AB020637.1	NT	Homo sapiens X transporter protein 3 (XTP3), mRNA
7100	18527	31519	0.89	2.0E-79	AF283613.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7317	20399	33861	2.09	2.0E-79	7382479	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7317	20398	33862	2.09	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 4, mRNA
8282	21374	34894	1.1	2.0E-79	4506442	NT	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 4, mRNA
8714	21794	35331	2.13	2.0E-79	11427428	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8965	22044	35987	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ11009 (FLJ11009), mRNA
8965	22044	35593	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9205	22283	35923	0.69	2.0E-79	11432184	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
10297	23332	36935	1.98	2.0E-79	S72869.1	NT	Homo sapiens hypothetical protein FLJ20276 (FLJ20276), mRNA
10297	23332	36936	1.98	2.0E-79	S72869.1	NT	Homo sapiens similar to A1Pase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-8 (H. sapiens) (LOC83991), mRNA
10297	23332	36938	1.98	2.0E-79	S72869.1	NT	associated protein M8-8 (H. sapiens) (LOC83991), mRNA
10297	23332	36938	1.98	2.0E-79	S72869.1	NT	H4(D105170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
1284	24350	37987	2.94	2.0E-79	BE094386.1	EST_HUMAN	H4(D105170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
							RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11284	24350	37988	2.94	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
12208	19498	31534	4.27	2.0E-78	7682357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12208	25219	32100	2.3	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12531	25362	32067	3.08	2.0E-78	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6718	25830		3.28	1.0E-79	BF363071.1	EST_HUMAN	MRD-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA
6833	19866	33394	0.65	1.0E-79	AI613480.1	EST_HUMAN	Y937e03.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
6833	19866	33395	0.65	1.0E-79	AI613480.1	EST_HUMAN	Y937e03.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
8438	21520	35049	0.9	1.0E-79	BE394211.1	EST_HUMAN	TEKTIN C1.1
11922	24908	38609	1.9	1.0E-79	BF087405.1	EST_HUMAN	TEKTIN C1.1
12329	25107	29309	1.44	1.0E-79	AI460115.1	EST_HUMAN	QV2-HT0840-120900-358-a05 HT0540 Homo sapiens cDNA
3215	16389	28400	6.95	9.0E-80	AA725848.1	EST_HUMAN	ar78a04.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
3215	16389	28400	6.95	9.0E-80	AA725848.1	EST_HUMAN	ar78a04.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
10217	29263	36842	1.3	9.0E-80	BE788603.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
11554	24609	38288	7.63	9.0E-80	11433924	NT	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
11554	24609	38289	7.63	9.0E-80	11433924	NT	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3691	16853		1.01	8.0E-80	U94387.1	NT	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
7780	20839	34328	2.82	8.0E-80	11422647	NT	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
7780	20836	34329	2.82	8.0E-80	11422647	NT	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
9802	22957	36228	2.2	8.0E-80	6005921	NT	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
9802	22957	36229	2.2	8.0E-80	6005921	NT	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
7114	18540	31497	0.61	7.0E-80	AF127882.1	NT	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
923	14098	27162	0.74	6.0E-80	AI422197.1	EST_HUMAN	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
1675	14827	27910	2.41	6.0E-80	U64998.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
2372	15603	28628	1.14	6.0E-80	6631094	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
2372	15603	28629	1.14	6.0E-80	6631094	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
5922	19109	32422	1.46	6.0E-80	11421462	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
6200	19375	32726	3.35	6.0E-80	AJ404488.1	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
							Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
							Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
							Callithrix jacchus diffractory receptor (CJAB0) gene, partial cds
							Q16795 NADHUBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
							Homo sapiens NRD convertase mRNA, complete cds
							Homo sapiens minichromosome maintenance deficient 3 (MCM3), mRNA
							Homo sapiens minichromosome maintenance deficient 3 (MCM3), mRNA
							Homo sapiens minichromosome maintenance deficient 3 (MCM3), mRNA
							Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
							Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6358	19528	32886	4.07	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6402	19571		1.08	6.0E-80	7862393	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
6452	19519	32982	0.92	6.0E-80	M18533.1	NT	Homo sapiens dystrophin (DMD), mRNA, complete cds
6024	22103	35643	3.4	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9024	22103	35644	3.4	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9221	22289	36842	1.57	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C010
9559	22824	36196	0.96	6.0E-80	AF161495.1	NT	Homo sapiens HSPC146 mRNA, complete cds
10085	23103	36708	1.83	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
11183	24252	37687	2	6.0E-80	11427366	NT	Human cdc37-related A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11499	24566	38231	20.85	6.0E-80	AF228730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
12053	25034	38740	1.48	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
12176	14088	27162	1.75	6.0E-80	AI422197.1	EST_HUMAN	158402.x1 NCL_GAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ; Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12309	25972		2	6.0E-80	AF240786.1	NT	Homo sapiens CST gene for cerebroside sulfolipase, exon 1, 2, 3, 4, 5
12512	25351		3.32	6.0E-80	AB025900.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
13081	28115		2.69	6.0E-80	AI133127.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
601	15790	26811	1.7	5.0E-80	4506228	NT	Homo sapiens serine-threonine protein kinase (MNBI) mRNA, complete cds
868	14035	27097	1.89	5.0E-80	AF108890.1	NT	Homo sapiens serine-threonine protein kinase (MNBI) mRNA, complete cds
858	14035	27098	1.89	5.0E-80	AF108890.1	NT	Homo sapiens serine-threonine protein kinase (MNBI) mRNA, complete cds
1218	14377		1.49	5.0E-80	X91847.1	NT	H-sapiens next1 gene (exon 12)
1485	14638		2.69	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2801	15628	28748	3.51	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2865	15969	29078	1.78	5.0E-80	AB019038.1	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4150	17302	30295	0.9	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1.4 mannosyltransferase, complete cds
4150	17302	30296	0.9	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1.4 mannosyltransferase, complete cds
5088	18195	31170	1.23	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C068
8552	21633	35170	1.28	5.0E-80	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9458	22574	36140	5.03	4.0E-80	F26915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
223	13445		6.03	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5028	18157		2.3	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA 0023612.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1687064 3' similar to TR:Q35780 Q38790 PIG-L ;
5941	19127	32440	1.78	3.0E-80	AI081675.1	EST_HUMAN	

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1841	14987	28087	4.85	2.0E-80	R35321.1	EST_HUMAN	y95608.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38080 5'
1908	15031	28163	1.57	2.0E-80	A144821.1	EST_HUMAN	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2116	15283	28372	7.03	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323.t1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434D1323 5'
6844	20257	33696	0.95	2.0E-80	AA582852.1	EST_HUMAN	nm80001.s1 NCL CGAP_C69 Homo sapiens cDNA clone IMAGE:1090177 3'
7053	20106	33522	1.89	2.0E-80	11421930	NT	Homo sapiens Gdgl transport complex protein (90 kDa) (GTC60), mRNA
7401	20479	33947	0.89	2.0E-80	T75215.1	EST_HUMAN	yc86112.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to
8360	22435	35994	1.21	2.0E-80	AW694270.1	EST_HUMAN	SP-K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B :
8970	23089	36603	0.99	2.0E-80	AJ007378.1	NT	EST376343 MAGE resequencing, MAGH Homo sapiens cDNA
11108	24181	37815	6.84	2.0E-80	AA393362.1	EST_HUMAN	Homo sapiens GGT gene, exon 6
350	13561		1.52	1.0E-80	AL163303.2	NT	z70712.t1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
822	14001	27055	1.3	1.0E-80	AF231620.1	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
2009	15149		2.42	1.0E-80	AI732656.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4583	17720	30703	0.85	1.0E-80	AF077188.1	NT	Homo sapiens chromosome 21 unknown mRNA
5343	18456		3.32	1.0E-80	Y13932.1	NT	nm0112.x5 NCL CGAP_C69 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR
5442	18642		5.25	1.0E-80	BE386615.1	EST_HUMAN	repetitive element ;
6083	19274	32603	6.12	1.0E-80	L10347.1	NT	Homo sapiens PRKY exon 7
6827	19787	33175	1.17	1.0E-80	5174540	NT	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
7356	20435	33897	1.18	1.0E-80	AJ224172.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7747	20807	34298	8.03	1.0E-80	A1948731.1	EST_HUMAN	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial
7747	20807	34287	8.03	1.0E-80	A1948731.1	EST_HUMAN	protein, mRNA
8426	21607	35039	0.67	1.0E-80	11421211	NT	Homo sapiens mRNA for lipophilin B
8897	21978	35514	0.78	1.0E-80	11421211	NT	wq25605.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472298 3'
8897	21978	35515	0.76	1.0E-80	AF245219.1	NT	wq25605.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472298 3'
9485	22542	36104	1.17	1.0E-80	AF245219.1	NT	wq25605.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472298 3'
9485	22542	36105	1.17	1.0E-80	AF245219.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
10640	23674	37284	0.7	1.0E-80	D63478.2	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
10887	23871	37601	4.8	1.0E-80	11641276	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
10887	23871	37602	4.9	1.0E-80	11641276	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
12593	25399	32042	1.32	1.0E-80	11417901	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
12682	25573		1.28	1.0E-80	AB011398.1	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
							Homo sapiens similar to rat myomegalin (LOC64182), mRNA
							Homo sapiens similar to rat myomegalin (LOC64182), mRNA
							Homo sapiens meningo (disrupted in balanced translocation) 1 (MNT), mRNA
							Homo sapiens gene for AF-6, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10923	24006	37840	1.93	8.0E-81	AI251752.1	EST_HUMAN	qh90g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854295 3'
10923	24006	37841	1.93	8.0E-81	AI251752.1	EST_HUMAN	qh90g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854295 3'
11422	24483	38147	6.99	8.0E-81	BE394525.1	EST_HUMAN	60131053F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
							ze21d10.r1 Soares_fetal_heart_NbHL19W Homo sapiens cDNA clone IMAGE:359835 5' similar to SW:KRHA_RABIT_Q02957 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1] contains element MER22 repetitive element:
2280	15412	28543	0.94	7.0E-81	AA011080.1	EST_HUMAN	zab9c08.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289918 3'
7402	20480	33948	3.69	7.0E-81	AI822115.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4506	17845	30632	3.73	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4506	17845	30633	3.73	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5397	18599	31569	2.28	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5397	18599	31570	2.28	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
9437	22511	36076	1.24	6.0E-81	AA360017.1	EST_HUMAN	EST16128 Fetal Lung II Homo sapiens cDNA 5' end
12747	25495	32030	3.38	6.0E-81	BF678022.1	EST_HUMAN	602153686F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
12747	25495	32031	3.38	6.0E-81	BF678022.1	EST_HUMAN	602153686F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2291	15423	28557	2.98	5.0E-81	BE268042.1	EST_HUMAN	601125503F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8607	21688	35226	3.06	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8607	21688	35227	3.06	5.0E-81	AB007923.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9848	22888	36467	1.25	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9848	22888	36468	1.25	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11883	24871	38568	1.76	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
							h60et2.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
720	13902	28943	0.84	4.0E-81	AI521435.1	EST_HUMAN	h60et2.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
1887	15013	28121	1.54	4.0E-81	AW779612.1	EST_HUMAN	h60et2.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
3239	16413	29428	3.91	4.0E-81	AB037768.1	NT	P53820 COATOMER GAMMA SUBUNIT
							Homo sapiens mRNA for KIAA1345 protein, partial cds
3718	16879	29884	0.89	4.0E-81	AW004608.1	EST_HUMAN	ws90j03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:Q43815 Q43815
4276	17421	30406	2.84	4.0E-81	AF263306.1	NT	STRIATIN;
4276	17421	30409	2.84	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
							Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7427	20504	33974	0.91	4.0E-81	4757893	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2) mRNA
7559	20631	34106	0.59	4.0E-81	11420544	NT	Homo sapiens ets variant gene 1 (ETV1), mRNA
8482	21563	35098	2.36	4.0E-81	X06989.1	NT	Human mRNA for amyloid A4(761) protein
8742	21821	35355	2.2	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8742	21821	35356	2.2	4.0E-81	U20187.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3
9427	22601	36067	3.35	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10306	23341	36946	1.4	4.0E-81	11425281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10374	23409	37018	0.65	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
10374	23409	37019	0.65	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11461	24520	38189	4.74	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B), mRNA
11461	24520	38190	4.74	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B), mRNA
12200	26039	31682	8.38	4.0E-81	11417682	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12200	26039	31683	8.38	4.0E-81	11417682	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12766	25332	32009	1.63	4.0E-81	11417671	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12766	25332	32010	1.63	4.0E-81	11417671	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12856	25823	31978	4.21	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1286	14452	27516	9.06	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1290	14452	27517	9.06	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2444	15572	28701	1.72	3.0E-81	AF07188.1	NT	Homo sapiens cullin 4A (CUL4A), mRNA, complete cds
3055	16231	29250	6.11	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
3055	16231	29261	6.11	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
2894	16073	29090	2.29	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3677121 5'
2894	16073	29091	2.29	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3677121 5'
3873	17032	30031	0.8	2.0E-81	AW611542.1	EST_HUMAN	Hg88601.x1 NCI_CGAP_Ki6711 Homo sapiens cDNA clone IMAGE:2952384 3'
8144	21226	34746	0.69	2.0E-81	8923839	NT	Homo sapiens hypothetical protein (LOC55586), mRNA
13128	17032	30031	5.68	2.0E-81	AW611542.1	EST_HUMAN	Hg88601.x1 NCI_CGAP_Ki6711 Homo sapiens cDNA clone IMAGE:2952384 3'
4638	17774	30754	2.86	1.0E-81	AA040370.1	EST_HUMAN	2k45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:495825 5' similar to
4768	17903	30885	9.54	1.0E-81	BE047996.1	EST_HUMAN	PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly
5241	18363	31331	0.6	1.0E-81	980844	NT	1245c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291525 5'
5351	18478	38821	6.18	1.0E-81	U87928.1	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
5459	18669	31648	3.8	1.0E-81	11432966	NT	Human acotinate hydratase (AC02) gene, exon 3
5459	18669	31649	3.8	1.0E-81	11432966	NT	Homo sapiens polymorax (DNA directed), gamma (POLG), mRNA
5619	18813	31881	0.76	1.0E-81	AA255569.1	EST_HUMAN	285508.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:682475 5' similar to SW:PRI2_HUMAN
5771	18963	32284	3.18	1.0E-81	U52351.1	NT	P49943 DNA PRIMASE 58 KD SUBUNIT ; Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2), mRNA, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5771	18083	32265	3.18	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAIP/neurujin (CTNND2) mRNA, partial cds
6274	19448	32787	1.81	1.0E-81	BF674641.1	EST_HUMAN	602137854F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
6877	20029	33439	1.09	1.0E-81	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7949	20959	34509	7.94	1.0E-81	11432866	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7972	21022	34535	0.81	1.0E-81	AJ250408.1	NT	Homo sapiens GLI3 gene for GLI3 protein
9978	23017	36610	0.89	1.0E-81	BE968278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9978	23017	36611	0.89	1.0E-81	BE968278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
10174	23211	36804	5.13	1.0E-81	BE564367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
10308	23343	36948	0.81	1.0E-81	AA630754.1	EST_HUMAN	act1406.a1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:866427 3' similar to SW:YB36, YEAST P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION:
10310	23345	36950	3.72	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10310	23345	36961	3.72	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10726	23759	37367	1.41	1.0E-81	AW897550.1	EST_HUMAN	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA
10884	23896	37619	0.49	1.0E-81	AW250322.1	EST_HUMAN	2822127.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822127 5'
11182	24251	37886	1.97	1.0E-81	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11347	24409	38061	1.56	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11347	24409	38062	1.56	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11352	24414	38068	2.93	1.0E-81	AW798167.1	EST_HUMAN	RC3-JM0046-290200-011-a06 UM0046 Homo sapiens cDNA
11550	24414	38069	2.93	1.0E-81	AW798167.1	EST_HUMAN	RC3-JM0046-290200-011-a06 UM0046 Homo sapiens cDNA
11550	24490	31528	2.48	1.0E-81	AW860658.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
11812	24802	38501	1.89	1.0E-81	BF204253.1	EST_HUMAN	60188771.4F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12417	25295	32085	3.6	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
13	13251	26251	1.59	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
109	13251	26251	1.35	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
274	13492	26523	1.58	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
837	14015	27070	1.87	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
910	14095	27150	1.84	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1520	14673	27755	2.24	8.0E-82	AB037148.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1690	14842	27827	1.39	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4198	17348	30339	0.74	8.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4358	17501	30483	0.83	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461, mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1481	14634		1.18	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862086 5'
2825	15039	28049	1.82	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
1705	14857	27944	22.64	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5613	18807	31874	0.87	4.0E-82	BF331091.1	EST_HUMAN	QV2-HT0540-120900-362-008 HT0540 Homo sapiens cDNA
5613	18807	31875	0.87	4.0E-82	BF331091.1	EST_HUMAN	QV2-HT0540-120900-362-008 HT0540 Homo sapiens cDNA
5878	19068	32374	1.1	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9
12018	25000	38702	4.71	4.0E-82	AI937300.1	EST_HUMAN	wp75e09.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467824 3' similar to TR:075276
12683	25455		3.78	4.0E-82	AF029701.2	NT	O75276 PKD1;
							Homo sapiens presenilin-1 gene, exons 1 and 2
288	13508	26540	15.3	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
721	13903	26944	2.5	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
810	13689	27043	8.44	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
893	14069	27134	5.31	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1086	14252		15.73	3.0E-82	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1386	14641	27617	1.22	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1494	14647	27729	5.59	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C086
1950	15093	28194	2.14	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-280700-018-g04 BN0005 Homo sapiens cDNA
2062	15202	28318	1.11	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1) mRNA
3345	16518		2.42	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
8346	21427	34952	2.66	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8753	21832	35371	0.89	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8753	21832	36372	0.89	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
10029	23067	36665	4.01	3.0E-82	AB028000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10029	23067	36666	4.01	3.0E-82	AB028000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
610	13799	26819	2.49	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
610	13799	26819	2.49	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1720	14870	27962	2.23	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M117 5'
3949	17107	30104	0.93	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4131	17284	30279	0.68	2.0E-82	U78833.1	NT	Human integral membrane sialin protease Sepsin mRNA, complete cds
4348	17491	30473	0.9	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4680	17815	30803	1.52	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4880	17915	30804	1.62	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4992	18121	31100	2.86	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSORF1) and wbscr5 (WBSORF5) genes, complete cds, alternatively spliced and
5191	18313	31280	1.56	2.0E-82	4507580	NT	replication factor C subunit 2 (RFC2) gene, complete cds
5191	18313	31281	1.56	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5587	18782	31827	2.89	2.0E-82	AB018270.1	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
6304	19477	32832	4.83	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7858	28222		1.19	2.0E-82	AI476428.1	EST_HUMAN	hm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
7988	21038	34560	0.8	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8500	21581	35117	1.81	2.0E-82	11321670	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
8869	21948	35482	0.58	2.0E-82	7657340	NT	Homo sapiens microtubulin (mouse) homolog (MORC), mRNA
8869	21948	35483	0.58	2.0E-82	7657340	NT	Homo sapiens microtubulin (mouse) homolog (MORC), mRNA
10315	23350	36958	1.16	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10315	23350	36959	1.16	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11547	24603	38279	1.74	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11547	24603	38280	1.74	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11588	24841	38322	2.8	2.0E-82	U80736.1	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11588	24841	38323	2.8	2.0E-82	U80736.1	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
12230	25177		3.72	2.0E-82	AA011278.1	EST_HUMAN	Homo sapiens CAGF9 mRNA, partial cds
12818	25545		1.69	1.0E-82	11543921	NT	Homo sapiens CAGF9 mRNA, partial cds
605	13794	26813	3.19	1.0E-82	BE885106.1	EST_HUMAN	Homo sapiens CAGF9 mRNA, partial cds
1235	14394		1.38	1.0E-82	BE064386.1	EST_HUMAN	Homo sapiens CAGF9 mRNA, partial cds
1314	14470	27536	0.8	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
1315	14471	27537	0.9	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
8143	22222	35785	0.51	1.0E-82	AB014962.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
9953	22893	36474	1.4	1.0E-82	BF515938.1	EST_HUMAN	UIH-BW1-aca-F03-Q-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084083 3'
10451	23486		2.49	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10884	24083	37698	1.49	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11258	24327	37966	1.05	9.0E-83	AF224686.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANSA) gene, and ubiquitin-conjugating enzyme E2D 3
5307	18424	31394	4.96	9.0E-83	BF672220.1	EST_HUMAN	(UBE2D3) genes, complete cds
8972	21991	35530	0.72	9.0E-83	BE253347.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281861 5'
10481	23516	37128	2.97	8.0E-83	BE383973.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1446	14599	27676				EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 6'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1715	15992	27656	10.59	8.0E-83	N68951.1	EST_HUMAN	z449f12.s1 Soares fetal liver spleen 1NFL3 Homo sapiens cDNA clone IMAGE:295823 3'
1388	14543	27618	1.2	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271295-068-111 LT0016 Homo sapiens cDNA
2928	46105		1.64	7.0E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4838	18088		8.85	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316
6176	18362	32699	0.95	7.0E-83	11428657	NT	DJ207H1.1;
416	13611	26850	1.39	6.0E-83	M33320.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
1828	14676	28071	1.79	6.0E-83	AW573088.1	EST_HUMAN	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
3082	16258	29277	0.98	6.0E-83	AW816405.1	EST_HUMAN	h31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833528 3' similar to
3116	19292		0.7	6.0E-83	AF231919.1	NT	SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034.;
3653	18816	29828	0.92	6.0E-83	11430241	NT	QV4-S10234-181189-037-105 S10234 Homo sapiens cDNA
5408	18810	31582	1.73	6.0E-83	4507888	NT	Homo sapiens chromosome 21 unknown mRNA
6147	19324	32659	1.31	6.0E-83	AJ010770.1	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
7871	20737	34215	2	6.0E-83	11422024	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
9878	22918	36503	3.51	6.0E-83	4505314	NT	Homo sapiens hyperion gene, exons 1-50
9971	23010	36504	0.71	6.0E-83	11430647	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
8971	23010	36505	0.71	6.0E-83	11430647	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
11821	24810		2.31	6.0E-83	AA486105.1	EST_HUMAN	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Ptp18 (PRP18), mRNA
12179	25139		4.14	6.0E-83	AF240786.1	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Ptp18 (PRP18), mRNA
989	14142		1.24	5.0E-83	U17883.1	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Ptp18 (PRP18), mRNA
2108	16968		3	5.0E-83	AF006305.1	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Ptp18 (PRP18), mRNA
3728	16889	29893	0.91	5.0E-83	AL133207.2	NT	ab14e10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element;
4015	17172	30180	0.73	5.0E-83	4885190	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4554	17852	30872	0.61	5.0E-83	AL163210.2	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
5190	18312	31278	13.87	5.0E-83	4557013	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
5190	18312	31279	13.87	5.0E-83	4557013	NT	Homo sapiens gene mapping to chromosome X
667	13843	26870	1.87	4.0E-83	AF224669.1	NT	Novel human gene mapping to chromosome X
1022	14193		4.09	3.0E-83	AA368311.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens catalase (CAT) mRNA
							Homo sapiens catalase (CAT) mRNA
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
							EST78942 Placenta Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2837	15951		1.6	3.0E-83	AA632654.1	EST_HUMAN	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.12 THR repetitive element;
6708	10986		0.82	3.0E-83	AI217223.1	EST_HUMAN	q173506.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1785882 3'
							q164g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614
1843	14989	28089	1.37	2.0E-83	AA993492.1	EST_HUMAN	Q92814 MYELOBLAST KIAA0216.;
1843	14989	28090	1.37	2.0E-83	AA993492.1	EST_HUMAN	Q92814 MYELOBLAST KIAA0216.;
1978	15121	28222	9.11	2.0E-83	N68951.1	EST_HUMAN	z448112.s1 Soares_fetal_liver_spleen TNFSL Homo sapiens cDNA clone IMAGE:295823 3'
2251	15384	28512	1.57	2.0E-83	AB033098.1	NT	Homo sapiens mRNA for KIAA1272 protein, partial cds
2913	16091	29103	1.33	2.0E-83	BE828694.1	EST_HUMAN	RC6-E10049-280600-013-H12 ET0046 Homo sapiens cDNA
3342	16515		2.16	2.0E-83	11430834	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3874	17033		0.94	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4466	17598	30576	4.95	2.0E-83	AF202870.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4776	17910	30893	3.19	2.0E-83	AF202870.1	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4775	17910	30894	3.19	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5385	18587	31559	0.91	2.0E-83	U06679.1	NT	Human carcinoembryonic antigen gene family member 18 (CGM18) gene, exons A1 and B1
5967	19153	32468	0.87	2.0E-83	11428081	NT	Homo sapiens membrane protein GH1 (GH1), mRNA
6086	19288	32597	1.2	2.0E-83	BE885401.1	EST_HUMAN	601507482F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3903098 5'
6885	20037	33446	0.72	2.0E-83	AF126533.1	NT	Homo sapiens F-box protein Fb3b (FBL3B) mRNA, partial cds
7593	20684	34140	5.15	2.0E-83	AF126533.1	NT	Homo sapiens F-box protein Fb3b (FBL3B) mRNA, partial cds
7987	21036	34548	0.58	2.0E-83	BF105097.1	EST_HUMAN	601822090F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042318 5'
8028	21109	34625	0.63	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
8028	21109	34627	0.63	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
8175	21257	34779	1.46	2.0E-83	AF011920.1	NT	Rattus norvegicus densin-180 mRNA, complete cds
8509	21590	35124	2.52	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8909	21590	36126	2.52	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8909	21590	36126	2.52	2.0E-83	AF011920.1	NT	Homo sapiens phosphotyrosine kinase, gamma 1 (muscle) (PHKG1) mRNA
9793	22833	36413	0.54	2.0E-83	5453881	NT	Homo sapiens phosphotyrosine kinase, gamma 1 (muscle) (PHKG1) mRNA
10240	23275	36966	3.2	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10240	23275	36967	3.2	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10322	23357	36967	1.35	2.0E-83	AF117659.1	EST_HUMAN	U117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001970 5'
10392	23427	37034	0.78	2.0E-83	AW509600.1	EST_HUMAN	U1-HF-BNO-amd-4-07-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081852 5'
11086	24160	37796	3.24	2.0E-83	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11168	24239	37870	1.64	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_11 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547J136 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11168	24239	37871	1.64	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547J135 5'
12859	25570		3.26	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
1444	14597	27673	2.26	1.0E-83	4504326	NT	Homo sapiens hydroxyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1444	14597	27674	2.26	1.0E-83	4504326	NT	Homo sapiens hydroxyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2076	15216	28335	1.15	1.0E-83	4503652	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2722	15840	28951	1.21	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3251	16425	29443	0.72	1.0E-83	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0898), mRNA
3972	17128	30132	7.76	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4359	17502	30484	2.22	1.0E-83	Z25822.1	NT	H.sapiens gene for mitochondrial dodecenyl-CoA delta-isomerase, exon 3
5006	18137	31111	2.74	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
6835	19888	33397	1.59	1.0E-83	AI027614.1	EST_HUMAN	ov69608.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM
3897	17056	30056	3.62	7.0E-84	BE901209.1	EST_HUMAN	PROTEIN (HUMAN);
1323	14479	27544	2.96	6.0E-84	BE838864.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3968853 5'
1323	14479	27545	2.96	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200800-011-g05 FN0119 Homo sapiens cDNA
2471	15598	28723	17.98	6.0E-84	AA778574.1	EST_HUMAN	RC2-FN0119-200800-011-g05 FN0119 Homo sapiens cDNA
5354	18481		2.18	6.0E-84	AL042833.2	EST_HUMAN	es86a03.s1 Stralagens schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5635	18828	31905	1.91	6.0E-84	AA897339.1	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434H0322 5'
5777	18869	32273	0.99	6.0E-84	11426718	NT	el47q03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338
5777	18869	32274	0.99	6.0E-84	11426718	NT	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
7642	20711	34190	3.14	6.0E-84	BE810371.1	EST_HUMAN	Homo sapiens acyl LDL receptor, SREC= scavenger receptor expressed by endothelial cells (SREC), mRNA
7868	20822	34429	1.05	6.0E-84	AF038391.1	NT	Homo sapiens acyl LDL receptor, SREC= scavenger receptor expressed by endothelial cells (SREC), mRNA
8264	21346	34861	2	6.0E-84	BE770199.1	EST_HUMAN	PM0-L70019-180600-004-F02 LT0019 Homo sapiens cDNA
732	13914	26956	1.32	5.0E-84	AA382811.1	EST_HUMAN	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
3079	18255		1.91	5.0E-84	AF109718.1	NT	PM4-FT0054-160600-004-e10 FT0054 Homo sapiens cDNA
6232	19407	32756	0.62	5.0E-84	AA167878.1	EST_HUMAN	EST196094 Testis I Homo sapiens cDNA 5' end
							Homo sapiens chromosome 3 subtelomeric region
							zq39e07.r1 Stralagens hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632100 5' similar to
							TR:G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11838	24827	38510	2.85	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11952	24938	38640	1.99	6.0E-84	AB032967.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11952	24938	38641	1.99	6.0E-84	AB032967.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1407	14581	27635	1.34	4.0E-84	AB037355.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds
1443	14596	27672	4.47	4.0E-84	AF685321.1	EST_HUMAN	wa76c04.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN 043847 NARDILYSIN PRECURSOR;
5084	18192	31167	0.66	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
5065	18193	31168	1.52	4.0E-84	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5377	18579	31448	1.62	4.0E-84	AF022835.1	NT	Homo sapiens multidrug resistance protein (MRP), exon 13
5680	18874	32162	1.8	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5680	18874	32163	1.8	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6398	19537	32928	2.14	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7825	20880	34381	13.68	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9112	22191	35736	1.12	4.0E-84	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9112	22191	35736	1.12	4.0E-84	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
11156	24229	37859	4.76	4.0E-84	AB032966.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
326	13540	26872	2.16	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1178	14341	27395	1.53	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2015	15155	28260	2.39	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2063	15203	28319	2.36	3.0E-84	AL056880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3843	17002	30005	5.93	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRP1) mRNA, complete cds
11118	24190		6.78	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares Dieckgraebe, colon_NHCO Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2172	15307	28435	6.46	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272408 BT0795 Homo sapiens cDNA
2172	15307	28436	6.46	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272408 BT0795 Homo sapiens cDNA
3009	16185	29209	9.21	2.0E-84	AF036043.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
3027	16203	29228	1.22	2.0E-84	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
5643	18837	31914	0.93	2.0E-84	BF511575.1	EST_HUMAN	U1-H-B14-act-a-02-0-U1.e1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084863 3'
5643	18837	31915	0.93	2.0E-84	BF511575.1	EST_HUMAN	U1-H-B14-act-a-02-0-U1.e1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084863 3'
6774	19929	33325	0.92	2.0E-84	H63370.1	EST_HUMAN	yr58e11.s1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:208324 3'
8247	21328		1.55	2.0E-84	AI299674.1	EST_HUMAN	gm87c09.x1 NCI CGAP LU5 Homo sapiens cDNA clone IMAGE:1895728 3'
8579	21660	35200	0.58	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8579	21660	35201	0.58	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9546	22811	36179	1.24	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'

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9933	22972	36564	0.64	2.0E-84	H22841.1	EST_HUMAN	ym49e11.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:51393 5' similar to SP-APOH_RAT
12449	25316	32092	1.81	2.0E-84	BF448000.1	EST_HUMAN	P26644 BETA-2-GLYCOPROTEIN 1; nae30a02.x1 Lupekl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q8UGS3 Q8UGS3 DJ756G23.1; nae30a02.x1 Lupekl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to nae30a02.x1 Lupekl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
12449	25316	32093	1.81	2.0E-84	BF448000.1	EST_HUMAN	TR:Q8UGS3 Q8UGS3 DJ756G23.1; nae30a02.x1 Lupekl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
322	13536	26568	1.5	1.0E-84	AF114488.1	NT	Homo sapiens interferon short isoform (ITSN) mRNA, complete cds Homo sapiens tyrosine 3-monooxygenase/tyrosine 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
563	13755	26781	10.87	1.0E-84	4507952	NT	Homo sapiens complement component 5 (C5), mRNA
739	13920		1.19	1.0E-84	11427631	NT	am85b11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629855 3'
1321	14471	27842	2.93	1.0E-84	AA984379.1	EST_HUMAN	601308006f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628257 5'
2114	15252	28371	3.11	1.0E-84	BE392137.1	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCM1), mRNA
2298	15430	28562	1.53	1.0E-84	11427197	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3845	17005	30007	2.78	1.0E-84	AA720851.1	EST_HUMAN	nm12e06.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4538	17676	30659	5.89	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4821	17954	30639	3.03	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4821	17954	30940	3.03	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
5031	17676	30659	3.56	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6043	19226	32549	0.88	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA uterine water channel=28 kDa erythrocyte integral membrane protein homolog (human, uterus, mRNA, 1340 nt)
6319	19491	32649	2.84	1.0E-84	S73482.1	NT	Novel human gene mapping to chromosome 13
7020	20156	33676	1.42	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7020	20156	33677	1.42	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7256	20339	33789	2.53	1.0E-84	AL049784.1	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7637	20706	34185	10.45	1.0E-84	8393994	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7737	20798	34287	1.07	1.0E-84	11430848	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7777	20798	34287	2.34	1.0E-84	11430848	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15), mRNA
9735	22800		2.79	1.0E-84	5031984	NT	Homo sapiens Ca2+-binding protein CABP3 (CABP3) gene, exon 6 and partial cds
9972	23011	36606	0.6	1.0E-84	AF224511.1	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
9984	19488	31527	1.6	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
9984	19488	31528	1.6	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
12323	25236		2.62	1.0E-84	11417812	NT	Homo sapiens purine receptor P2X-like 1, orphan receptor (P2RXL-1), mRNA
12438	25311	32088	3.77	1.0E-84	11417812	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
989	14161		1.94	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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1098	14263	27319	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1098	14263	27320	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1608	14762	27841	1.12	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1609	14762	27842	1.12	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1709	14860	27849	3.59	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
3870	17029		0.8	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C089
4368	17509	30490	0.92	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5001	18130	31105	0.99	9.0E-85	5801979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5032	18160	31137	1.16	9.0E-85	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
13046	14860	27849	1.78	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
1159	14323	27378	4.64	7.0E-85	L06094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11843	24826		5.61	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11702	24698	38391	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11702	24699	38392	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
12060	25041	38750	2	6.0E-85	AA403053.1	EST_HUMAN	z62b01.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
2410	15540	28698	4.08	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4652	17690		0.71	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA11) mRNA, complete cds
5567	18784	31804	1.59	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3862402 5'
5567	18784	31805	1.59	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3862402 5'
11381	24442	38101	2.31	5.0E-85	AF224659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
13127	17690		1.72	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA11) mRNA, complete cds
6276	19450	32798	1.39	4.0E-85	BF077910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6276	19450	32799	1.39	4.0E-85	BF077910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
8021	21074	34658	3.43	4.0E-85	BE88284.1	EST_HUMAN	601605022F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906940 5'
10799	23831		1.8	4.0E-85	BE078263.1	EST_HUMAN	RC1-8T0623-120200-011-007 B10623 Homo sapiens cDNA
1327	14484	27551	0.91	3.0E-85	AF098157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1821	14970	28062	4.8	3.0E-85	T87495.1	EST_HUMAN	y63g06r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
5019	18148	31125	1.03	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA

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5019	18148	31126	1.03	3.0E-85	11024895	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5080	18208	31180	0.91	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5517	18715	31729	6.35	3.0E-85	11436001	NT	Homo sapiens lacrima proline rich protein (LPRP), mRNA
6210	19385	32734	0.72	3.0E-85	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6282	19436	32782	4.82	3.0E-85	7662303	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6282	19438	32783	4.92	3.0E-85	7662303	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
7091	20185		7.95	3.0E-85	AJ404463.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7555	20627	34103	0.84	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125 (FAK); KIAA0621 protein (KIAA0621), mRNA
8056	21139	34659	1.44	3.0E-85	U4953.1	NT	Homo sapiens DENN mRNA, complete cds
8706	21766	35319	0.48	3.0E-85	11525623	NT	Homo sapiens CGL-81 protein (LOC51108), mRNA
9178	22258	35798	4.39	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9506	22772	36343	0.84	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
9508	22772	36344	0.84	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
10700	23733	37338	0.72	3.0E-85	AF098642.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11798	24786	38484	1.48	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discordin-like domains 3 (EDIL3), mRNA
12886	25648		3.02	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
985	14157	27218	0.62	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1085	14231	27289	2.35	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1436	14589	27662	1.19	2.0E-85	7708203	NT	Homo sapiens CGL-201 protein (LOC51340), mRNA
1451	14904	27682	13.02	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1451	14904	27683	13.02	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2304	15438	28568	2.92	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2884	14623		4.22	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3087	16263	29280	3.57	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4454	17584	30574	4.66	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4687	17822	30810	0.74	2.0E-85	4829377	NT	Homo sapiens reelin (RELN) mRNA
5030	18159	31136	1.21	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9473	22530	36094	1.78	2.0E-85	AJ760820.1	EST_HUMAN	w6708.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element
9849	22889	36469	0.82	2.0E-85	AJ914456.1	EST_HUMAN	MSR1 repetitive element 1
10469	23504	37118	0.94	2.0E-85	AI886384.1	EST_HUMAN	w449c03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2331461 3'
2360	15491		3.55	1.0E-85	BE794303.1	EST_HUMAN	w894d12.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
							601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2467	15594	28719	9.36	1.0E-85	BE618392.1	EST_HUMAN	901462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2467	15594	28720	9.36	1.0E-85	BE618392.1	EST_HUMAN	901462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7983	21032	34545	0.81	1.0E-85	BE082851.1	EST_HUMAN	MR0-BT0284-221189-002-03 BT0284 Homo sapiens cDNA
8984	23023	36615	2.13	1.0E-85	BE267917.1	EST_HUMAN	901100738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350553 5'
10415	23450	37055	0.76	1.0E-85	AW813525.1	EST_HUMAN	RC1-ST0195-081099-011-005 ST0195 Homo sapiens cDNA
11184	24235	37865	2.79	1.0E-85	AA778785.1	EST_HUMAN	Z4503.s1 Soares fetal liver spleen INFIL S1 Homo sapiens cDNA clone IMAGE:463245 3'
11184	24235	37866	2.79	1.0E-85	AA778785.1	EST_HUMAN	Z4503.s1 Soares fetal liver spleen INFIL S1 Homo sapiens cDNA clone IMAGE:463245 3'
11245	24314	37953	1.86	1.0E-85	AA778785.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
11245	24314	37954	1.86	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
12098	25049	38757	3.29	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
12300	25404	32045	4.68	1.0E-85	AI198420.1	EST_HUMAN	q16607.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1860468 3'
12601	25404	32045	2.92	1.0E-85	AI198420.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1460	14613	32774	0.62	8.0E-86	11474140	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
6254	19428	26480	2.2	7.0E-86	7862247	NT	Homo sapiens similar to CDC28 protein kinase 1 (H_sapiens) (LOC63041), mRNA
233	13454	27192	1.03	7.0E-86	AA860801.1	EST_HUMAN	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
960	14133	27183	1.03	7.0E-86	AA860801.1	EST_HUMAN	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
6325	19497	32853	0.97	7.0E-86	9966886	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
6325	19497	32854	0.97	7.0E-86	9966886	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
7118	18542	31499	6.43	7.0E-86	11421737	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
8943	22022	35562	3.98	7.0E-86	L38557.1	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
9801	22941	36595	1.13	7.0E-86	5453997	NT	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
9960	22999	36595	1.86	7.0E-86	11526307	NT	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
11204	24273	37909	1.44	7.0E-86	11417012	NT	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
11204	24273	37910	1.44	7.0E-86	11417012	NT	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
12117	25097	38802	1.99	7.0E-86	11418903	NT	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
1322	14478	27543	1.87	6.0E-86	4505492	NT	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
217	13439	26471	2.15	4.0E-86	BE547173.1	EST_HUMAN	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
6159	18339	32080	11.61	4.0E-86	BE265943.1	EST_HUMAN	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
11517	13439	26471	2.34	4.0E-86	BE547173.1	EST_HUMAN	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
4404	17847	30631	0.94	3.0E-86	BE887703.1	EST_HUMAN	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
5713	18906	32201	6.19	3.0E-86	AW340946.1	EST_HUMAN	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
8457	21538	35067	1.21	3.0E-86	AV722329.1	EST_HUMAN	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
10425	23460	37055	3.54	3.0E-86	BE888479.1	EST_HUMAN	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10425	23480	37066	3.54	3.0E-86	BE886476.1	EST_HUMAN	601506696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:391303 5'
11720	23906	37529	4.87	3.0E-86	AI659240.1	EST_HUMAN	U18002.X1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2251371 3'
11803	24793	38491	1.37	3.0E-86	AV690469.1	EST_HUMAN	AV690469 GKC Homo sapiens cDNA clone GKCBSE02 5'
12300	25971		3.38	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3630753 5'
277	13495	28525	1.56	2.0E-86	AA306284.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
427	13622		2.69	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1217	14378	27437	3.33	2.0E-86	N58977.1	EST_HUMAN	Yz18a08.r1 Soares_multiple_sclerosis_2/NbHMSF Homo sapiens cDNA clone IMAGE:283478 5'
2285	15398	28526	8.53	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2342	16473	28607	1.56	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3002	16689	29679	1.61	2.0E-86	AW966142.1	EST_HUMAN	EST378216 MAGE resequences, MAGI Homo sapiens cDNA
3840	16989	30001	2.29	2.0E-86	AF156776.1	NT	Homo sapiens tyrosinase-like acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3840	16989	30002	2.29	2.0E-86	AF156776.1	NT	Homo sapiens tyrosinase-like acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4151	17303		2.69	2.0E-86	AW515742.1	EST_HUMAN	hd87g08.X1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2816542 3'
4910	18040	31030	3.21	2.0E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5993	19178	32499	1.32	2.0E-86	Z18411.1	NT	H. sapiens mRNA encoding phospholipase c
5993	19178	32500	1.32	2.0E-86	Z18411.1	NT	H. sapiens mRNA encoding phospholipase c
							Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
7221	25837	33501	0.78	2.0E-86	11419429	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8199	21281	34803	0.58	2.0E-86	U84744.1	NT	Homo sapiens butyrobetaine (gamme), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8772	21851	35392	2.52	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamme), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8772	21851	35393	2.52	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamme), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9104	22183	35728	0.68	2.0E-86	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9518	22594	36153	1.98	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog) like (CSE1L), mRNA
10684	23898	37307	2.9	2.0E-86	11545848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10684	23898	37308	2.9	2.0E-86	11545848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10687	23701	37311	0.48	2.0E-86	11417120	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20125), mRNA
10721	23754	37360	1.25	2.0E-86	AB037822.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11143	24215	37842	1.78	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
12789	25527	32006	6.3	2.0E-86	11478189	NT	Homo sapiens thyroid autoantigen 70kD [Ku antigen] (G22P1), mRNA
12980	25638		2.58	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
1627	14779	27864	2.15	1.0E-86	4826955	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3231	16405	29417	1.68	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3307	18481	29502	2.39	1.0E-86	L20482.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3368	16540	29563	1.74	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
3368	16540	29564	1.74	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4390	17523	30504	5.41	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4743	17878	30861	0.84	1.0E-86	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
5670	18864	32149	1.85	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11905	18864	32149	1.53	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5472	18872		1.84	9.0E-87	AI150709.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1706128 3' similar to
7606	20876	34150	1.82	9.0E-87	4757721	NT	qbt7c09.x1 Scores: fetal heart NDRH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to
7606	20876	34151	1.82	9.0E-87	4757721	NT	SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
492	13686	26720	49.59	8.0E-87	X62246.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
2369	15500	28626	3.27	7.0E-87	BF063211.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
2369	15500	28627	3.27	7.0E-87	BF063211.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6330	18694	33067	1.38	7.0E-87	AW890336.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
8384	21465	34990	3	7.0E-87	BF352776.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
9683	21096	34610	0.66	7.0E-87	BE172961.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
10276	23311	36607	3.38	7.0E-87	AL043314.2	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
10276	23311	36608	3.38	7.0E-87	AL043314.2	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
10686	25865		0.53	7.0E-87	AI081595.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
11129	24201	37825	6.59	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
11129	24201	37826	6.59	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
3815	16779	29794	1.19	6.0E-87	7657213	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
6551	18713	33089	1.47	6.0E-87	AB028004.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
10963	24044		4.48	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1184	14347	27404	1.62	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
12003	14347	27404	2.58	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
988	14160	27220	1.37	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1189	14361	27420	7.91	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1461	14614	27696	1.31	4.0E-87	R78133.1	EST_HUMAN	y80110.r1 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:146579 5' similar to contains Alu repetitive element
2086	15226	28348	2.28	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2143	15279	28402	1.29	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2143	15279	28403	1.29	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2493	15620	28738	0.99	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51628), mRNA
2493	15620	28739	0.99	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51628), mRNA
3553	18718	29732	3.61	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) translocation), translocated to, 4 (MLL14) mRNA
5562	18759	31798	4.9	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLATION VARIANT 2)
5569	19099	32366	0.58	4.0E-87	U85429.1	NT	Human transcription factor NFATx2 mRNA, complete cds
6170	19348	32692	4.34	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4031 Pediatric pre-B cell acute lymphoblastic leukemia Bayor-HcSC project=TCBAP1E4031 cDNA clone TCBAP-4031
7848	20903	34406	0.71	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7848	20903	34407	0.71	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7950	21000	34910	3.64	4.0E-87	L48524.1	NT	Homo sapiens tuberin (TSC2) gene, exon 10
11437	24498	38165	3.42	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
12705	26023	31671	1.27	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12705	26023	31672	1.27	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12898	25593		58.7	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RX1), mRNA
2839	15950	28057	14.35	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
3894	17043	30042	1.02	2.0E-87	AU116935.1	EST_HUMAN	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
5033	18161	31138	3.2	2.0E-87	BF37631.1	EST_HUMAN	CMO-TN0038-150900-552-109 TN0038 Homo sapiens cDNA
5076	18204	31176	0.8	2.0E-87	BE175478.1	EST_HUMAN	RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
5778	18970	32275	12.22	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5778	18970	32276	12.22	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6456	18923		4.87	2.0E-87	BE507193.1	EST_HUMAN	601341393F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5'
6838	18991	33399	0.79	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:243396 5'
6920	20235	33668	0.75	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDS G04 3'
7324	20406	33958	1.35	2.0E-87	BE294432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7374	20463	33918	0.7	2.0E-87	11433043	NT	Homo sapiens hex domain and RLD 2 (HERC2), mRNA
7611	20681	34157	36.59	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:243396 5'
7864	20918	34424	35.3	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:243396 5'
8589	21670	36209	3.35	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
9988	23027		4.96	2.0E-87	BE531136.1	EST_HUMAN	601278316F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1209	15989		2.2	1.0E-87	7705883	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1463	14616	27698	1.61	1.0E-87	AW361877.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1463	14616	27698	1.61	1.0E-87	AW361877.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3801	16862	28968	5.18	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3828	16988	29991	2.3	1.0E-87	4758827	NT	Homo sapiens neurexin III (NRXN3), mRNA
6356	19526	32883	1.93	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6356	19526	32884	1.63	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7333	20414	33876	1.09	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7558	20630	34105	1.05	1.0E-87	11431560	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7707	20772	34257	0.92	1.0E-87	4506788	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
8307	21389	34912	9.93	1.0E-87	AF214582.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9110	22189	35732	0.95	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9110	22189	35733	0.95	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9833	22873	36457	2.92	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
9833	22873	36457	2.92	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
10364	23619	37225	0.88	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' end
10970	24050	37683	2.11	1.0E-87	5729867	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
11247	24316		1.66	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12701	26190		2.31	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
13228	25798	31890	1.22	1.0E-87	AF169558.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
13228	25798	31891	1.22	1.0E-87	AF169558.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
1730	14295	27350	8.48	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1380	14535	27609	2.94	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1380	14535	27610	2.94	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2189	16324	28449	0.99	9.0E-88	7661701	NT	Homo sapiens DKFZP589P1522 protein (DKFZP589P1522), mRNA
3717	16878	29883	1	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4384	17527	30508	2.97	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)
4384	17527	30509	2.97	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)
9223	22301	36845	4.04	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1875	15019		1.22	5.0E-88	7681867	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2704	15822	28839	3.65	5.0E-88	N88399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3064	16240	29280	0.62	6.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3076	16251	29272	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3075	16251	29273	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3476	16643		2.78	5.0E-88	AF114488.1	EST_HUMAN	wd88h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element;
3625	16789	29808	0.75	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
4859	17692	30979	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
6910	20226	33656	2.87	5.0E-88	AF114488.1	EST_HUMAN	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
8114	21196	34715	2.87	5.0E-88	AF114488.1	EST_HUMAN	ym06b10.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:47129 5'
9512	22577	36143	0.63	5.0E-88	AF114488.1	EST_HUMAN	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
1360	14515	27589	0.96	5.0E-88	AF114488.1	EST_HUMAN	602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5'
1360	14515	27590	0.96	5.0E-88	AF114488.1	EST_HUMAN	PM1-TN0028-050800-004-110 TN0028 Homo sapiens cDNA
5244	18365	31333	0.65	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050800-004-110 TN0028 Homo sapiens cDNA
7392	20470	33936	1.7	4.0E-88	BF091229.1	EST_HUMAN	802149702F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290975 5'
11150	24221	37849	1.64	4.0E-88	BF091229.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68kd (TGFB1), mRNA
11779	24769	38464	1.72	4.0E-88	BF091229.1	EST_HUMAN	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11779	24769	38465	1.72	4.0E-88	BF091229.1	EST_HUMAN	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
750	13931	26974	1.25	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
1855	15001	29214	6.08	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
3013	16189	30477	0.81	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
4355	17498	30477	0.81	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
4355	17498	30478	0.81	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
4800	17737	31590	2.79	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
5414	18616	32188	3.63	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
5703	18896	32188	3.63	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
5822	18012	32318	0.72	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
6280	19493	32815	0.84	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
6543	26826	33080	0.84	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
6543	26826	33081	0.84	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
7211	20076	33489	15.52	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
7712	20777	34253	5.63	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
8105	21187	34707	9.3	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA
8390	21471	34997	1.58	3.0E-88	BF091229.1	EST_HUMAN	Homo sapiens zinc finger protein 269 (ZNF269) mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9834	21077	34589	2.14	3.0E-98	11529252	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
10132	23170	36767	0.76	3.0E-98	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10132	23170	36768	0.76	3.0E-98	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10162	23169	36784	0.6	3.0E-98	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12424	26301		2.49	3.0E-98	11477974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
12439	26300	31676	1.63	3.0E-98	11430460	NT	Homo sapiens protease, serine, 7 (serine protease) (PRSS7), mRNA
13223	25706	31889	1.31	3.0E-98	11529140	NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1061	14227	27283	6.85	2.0E-98	7305198	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1853	14806	27891	4.24	2.0E-98	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1789	14838	28031	6.83	2.0E-98	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3554	16719	29733	2.9	2.0E-98	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4545	17883	30865	1.93	2.0E-98	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
6032	19215	32536	4.98	1.0E-98	AW139565.1	EST_HUMAN	U1H-B11-acc-d-04-0-U1.s1 NCI_GGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718760 3'
6032	19215	32537	4.98	1.0E-98	AW139565.1	EST_HUMAN	U1H-B11-acc-d-04-0-U1.s1 NCI_GGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718760 3'
6783	19838	33335	21.66	1.0E-98	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7271	20354	33807	1.52	1.0E-98	AI69034.1	EST_HUMAN	Homo sapiens KIAA0417 mRNA, complete cds
7334	20415	33877	3.7	1.0E-98	AA489981.1	EST_HUMAN	Homo sapiens KIAA0417 mRNA, complete cds
8331	21413	34939	0.51	1.0E-98	AF135183.1	NT	Homo sapiens Recq helicase 5 (RECQ5) gene, alternative splice products, complete cds
9443	22559	36122	0.76	1.0E-98	AA190388.1	EST_HUMAN	SW:POL.1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN :
9778	22818	36396	2.83	1.0E-98	AL048314.2	EST_HUMAN	DKFZp434N0323.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
11730	23916	37541	3.35	1.0E-98	AA981479.1	EST_HUMAN	cs91g03.s1 NCI_GGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342
12805	25442		4.28	1.0E-98	AL163246.2	NT	HETEROGENEOUS NUCLEOTIDE RIBONUCLEOPROTEINS C1/C2 (HUMAN);
13232	25900	31850	1.54	1.0E-98	AW451790.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
11194	24283	37898	8.14	9.0E-98	11421238	NT	U1H-B13-alk-b-03-0-U1.s1 NCI_GGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737084 3'
2795	15910	29019	1.75	8.0E-98	BE311557.1	EST_HUMAN	Homo sapiens transgelin 2 (TAGLN2), mRNA
7072	20125	33541	1.14	8.0E-98	11421514	NT	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3606186 5'
446	13642	26680	1.41	7.0E-98	7657213	NT	Homo sapiens similar to some domain, immunoglobulin domain (ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
446	13642	26681	1.41	7.0E-98	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5005	18134	31108	2.71	7.0E-98	4557390	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
							Homo sapiens complement component 8, beta polypeptide (C8B) mRNA

Table 4

Table 4
Single Exon Probes Expressed in Placenta

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
129	13616	26665	0.73	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
129	13616	26657	0.73	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26656	0.89	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26657	0.89	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
543	13736	26760	0.63	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2845	16122	29135	1.53	2.0E-89	AJ222095.1	EST_HUMAN	q99c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
4263	17408	30394	1.18	2.0E-89	AF089897.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
4269	17414	30402	5.14	2.0E-89	X58742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4269	17414	30403	5.14	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4269	17414	30403	5.14	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4469	17509	30587	1.13	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4619	17758	30738	1	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5459	18659	31842	1.39	2.0E-89	BE541744.1	EST_HUMAN	60108599F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3462423 5'
5598	18793	32412	3.55	2.0E-89	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
5909	19098	32412	1.5	2.0E-89	U03985.1	NT	Homo sapiens gene for LECT2, complete cds
6339	19509	32865	0.79	2.0E-89	AL163285.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
7847	20902	34405	6.28	2.0E-89	U81004.1	NT	Homo sapiens chromosome 21 segment HS21C085
8119	21201	34722	3.11	2.0E-89	11428901	NT	Human GT24 (GT24) mRNA, partial cds
8612	21692	35229	0.9	2.0E-89	AJ245503.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
9453	22660	36136	0.72	2.0E-89	AB037764.1	NT	Homo sapiens partial mRNA for PEX3 related protein
10015	23053	36647	1.22	2.0E-89	AF170814.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10015	23053	36648	1.22	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
11655	24734	38425	2.63	2.0E-89	11434411	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
11871	24859	38554	3.62	2.0E-89	11433673	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
12017	25001	38703	1.64	2.0E-89	U10692.1	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
12877	25584	38561	4.25	2.0E-89	AF156981.1	NT	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
11877	24885	38561	6.88	1.0E-89	BF196052.1	EST_HUMAN	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
11877	24885	38562	6.88	1.0E-89	BF196052.1	EST_HUMAN	Homo sapiens human endogenous reovirus W gagC3 37 G gag (gag) gene, complete cds
							hr81d09.x1 NCL CGAP_K4111 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778
							SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN;
							hr81d09.x1 NCL CGAP_K4111 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778
							SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8422	21503	35035	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8422	21503	35036	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1088	14254	27308	4.38	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1089	14254	27309	2.91	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1361	16035	27591	3.26	8.0E-90	BE670561.1	EST_HUMAN	733608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1381	16035	27592	3.26	8.0E-90	BE670561.1	EST_HUMAN	733608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8757	21836	35377	0.8	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-508 HT0598 Homo sapiens cDNA
10939	24021	37654	1.38	8.0E-90	AI222095.1	EST_HUMAN	q99c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
10939	24021	37655	1.38	8.0E-90	AI222095.1	EST_HUMAN	q99c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
859	14036		6.81	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8619	21699		2.14	7.0E-90	AA782977.1	EST_HUMAN	ai83d08.s1 Soares_testis NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9166	22244	35787	2.13	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9166	22244	35788	2.13	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10220	23256	36844	0.46	7.0E-90	AW273794.1	EST_HUMAN	xv24a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814028 3'
10340	23375	36985	4.2	7.0E-90	H68849.1	EST_HUMAN	yf86e04.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:CTTC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10340	23375	36986	4.2	7.0E-90	H68849.1	EST_HUMAN	yf86e04.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:CTTC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10672	23706	37314	0.62	7.0E-90	BF526089.1	EST_HUMAN	602071208F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4214257 5'
3136	16312	29324	1.16	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
3136	16312	29325	1.16	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4342	17485	30467	11.21	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4342	17485	30468	11.21	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6105	19285	32618	2.84	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6105	19285	32619	2.84	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8522	21603	35140	4.01	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8522	21603	35141	4.01	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
159	13384		27.59	5.0E-90	AB035344.1	NT	Homo sapiens TCE6 gene, exon 1-10b
1219	14380	27439	6.22	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1864	15010	28116	1.07	5.0E-90	A1222095.1	EST_HUMAN	q99c08.x1 Scores_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb.J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
1864	15010	28117	1.07	5.0E-90	A1222095.1	EST_HUMAN	q99c08.x1 Scores_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb.J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
2622	16745	28869	2.37	5.0E-90	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
4662	17797	30784	4.51	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4693	17818	30806	0.78	5.0E-90	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
6709	18901	32196	2.85	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
3726	18919		0.72	5.0E-90	AF008915.1	NT	Homo sapiens EVI8 homolog mRNA, complete cds
5810	19000	32307	1.32	5.0E-90	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
5886	18901	32166	1.88	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6869	20021	33430	0.95	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC66934) mRNA
6869	20021	33431	0.95	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC66934) mRNA
7364	20443	33905	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7384	20443	33906	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7736	20797	34286	7.98	5.0E-90	4557258	NT	Homo sapiens adenylylase 9 (ADCY9) mRNA
8488	21668	35107	4.89	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222) mRNA
9882	22922	36806	1.17	5.0E-90	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10488	23623	37133	0.71	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10663	23697	37306	0.66	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10723	23756	37382	0.53	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10723	23756	37383	0.53	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
12948	25659		1.77	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13000	25649		4.54	5.0E-90	A1523366.1	EST_HUMAN	af78105.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2128761 3'
313	13529	26582	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
313	13529	26583	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1110	14275	27332	4.36	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1724	14874	27966	13.42	4.0E-90	X39033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
2823	18101	29114	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2823	16101	29115	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3088	16284	29281	0.93	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3088	16284	29282	0.93	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4778	17814	30800	3.63	4.0E-90	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4913	18049	31037	2.1	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cdc
4839	18059	31047	1.91	4.0E-90	M85967.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
12885	16101	29114	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12885	16101	29115	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8038	21119	34638	0.91	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-amy-b-04-0-UI.s1 NCI_OGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
8036	21119	34639	0.91	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-amy-b-04-0-UI.s1 NCI_OGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11830	24916	38619	28.7	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
220	13442	28473	4.5	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1200	14362	27421	6.46	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1200	14362	27422	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3948	17108	30103	2.95	2.0E-90	AI138213.1	EST_HUMAN	q64c02.x1 Scapies, placenta, 8w6weeks_2NbrIP8x6W Homo sapiens cDNA clone IMAGE:1713410 3'
4811	17944	30930	1.05	2.0E-90	AB006627.1	NT	similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3. ;
6029	18158	31139	10.16	2.0E-90	5729855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5886	19084	32395	0.8	2.0E-90	11525901	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5896	19084	32396	0.8	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5903	19092	32406	3.89	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
9893	23032	36623	0.99	2.0E-90	11427320	NT	be49d05.j3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3899881 5' similar to TR:075208 O75208
9893	23032	36624	0.99	2.0E-90	11427320	NT	HYPOTHETICAL 35.5 KD PROTEIN. ;
10165	23202	36795	1.46	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10165	23202	36796	1.46	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
11758	23844	37571	3.06	2.0E-90	11024711	NT	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
287	13505	26539	4.1	1.0E-90	4502166	NT	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
385	15983	26628	2.28	1.0E-90	AF231920.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
386	15983	26628	1.56	1.0E-90	AF231920.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
713	13895	26932	1.92	1.0E-90	AJ237589.1	NT	Homo sapiens chromosome 21 unknown mRNA
713	13895	26933	1.92	1.0E-90	AJ237589.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
748	13928	26971	17.93	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
748	13929	26972	17.93	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1134	14299		2.25	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1334	14491	27560	3.48	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1334	14491	27561	3.48	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1701	14853		2.61	1.0E-90	BE378884.1	EST_HUMAN	60115953F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5'
1951	15094	28195	3.73	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila))-like (LOC57187), mRNA
2915	16093	29106	6.46	1.0E-90	AB020710.1	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3054	17112	30112	0.59	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3954	17112	30113	0.59	1.0E-90	AB020710.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
4543	17681	30663	1.68	1.0E-90	AF167340.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5792	18983	32286	2.08	1.0E-90	AB014533.1	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
5959	19145	32480	0.9	1.0E-90	11426910	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7220	20085	33500	0.73	1.0E-90	U91934.1	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
7849	20904	34408	2.31	1.0E-90	11426758	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9021	22100	35640	3	1.0E-90	11422088	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9493	22550		0.92	1.0E-90	AF163884.1	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9518	22581	36148	1.4	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9518	22581	36149	1.4	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
4313	17458	30444	8.29	8.0E-91	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line, Homo sapiens cDNA clone s381 3'
8501	21592	35118	1.14	7.0E-91	11419234	NT	Homo sapiens makoln, ring finger protein, 1 (MKRN1), mRNA
10607	23542	37153	0.65	7.0E-91	A904151.1	EST_HUMAN	GM-BT043-090289-075 BT043 Homo sapiens cDNA
3563	16728	29744	1.85	5.0E-91	AA702794.1	EST_HUMAN	z950504.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4039	17775	30755	1.14	5.0E-91	AU143539	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4639	17775	30756	1.14	5.0E-91	AU143539	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4930	18060	31042	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4930	18060	31043	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6750	19808	33300	1.25	5.0E-91	A1879995.1	EST_HUMAN	au49709.x1 Schmeider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW:ASPG_FLAME_Q47898 N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR
8400	21481	35009	1.33	5.0E-91	BF314682.1	EST_HUMAN	601901624FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8960	22039	35581	1.47	5.0E-91	AV649876.1	EST_HUMAN	AV649876 GLC Homo sapiens cDNA clone GLCBYF08 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8960	22039	35582	1.47	5.0E-91	AV648878.1	EST_HUMAN	AV648878 GLC Homo sapiens cDNA clone GLOBYF08 3'
12871	26631		1.61	5.0E-91	AI193366.1	EST_HUMAN	qg70f11.x1 Soares_fetal_lung_NHLL19W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains
3272	16446	29465	1.58	4.0E-91	AF156776.1	NT	MIR.b2 MIR MIR repetitive element;
3272	16446	29466	1.58	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
11171	24242	37875	3.22	4.0E-91	AL163284.2	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
							Homo sapiens chromosome 21 segment HS21C084
12376	25287	32074	3.27	4.0E-91	M77894.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC80 similar to
							Retrovirus-related gag polyprotein
12376	25287	32119	3.27	4.0E-91	M77894.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC80 similar to
							Retrovirus-related gag polyprotein
12885	25457	32019	1.16	4.0E-91	M77894.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC80 similar to
							Retrovirus-related gag polyprotein
12885	25457	32020	1.16	4.0E-91	M77894.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC80 similar to
							Retrovirus-related gag polyprotein
1847	14800	27885	2.17	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1847	14800	27886	2.17	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1832	15983	28077	1.1	3.0E-91	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR domain enzyme APOLLON mRNA, complete cds
3420	15589	29605	1.29	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3551	18716	29729	4.85	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3551	18716	29730	4.85	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3888	17047	30047	0.93	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4714	17849	30832	4.41	3.0E-91	M30938.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
5094	18222	31193	1.48	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5094	18222	31194	1.48	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5803	18983	32296	3.55	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19.5kD) (HET), mRNA
6434	18602		2.56	3.0E-91	4602740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
							Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
8713	19871	33262	2.98	3.0E-91	11467811	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
8713	19871	33263	2.98	3.0E-91	11467811	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7816	20871	34368	4.48	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7816	20871	34369	4.48	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8132	21214	34735	0.69	3.0E-91	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8970	22049	35592	2.73	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9488	22545	38108	0.73	3.0E-91	AB011163.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11480	24539	38207	1.49	3.0E-91	AB028003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11480	24539	38208	1.49	3.0E-91	AB028003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
13037	18485	31430	8.54	3.0E-91	AF169556.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
13037	18485	31431	8.54	3.0E-91	AF169556.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
49	13288	26300	2.94	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1274	14431	27502	2.74	1.0E-91	AW449749.1	EST_HUMAN	U1H-B13-ake-d01-0-U1.8.1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
5529	18728	31742	0.78	1.0E-91	11434402	EST_HUMAN	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6983	20211	33940	1.98	1.0E-91	BF348182.1	EST_HUMAN	60202088F1 NCL CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4157804 5'
6983	20211	33941	1.98	1.0E-91	BF348182.1	EST_HUMAN	60202088F1 NCL CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4157804 5'
12130	25110	38814	1.48	1.0E-91	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSBEC05 5'
12540	28114		1.5	1.0E-91	H15212.1	EST_HUMAN	Yn30e03.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:49587 5'
1270	14428	27496	5.77	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1270	14428	27497	5.77	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5309	18428	31396	0.88	9.0E-92	AJ020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5579	18774	31820	5.98	9.0E-92	J03007.1	NT	Human Na ⁺ K ⁺ ATPase alpha-subunit mRNA, partial cds
5722	18915	32210	2.82	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
8583	19745	33127	3.77	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
8041	21124	34644	0.55	9.0E-92	AJ250586.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8041	21124	34645	0.55	9.0E-92	AJ250586.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8569	21650	35191	1.53	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8569	21650	35192	1.53	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9474	22531	36095	1.83	9.0E-92	11422036	EST_HUMAN	Homo sapiens brafadin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
95	13330	26357	6.63	8.0E-92	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
266	13513	26547	3.09	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614867 5'
1866	15012	28119	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90K) (DGKG), mRNA
1866	15012	28120	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90K) (DGKG), mRNA
5508	18707	31722	0.69	8.0E-92	AB046820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds
							Homo sapiens FVE domain-containing dual specificity protein phosphatase FVE-DSP2 mRNA, complete cds
5615	18809	31877	0.8	8.0E-92	AF284717.1	NT	Homo sapiens MCP-4 gene
6677	19836	33225	1.28	8.0E-92	AJ000979.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
6680	19839	33228	0.91	8.0E-92	AF178428.1	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8283	21365		0.55	8.0E-92	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8620	21700	35235	5.05	8.0E-92	L04163.1	NT	Human lens membrane protein (mp18) gene, exon 11

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8620	21700	35236	5.05	8.0E-92	L04193.1	NT	Human lens membrane protein (mp18) gene, exon 11
8721	21801	35337	0.71	8.0E-92	11426369	NT	Homo sapiens transcription termination factor, RNA polymerase II (TF2), mRNA
9262	22339	35889	2.33	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10232	23287	36857	0.91	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
11043	24121	37755	2.86	8.0E-92	AF074353.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11642	24722	38415	1.93	8.0E-92	4503340	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
12740	25491	32028	1.59	8.0E-92	11434704	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
68	13305	26328	1.91	7.0E-92	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
246	16008	26498	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
246	16008	26496	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
604	13793	27533	1.69	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Sepsase truncated isoform mRNA, complete cds
1309	14465	27533	1.94	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2260	15393	28619	3.85	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2260	15393	28620	3.85	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2630	15753	28868	6.13	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2787	15903	29010	5.84	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S158E), mRNA
3426	18466	29609	0.7	7.0E-92	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3426	18466	29610	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4710	17945	30828	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4710	17945	30829	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5284	18403	31371	0.98	7.0E-92	4508118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5376	18578	31446	5.51	7.0E-92	AA446208.1	EST_HUMAN	zfv6d12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:761175 5'
2178	15313	28441	0.96	3.0E-92	11434814	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA
2178	15313	28442	0.96	3.0E-92	11434814	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA
2824	15938	29048	2.74	3.0E-92	BE908714.1	EST_HUMAN	001501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
5997	19182	32504	3.96	3.0E-92	AA378336.1	EST_HUMAN	EST01020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
11002	24081	37716	3.26	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
11002	24081	37717	3.26	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12878	28198		1.87	3.0E-92	BF387138.1	EST_HUMAN	RC1-GN0021-240800-012-e11 GN0021 Homo sapiens cDNA
26	13284	28286	1.54	2.0E-92	4501888	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
183	13405	28433	4.28	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ482O23.2 (dJ482O23.2), mRNA
183	13405	28434	4.28	2.0E-92	11422948	NT	Homo sapiens hypothetical protein dJ482O23.2 (dJ482O23.2), mRNA
768	13949	28997	5.49	2.0E-92	BE298190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
768	13949	28998	5.49	2.0E-92	BE298190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1752	14901		1.82	2.0E-92	S78653.1	NT	mfg-mas-related [Human, Genomic, 2416 nt]
							Wk27407.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1990	15132	28238	2.53	2.0E-92	A1818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1990	15132	28237	2.53	2.0E-92	A1818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2020	15161	28285	1.01	2.0E-92	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2020	15161	28286	1.01	2.0E-92	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2108	15245	28366	5.35	2.0E-92	4506860	NT	Homo sapiens syndecan 4 (amphiglycan, rydooan) (SDC4) mRNA
2725	15943	28954	22.36	2.0E-92	6912457	NT	Homo sapiens calcitonin binding protein 1 (KIAA0330), mRNA
3701	16862	28864	1.02	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3701	16862	28865	1.02	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3777	16938	28944	7.02	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4403	17546	30530	1.17	2.0E-92	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete proviral segment
5108	18236		4.1	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5'
5878	19069	32377	0.84	2.0E-92	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6431	19599		7.19	2.0E-92	4504758	NT	Homo sapiens Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
6748	19904	33297	2.6	2.0E-92	AB028991.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7627	20697		0.81	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7657	20697		0.84	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
9056	22135	35680	1.28	2.0E-92	AW340174.1	EST_HUMAN	h0202.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
10987	24076	37709	4.68	2.0E-92	11434900	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
11257	24326	37965	3.22	2.0E-92	11434759	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
11409	24470	38134	5.71	2.0E-92	AW838290.1	EST_HUMAN	Homo sapiens zinc finger protein 198 (ZNF198), mRNA
11409	24470	38135	5.71	2.0E-92	AW838290.1	EST_HUMAN	GM4-L70028-161289-062-g08 L70028 Homo sapiens cDNA
12758	25502	32036	8.48	2.0E-92	AB028016.1	NT	GM4-L70028-161289-062-g08 L70028 Homo sapiens cDNA
							Homo sapiens mRNA for KIAA1063 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12782	25524	32005	1.36	2.0E-92	AF106558.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
13066	15843	28954	73.58	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIA0330), mRNA
1897	15040	28150	2.95	1.0E-92	R78078.1	EST_HUMAN	yf80e08.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1897	15040	28151	2.95	1.0E-92	R78078.1	EST_HUMAN	yf80e08.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2135	15271	28392	35.12	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8441	21522	35051	0.82	1.0E-92	BE439825.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
							ig01b02.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN
							Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element; contains element
							MER17 repetitive element
9385	22440	35999	3.24	1.0E-92	AI380356.1	EST_HUMAN	ig01b02.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN
							Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element; contains element
9385	22440	36000	3.24	1.0E-92	AI380356.1	EST_HUMAN	MER17 repetitive element
2085	15225	28347	3.53	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MANM1 Homo sapiens cDNA clone MAMMA1000738 5'
							EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2100	15240		20.41	9.0E-93	AA316723.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2712	15830		1.69	9.0E-93	AF223391.1	NT	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
3703	16864	29867	1.35	9.0E-93	BE388571.1	EST_HUMAN	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
11947	24933		7.79	9.0E-93	11418528	NT	601490521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
6723	19880	33271	2.4	8.0E-93	BF036364.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
256	13476	26506	7.25	7.0E-93	AF231919.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
3144	16320	29332	0.74	6.0E-93	11526176	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6819	19972	33380	0.97	6.0E-93	AB033093.1	NT	Homo sapiens PTH-related osteosarcoma B1 protein (B1) mRNA, complete cds
7056	20109	33525	7.64	6.0E-93	AF095771.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1412	14566	27840	0.99	5.0E-93	AB014511.1	NT	wd09c08.x1 NCL CGAP P-28 Homo sapiens cDNA clone IMAGE:2314670 3'
1439	14592	27666	4.61	5.0E-93	AI674184.1	EST_HUMAN	wd09c08.x1 NCL CGAP P-28 Homo sapiens cDNA clone IMAGE:2314670 3'
1439	14592	27667	4.61	5.0E-93	AI674184.1	EST_HUMAN	wd09c08.x1 NCL CGAP P-28 Homo sapiens cDNA clone IMAGE:2314670 3'
1504	14657		4.17	6.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
1869	19049	28123	1.03	5.0E-93	AJ297710.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
3305	16479	29500	3.73	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
5920	19107	32420	1.09	5.0E-93	M22878.1	NT	Human somatic cytochrome c (HCT) processed pseudogene, complete cds
							Homo sapiens wbscr1 (WBSCTR1) and wbscr5 (WBSCTR5) genes, complete cds, alternatively spliced and
							replication factor C subunit 2 (RFC2) gene, complete cds
6235	19410		1.75	5.0E-93	AF046555.1	NT	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7892	20944	34450	3.52	5.0E-93	AF067138.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8804	21883	35422	0.73	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8804	21883	35423	0.73	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9822	22892	36443	2.02	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10012	23080	36844	1.35	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10276	23310	36906	1.78	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
11084	24140	37775	1.92	5.0E-93	11439598	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12651	25781	31921	2.31	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
80	13325		6.63	4.0E-93	AA458933.1	EST_HUMAN	zx60c09.6.1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT
458	13653	26590	2.38	4.0E-93	4557879	NT	P97397 CALPONIN, ACIDIC ISOFORM ;
458	13653	26591	2.38	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
793	13972	27024	1.16	4.0E-93	7657464	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
793	13972	27025	1.16	4.0E-93	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1210	14371	27431	2.12	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
2033	15174	28284	4.37	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2318	15450	28582	1.19	4.0E-93	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2672	15792	28908	1.16	4.0E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3656	16819	29831	0.73	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4159	17310	30306	1.51	4.0E-93	4604854	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5138	16819	29831	0.75	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5760	18952	32286	5.01	4.0E-93	T46864.1	EST_HUMAN	y694c12.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:76833 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN ,
11398	24459	38123	10.47	4.0E-93	AY692051.1	EST_HUMAN	SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN ,
3742	16903	29906	12.26	3.0E-93	BF690630.1	EST_HUMAN	AY692051 GKX Homo sapiens cDNA clone GKDRP07 5'
3742	16903	29907	12.26	3.0E-93	BF690630.1	EST_HUMAN	60224654F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4350	17493		2.6	3.0E-93	AF225696.1	NT	60224654F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
6693	19851	33242	1.31	3.0E-93	11426182	NT	Homo sapiens tensin mRNA, complete cds
11040	24119	37752	2.86	3.0E-93	AB24829.1	EST_HUMAN	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast homolog)-like 2 (GCN5L2), mRNA
195	13418	26447	5.59	2.0E-93	AB015610.1	NT	w602805.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:2304489 3'
							Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
185	13418	26448	5.59	2.0E-93	AB015610.1	NT	Chlorocibius ethiops mRNA for ribosomal protein S4X, complete cds
333	13547	26578	13.77	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
334	13547	26578	6.74	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1646	14799	27884	3.9	2.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
2199	16334	28481	2.23	2.0E-93	U40763.1	NT	Human Cdk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2555	15680	28805	1.02	2.0E-93	BE25282.1	EST_HUMAN	601117596F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5254	18374	31340	1.19	2.0E-93	BE253201.1	EST_HUMAN	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
5533	18730	31749	5.08	2.0E-93	AW964388.1	EST_HUMAN	EST378458 MAGE resequences, MAGH Homo sapiens cDNA
5544	18741	31775	0.7	2.0E-93	4768153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5660	18854		0.64	2.0E-93	BF351468.1	EST_HUMAN	QV3-HT0513-280300-128-h04 HT0513 Homo sapiens cDNA
5754	18946	32248	1.08	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC81318), mRNA
5768	18960	32261	0.76	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-88
6822	18975		1.2	2.0E-93	AW502002.1	EST_HUMAN	UHF-BND-aks-g-09-Q.U.11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
11333	24398	38044	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
11333	24398	38045	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
12526	25358		1.78	2.0E-93	AA128735.1	EST_HUMAN	2129c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
12624	25420		3.25	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12930	25613		6.34	2.0E-93	BF035327.1	EST_HUMAN	901458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
105	13341	26368	1.38	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
105	13341	26369	1.38	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
531	13724	26750	7.78	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (D3328E19.C1.1), mRNA
613	13802	26822	3.32	1.0E-93	AI146755.1	EST_HUMAN	oy64b03.x1 NCJ CGAP CLL1 Homo sapiens cDNA clone IMAGE:1872503 3' similar to TR:082384 Q62384
896	14071	27136	3.43	1.0E-93	D87876.1	NT	ZINC FINGER PROTEIN.1
1194	14356	27414	0.6	1.0E-93	4903872	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1265	14422	27487	7.22	1.0E-93	8923270	NT	Homo sapiens glutamate decarboxylase 1 (brain, 87kD) (GAD1), transcript variant GAD67, mRNA
1265	14422	27488	7.22	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA
1376	14631	27604	9.7	1.0E-93	AF167706.1	NT	Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA
2414	15544	28672	1.08	1.0E-93	AF231981.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2534	15659	28763	3.06	1.0E-93	AF050586.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2576	15702		1.29	1.0E-93	AL137200.1	NT	Homo sapiens MHC class 1 region
2883	14480	27546	1.32	1.0E-93	BE297399.1	EST_HUMAN	Homo sapiens gene mapping to chromosome 1
2883	14480	27547	1.32	1.0E-93	BE297399.1	EST_HUMAN	601117886F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2883	14480	27547	1.32	1.0E-93	BE297399.1	EST_HUMAN	601117886F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3000	16176	29197	5.86	1.0E-93	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3287	16461		1.23	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4549	17687	30968	3.28	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5348	18461	31428	0.92	1.0E-93	AF123498.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
5348	18461	31427	0.92	1.0E-93	AF123498.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
5884	18878	32167	2.39	1.0E-93	U78508.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5884	18878	32168	2.39	1.0E-93	U78508.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5885	19074	32383	1.2	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6037	19220	32543	10.78	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6326	19498	32855	4.8	1.0E-93	7682241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
6931	20246	33679	1.94	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7400	20478	33946	3.24	1.0E-93	D42072.1	NT	Human mRNA for NF1 N1 isoform-exon11, complete cds
8455	21536	35066	2.29	1.0E-93	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8740	21819	35353	1.15	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEMD protein
8850	21929	35468	1.14	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9651	21094	34608	2.03	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9655	21098	34612	1.14	1.0E-93	AF091395.1	NT	Homo sapiens Trho isoform mRNA, complete cds
9767	22827	36403	3.9	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9767	22827	36404	3.9	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9926	22966	36556	1.24	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10349	23384	36994	0.59	1.0E-93	11433648	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
12820	25547		1.62	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12923	25608		3.71	1.0E-93	11417859	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
13108	25723	31941	1.36	1.0E-93	11417862	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
13123	26173		1.42	1.0E-93	AF240786.1	NT	Homo sapiens chromosome 21 segment HS21C009
10819	23862		1.13	8.0E-94	AL163209.2	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
4070	17226	30233	1.04	8.0E-94	AF142482.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5483	18682	31698	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5483	18682	31698	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6173	18349	32895	2.24	5.0E-94	AA722434.1	EST_HUMAN	z987g05.s1 Soares_Telomere1_NBHH19W Homo sapiens cDNA clone IMAGE:409594 3'
7150	20285	33726	1.45	5.0E-94	AJ015800.1	EST_HUMAN	cl83405.s1 Soares_Telomere1_NB2HFB_9w Homo sapiens cDNA clone IMAGE:1623368 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8940	21919	35457	0.85	5.0E-94	BF529115.1	EST_HUMAN	602042163F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4180023 5'
11216	24284	37922	1.43	5.0E-94	11423952	NT	Homo sapiens adenylylate kinase 2 (AK2), mRNA
11215	24284	37923	1.43	5.0E-94	11423962	NT	Homo sapiens adenylylate kinase 2 (AK2), mRNA
12503	26177	31558	3.6	5.0E-94	T89398.1	EST_HUMAN	Yd88b04.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:116239 3'
1890	18034		16.48	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2723	18841	28952	0.89	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3762	18923	28925	1.12	4.0E-94	AW197851.1	EST_HUMAN	x189f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3762	18923	28926	1.12	4.0E-94	AW197851.1	EST_HUMAN	x189f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4840	17973	30963	3.06	4.0E-94	AI591312.1	EST_HUMAN	hw1110.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15285 Q15285 PROTEIN TYROSINE PHOSPHATASE ;
6597	19757	33144	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6597	19757	33145	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7052	20106		0.8	4.0E-94	L27386.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
628	13811	28833	1.76	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
739	13921	28961	1.13	3.0E-94	4502508	NT	Homo sapiens complement component 5 (C5) mRNA
1779	14928	28021	12.9	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1779	14928	28022	12.9	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1813	14962	28055	3.18	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4306	17449	30435	0.67	3.0E-94	AA494605.1	EST_HUMAN	zw63g08.f1 Soares_fetal_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
4437	17577	30557	0.72	3.0E-94	AA781836.1	EST_HUMAN	ais9f06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376163 3'
5798	18988	32292	3.21	3.0E-94	11498288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6279	19453	32801	1.13	3.0E-94	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6581	18743	33125	3.84	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
7978	21027	34541	0.63	3.0E-94	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8363	21474	35001	0.96	3.0E-94	AF152309.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8787	21866	35408	4.41	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
9781	22831	36410	7.29	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
11362	24423	38079	1.94	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
11976	24960	38882	2.11	3.0E-94	U28711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
9954	22953	36587	0.67	2.0E-94	AI910393.1	EST_HUMAN	w130h11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
8854	22993	36588	0.67	2.0E-94	AI910393.1	EST_HUMAN	w130h11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
153	13378	26410	3.07	1.0E-94	BE298714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'

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Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3158	16333	28342	2.05	1.0E-94	BE253433.1	EST_HUMAN	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3159	16333	28343	2.05	1.0E-94	BE253433.1	EST_HUMAN	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4478	17618	30800	1.11	1.0E-94	9508892	NT	Homo sapiens hypothetical protein (FLJ20749), mRNA
6198	18373	32724	0.69	1.0E-94	AE000269.1	NT	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome
6306	18565	32825	1.91	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G0314 5'
6405	19574	32836	0.82	1.0E-94	H08270.1	EST_HUMAN	W87f02.r1 Spares infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'
6648	19807	33194	0.66	1.0E-94	AV725892.1	EST_HUMAN	AV725892 HTC Homo sapiens cDNA clone HTCEBF05 5'
8304	21386	34908	0.8	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8304	21386	34909	0.8	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9456	22572	36138	2.17	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
9880	23029	36620	1.35	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872088 5'
11321	24384	38028	3.11	1.0E-94	U85590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11587	24850	38334	1.88	1.0E-94	AI272244.1	EST_HUMAN	ap22a02.x1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1986122 3' similar to TR-Q82845
12051	25032	38728	1.34	1.0E-94	11418871	NT	Q82845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR, ;
12839	13378	28410	2.02	1.0E-94	BE298714.1	EST_HUMAN	Homo sapiens KIAA0184 gene product (KIAA0184), mRNA
12968	13378	28410	1.73	1.0E-94	BE298714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1508	14858	27741	6.05	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3224	16398	28409	1.09	9.0E-95	7682027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3224	16398	28410	1.09	9.0E-95	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5521	18718	31733	1.46	9.0E-95	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5521	18718	31734	1.46	9.0E-95	X82569.1	NT	Musculus glyt1 gene (exons 1c and 2)
8446	21527	35054	1.58	9.0E-95	AF274753.1	NT	Musculus glyt1 gene (exons 1c and 2)
149	13374	26407	2.9	8.0E-95	AF154830.1	NT	Homo sapiens progressive encephalitis-like protein (ANK) mRNA, complete cds
4658	17794	30779	1.68	8.0E-95	AI700998.1	EST_HUMAN	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
4658	17794	30780	1.68	8.0E-95	AI700998.1	EST_HUMAN	wed0804.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
7087	20181	33805	0.73	8.0E-95	11419376	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7390	20468	33934	1.4	8.0E-95	11428529	NT	wed0904.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
7390	20468	33935	1.4	8.0E-95	11428529	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
8391	21472	34998	2.08	8.0E-95	AF032897.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
9565	22707	36273	1.98	8.0E-95	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens KIAA0255 gene product (KIAA0255), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9565	22707	38274	1.98	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10053	23091	38693	2.45	8.0E-95	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH), mRNA
10083	23121		2.92	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10440	23475	37079	0.81	8.0E-95	9845523	NT	Homo sapiens early growth response 2 (Krox-20) (Drosophila) homolog (EGR2), mRNA
10953	24035	37670	1.59	8.0E-95	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
11773	24765	38461	1.72	8.0E-95	10864024	NT	Homo sapiens HGF-binding transcription factor Zhangfei (ZF), mRNA
11982	24887	38669	1.32	8.0E-95	7019572	NT	Homo sapiens zincfin (ZNF), mRNA
11982	24887	38670	1.32	8.0E-95	7019572	NT	Homo sapiens zincfin (ZNF), mRNA
12887	25988		17.21	8.0E-95	AA629056.1	EST_HUMAN	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744849 3' similar to contains L1.L1 repetitive element
288	13504	26537	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
286	13504	26538	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2519	15645	28767	1.37	7.0E-95	M75073.1	NT	Human hepatocyte growth factor gene, exon 8
2519	15645	28768	1.37	7.0E-95	M75073.1	NT	Human hepatocyte growth factor gene, exon 8
4488	17628	30608	15.92	7.0E-95	M95708.1	NT	Homo sapiens Ly-8-like protein (CD59) mRNA, complete cds
4535	17673		1.09	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9418	22492	36058	0.82	4.0E-95	BE439825.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
215	13438	26468	0.82	3.0E-95	AV648361.1	EST_HUMAN	AV648361 GLC Homo sapiens cDNA clone GLCBF01 3'
5558	18756	31794	1.52	3.0E-95	BF526041.1	EST_HUMAN	802071146F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4214147 5'
5791	25811	32285	0.94	3.0E-95	4503354	NT	Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA
7315	20397	33859	0.73	3.0E-95	AA412321.1	EST_HUMAN	287401.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7315	20397	33860	0.73	3.0E-95	AA412321.1	EST_HUMAN	287401.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7525	20598	34071	2.01	3.0E-95	AW958121.1	EST_HUMAN	EST370181 IMAGE resequences, IMAGE Homo sapiens cDNA
7525	20598	34072	2.01	3.0E-95	AW958121.1	EST_HUMAN	EST370181 IMAGE resequences, IMAGE Homo sapiens cDNA
9555	22620	36190	1.62	3.0E-95	7662280	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9555	22620	36191	1.62	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9948	22987	36581	0.86	3.0E-95	BF213446.1	EST_HUMAN	801845212F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070451 5'
1876	14828	27911	3.52	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1876	14828	27912	3.52	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1996	15136	28242	73.27	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
1998	15139	28245	3.97	2.0E-95	BE393873.1	EST_HUMAN	801312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2497	15624	28743	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19), mRNA
2497	15624	28744	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2536	15661	28784	3.62	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2582	15707	28828	1.34	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2662	15784		0.89	2.0E-95	RI6245.1	EST HUMAN	ya49d08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53393 3'
3228	16400	29412	2.1	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3655	16818	28629	3.6	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3655	16818	28630	3.6	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3706	16867	29870	0.81	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3844	17004	30009	0.62	2.0E-95	AI290264.1	EST HUMAN	qin01c02.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4
4481	17521	30602	1.38	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5151	18273	31242	3.5	2.0E-95	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5230	18352	31321	0.99	2.0E-95	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5597	18792	31840	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5597	18792	31841	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5815	19005	32310	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5815	19005	32311	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5855	19045	32352	0.63	2.0E-95			Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6270	19444	32793	3.86	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFKM) gene, exon 7
6579	19741	33122	0.9	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6579	19741	33123	0.9	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6700	19858	33248	3.25	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6903	20218	33647	1.47	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9343	22419	35973	1.48	2.0E-95	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10592	23627	37236	0.56	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10982	24043	37678	1.88	2.0E-95	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRIA) mRNA
11138	24210	37836	1.35	2.0E-95	7661983	NT	Homo sapiens Ste20-related serine/threonine kinase (KIAA0204), mRNA
12002	24987	38691	1.69	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12002	24987	38692	1.69	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12103	25083		1.57	2.0E-95	AF161420.1	NT	Homo sapiens HSPC302 mRNA, partial cds
12608	25407	32047	2.31	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12721	25480		1.3	2.0E-95	11417860	NT	Homo sapiens hypothetical protein (H5322B1A), mRNA
13087	25698	31966	7.4	2.0E-95	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
						EST_HUMAN	Homo sapiens ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
						EST_HUMAN	z223h04.1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
						EST_HUMAN	TR:G1087084 G1087084 F59H2.6 ;
						EST_HUMAN	z223h04.1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
5732	18925	32219	8.06	1.0E-95	AA284651.1	EST_HUMAN	TR:G1087084 G1087084 F59H2.6 ;
						EST_HUMAN	TR:G1087084 G1087084 F59H2.6 ;
5732	18925	32220	8.06	1.0E-95	AA284651.1	EST_HUMAN	TR:G1087084 G1087084 F59H2.6 ;
7683	20748	34228	4.11	1.0E-95	BF370000.1	EST_HUMAN	RC8-FN0019-290800-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:31763 5'
7683	20748	34230	4.11	1.0E-95	BF370000.1	EST_HUMAN	RC8-FN0019-290800-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3922423 5'
9663	22826	36197	0.45	1.0E-95	R17806.1	EST_HUMAN	y09b06.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:3899781 5'
9388	21469	34996	1.98	9.0E-96	BE807259.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3899781 5'
455	16012	26687	0.88	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899781 5'
455	16012	26688	0.88	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899781 5'
5628	18822	30183	1.25	7.0E-96	AF231920.1	EST_HUMAN	PMO-L70019-090300-002-409 L70019 Homo sapiens cDNA
4018	17175	28600	2.48	6.0E-96	BE171984.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
2334	15485	28600	0.71	6.0E-96	AL163201.2	NT	MIR0-HT0559-250200-002-407 HT0559 Homo sapiens cDNA
3394	18564	28579	10.25	6.0E-96	M26873.1	NT	Homo sapiens chromosome 21 segment HS21C001
3571	16736	29751	2.41	6.0E-96		NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
11839	24828	38517	2.41	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11891	24879	38576	1.94	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12084	25045	38753	1.32	6.0E-96	7662289	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
12064	25045	38754	1.32	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
330	13544	28574	3.95	5.0E-96	AB032998.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
865	14041	27104	3.4	5.0E-96	AB032998.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
865	14041	27105	3.4	5.0E-96	AB032998.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
2684	16804	29284	1.72	5.0E-96	XG0812.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
3092	16268	31381	0.71	5.0E-96	XG0812.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
5024	18153	31381	0.79	5.0E-96	AF264750.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
5296	18414	33341	1.1	5.0E-96	AF149773.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6788	19943	33341	1.1	5.0E-96	AF149773.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6851	20004	33413	0.58	5.0E-96	AJ277557.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6921	20236	33669	3.68	5.0E-96	11424399	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6921	20236	33670	3.68	5.0E-96	11424399	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA

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7163	20299	33740	0.91	5.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7684	20749	34231	0.76	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8267	21379	34900	1.87	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8267	21379	34901	1.87	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 6
12063	25063	38769	1.33	5.0E-96	7661973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4308	17451		15.95	3.0E-96	H86666.1	EST_HUMAN	Yr87h12.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:212327 5'
428	13623		5.76	2.0E-96	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
766	13947	28994	1.1	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1834	14981	28079	1.03	2.0E-96	7706205	NT	Homo sapiens CGI-201 protein (LOC61340), mRNA
4880	18011	30995	1.56	2.0E-96	BE148074.1	EST_HUMAN	RC3-H1T0230-040500-110-p02 HT0230 Homo sapiens cDNA
7620	20690	34165	0.59	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250800-427-512 GN0120 Homo sapiens cDNA
7620	20690	34166	0.59	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250800-427-512 GN0120 Homo sapiens cDNA
9181	22259		4.9	2.0E-96	AV889461.1	EST_HUMAN	AV889461 GKCC Homo sapiens cDNA clone GKCFMD07 5'
12288	25214		2.54	2.0E-96	AW246440.1	EST_HUMAN	2819351 Sprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2819351 5'
638	13623	26845	0.86	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA
638	13623	26846	0.86	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA
688	13672	26905	3.08	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1822	14971	28063	9.97	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1822	14971	28064	9.97	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
5331	18444		1.59	1.0E-96	5453913	NT	Homo sapiens phospholipid transfer protein (PLTP), mRNA
7105	16532	31487	1.19	1.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7184	20059	33470	0.71	1.0E-96	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8407	21488	35017	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8407	21488	35018	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8913	21692	35531	21.44	1.0E-96	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
9051	22130	35674	2.22	1.0E-96	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10362	23397	37007	0.68	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
10362	23397	37008	0.68	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
12274	13823	26845	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA
12274	13823	26846	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA
3405	16575	28590	0.72	6.0E-97	BF245240.1	EST_HUMAN	801863712F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4081202 5'
7730	20762		3.4	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011069-004-D07 HT0117 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9134	22213	35757	0.75	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
9134	22213	35758	0.75	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10821	23854	37476	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST22872 Adipose tissue, white II Homo sapiens cDNA 5' end
10821	23854	37478	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST22872 Adipose tissue, white II Homo sapiens cDNA 5' end
11892	24680	38381	2.42	6.0E-97	X15804.1	NT	Human mRNA for alpha-actinin
8204	21286	34809	1.73	6.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hta53) Homo sapiens cDNA clone DKFZp434N0323 5'
8336	21417	34943	11.21	6.0E-97	AA418026.1	EST_HUMAN	z07e12.s1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:787788 3' similar to TR:G1304126
9877	22917	36502	3.12	5.0E-97	BF164912.1	EST_HUMAN	RCO-BT0812-250800-032-a09 BT0812 Homo sapiens cDNA
11840	24829	38519	1.68	5.0E-97	BE148597.1	EST_HUMAN	MRQ-HT0241-150800-010-502 H70241 Homo sapiens cDNA
11840	24829	38520	1.68	5.0E-97	BE148597.1	EST_HUMAN	MRQ-HT0241-150800-010-502 H70241 Homo sapiens cDNA
982	14135	27196	2.13	4.0E-97	BE004436.1	EST_HUMAN	CMO-BN0108-170300-293-a06 BN0108 Homo sapiens cDNA
1959	15102	28202	1.41	4.0E-97	5463572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
5683	18871	32166	0.82	4.0E-97	4557326	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
6862	20180	33615	6.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
6862	20180	33616	6.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7161	20284	33737	1.08	4.0E-97	7710125	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7214	20079	33492	0.82	4.0E-97	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8328	21411	34837	1.06	4.0E-97	4557708	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8553	21634	35171	1.43	4.0E-97	11421783	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8778	21858	35401	0.51	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) Interactor (NMI), mRNA
8820	21869	35438	0.82	4.0E-97	11423233	NT	Homo sapiens cytochrome P450, subfamily VB, polypeptide 1 (CYP4B1), mRNA
9449	22565	36128	1.06	4.0E-97	AB011186.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9449	22565	36129	1.06	4.0E-97	AB011186.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10652	23698	37296	0.55	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) Interactor (NMI), mRNA
11435	24498	38162	1.99	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11435	24498	38163	1.99	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11719	23905	37528	4.61	4.0E-97	AB042557.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
12472	25325		5.26	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
253	13473	26504	1.58	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
897	14073	27138	7.16	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

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897	14073	27139	7.16	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1473	16039	27712	1.94	3.0E-97	4768813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2508	15998	28755	2.4	3.0E-97	U36255.1	NT	Human beta-prime-adipin (BAM22) gene, exon 7
3333	16508	29523	0.96	3.0E-97	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
4902	18032	31021	22.23	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6557	19719	33095	2.72	1.0E-97	BE566486.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
7039	20092	33509	0.69	1.0E-97	9453881	NT	Homo sapiens phosphotyrosine kinase, gamma 1 (muscle) (PHKG1) mRNA
9988	23005	36600	1.02	1.0E-97	R10887.1	EST_HUMAN	yf38c08.s1 Soares fetal liver spleen 1NF5S Homo sapiens cDNA clone IMAGE:129134 3'
10945	24027	37663	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
10945	24027	37684	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
11589	24642	38324	1.38	1.0E-97	AA553761.1	EST_HUMAN	nk28g02.s1 NCL CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014862 3'
11768	23942	37668	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11768	23942	37569	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
924	14099	27163	2.34	9.0E-98	BE090873.1	EST_HUMAN	PM4-BT0724-010400-008-at12 BT0724 Homo sapiens cDNA
1305	14461	27528	1.32	9.0E-98	8393082	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6432	18600		0.70	9.0E-98	AL250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
8020	21072	34583	4.13	9.0E-98	AB046956.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8020	21072	34584	4.13	9.0E-98	AB046956.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8109	21191	34711	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8109	21191	34712	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9316	22392	35943	1.78	9.0E-98	X06989.1	NT	Human mRNA for amyloid A4(751) protein
9425	22499	36064	1.12	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9492	22549	36112	1.6	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9640	22605		0.61	9.0E-98	AF05726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9687	22709	36276	1.28	9.0E-98		NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9687	22709	36277	1.28	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10467	23502	37115	0.67	9.0E-98	AF141325.2	NT	Homo sapiens insect polyphospho 1-phosphatase (INPP1) gene, complete cds
10575	23610	37215	0.5	9.0E-98	11431544	NT	Homo sapiens protease-activated receptor 3 (PAR3), mRNA
11253	24322	37802	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11253	24322	37863	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12487	14099	27163	4.97	9.0E-98	BE090873.1	EST_HUMAN	PM4-BT0724-010400-008-at12 BT0724 Homo sapiens cDNA

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1403	14557	27631	0.93	8.0E-08	AB033798.1	NT	Homo sapiens HPAD-colony10 mRNA for peptidylarginine deaminase type I, complete cds
1591	14743	27825	1.1	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1591	14743	27826	1.1	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1785	14814	28009	2.79	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1785	14914	28010	2.79	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3886	17055	30055	6.45	8.0E-08	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
6207	19382	32732	0.96	5.0E-08	BE895873.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 5'
2247	15380	28508	1.35	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2873	16793	28910	2.1	3.0E-08	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2807	15921		5.04	3.0E-08	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7085	20179	33602	1.99	3.0E-08	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7085	20179	33603	1.99	3.0E-08	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
8951	22030	35571	4.07	3.0E-08	H46698.1	EST_HUMAN	ye17g08.r1 Soares adult brain N265HB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9497	22553	36116	0.54	3.0E-08	8922096	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
10087	23125	36726	1.82	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10087	23125	36727	1.82	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10691	23724	37330	0.89	3.0E-08	BE900454.1	EST_HUMAN	601673886F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
11165	24264	37859	2.56	3.0E-08	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
11819	24808	38504	2.22	3.0E-08	AI159975.1	EST_HUMAN	qb80h02.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1708451 3'
13138	25739		3.01	3.0E-08	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
754	13935	26980	0.67	2.0E-08	BE261694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2141	15277	28309	4.06	2.0E-08	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2311	15443	28578	2.21	2.0E-08	AL163202.2	NT	Homo sapiens chromosome 21 segment HS27C002
4411	17553	30538	0.82	2.0E-08	AF032887.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4459	17599	30577	4.23	2.0E-08	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4948	18078	31052	1.39	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 16
4948	18078	31053	1.39	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 16
5482	18691	31708	4.78	2.0E-08	7708512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6793	19948	33347	1.7	2.0E-08	4505798	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7801	20857	34348	1.25	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7801	20857	34349	1.25	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8807	21866	35428	4.44	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8807	21866	35427	4.44	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8889	21988	35503	0.8	2.0E-98	L76656.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8889	21988	35504	0.8	2.0E-98	L76656.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9737	22802	36376	1.56	2.0E-98	X12684.1	NT	H. sapiens arginase gene exon 3 (EC 3.5.3.1)
10624	23668		1.66	2.0E-98	7708668	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
12136	25116		1.61	2.0E-98	AB046613.1	NT	Homo sapiens mRNA for KIAA1869 protein, partial cds
12492	25340	32062	2.23	2.0E-98	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
418	13613	26953	27.52	1.0E-98	AI882007.1	EST_HUMAN	tm66504.x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN
467	13682	26808	3.27	1.0E-98	AW988511.1	EST_HUMAN	P28318 60S RIBOSOMAL PROTEIN L23A.
1840	14986	28086	28.16	1.0E-98	N49818.1	EST_HUMAN	PMD-BN0085-100300-001-c08 BN0085 Homo sapiens cDNA
5432	18632	31610	3.3	1.0E-98	AA195854.1	EST_HUMAN	Y2305.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to
5687	18881	32172	0.97	1.0E-98	BE390627.1	EST_HUMAN	PIR:S54204 S54204 ribosomal protein L28 - human;
5687	18881	32173	0.97	1.0E-98	BE390627.1	EST_HUMAN	z08609.1 Striatogene muscle 937208 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562
9199	22277	35815	0.58	1.0E-98	AF141349.1	NT	G806562 NEBULIN.
9199	22277	35816	0.58	1.0E-98	AF141349.1	NT	801284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3806892 5'
5939	19125	32438	1.05	9.0E-99	AI905004.1	EST_HUMAN	801284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3806892 5'
5939	19125	32439	1.05	9.0E-99	AI905004.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
6166	19341	32588	4.01	9.0E-99	AW988635.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
11384	24445	38105	1.86	9.0E-99	AI479829.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
11384	24445	38106	1.85	9.0E-99	AI479829.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
11700	24697	38389	1.72	9.0E-99	AA134604.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
8924	22003	35542	1.19	8.0E-99	AF035808.1	NT	EST380711 IMAGE resequences, MAGJ Homo sapiens cDNA
5956	19142	32458	0.25	7.0E-99	AF001886.1	NT	tm68h07.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
11909	24896	38599	1.91	7.0E-99	U10981.1	NT	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST
484	13678	28713	0.72	8.0E-99	U10981.1	NT	tm68h07.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
2196	15331	28456	6.2	6.0E-99	11430555	NT	tm68h07.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
2196	15331	28457	6.2	6.0E-99	11430555	NT	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST
3985	17152	30160	2.8	6.0E-99	AW978364.1	EST_HUMAN	z190d02.1 Striatogene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565443 5' similar to
4870	18003	30986	1.42	8.0E-99	4502660	NT	TR:G862894 G862894 GPI-ANCHORED PROTEIN P137.;
							Human endogenous retrovirus, complete genome
							Homo sapiens bacillin (hln) gene, exon 5
							Homo sapiens NK-receptor (KIR-32) gene, linker region exon
							Human G2 protein mRNA, partial cds
							Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
							Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
							EST388473 IMAGE resequences, MAGN Homo sapiens cDNA
							Homo sapiens CD34 antigen (CD34) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6732	19888	33290	0.94	6.0E-99	7706138	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
6816	19868	33378	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6816	19868	33377	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8298	21378	34899	1.85	6.0E-99	X99101.1	NT	H. sapiens mRNA for estrogen receptor
8314	21396	34921	0.59	6.0E-99	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8684	22043	35586	2.67	6.0E-99	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/sulfotransferase 4, complete cds
9084	22143	35688	7.6	6.0E-99	AF080255.1	NT	Homo sapiens lodeslar protein mRNA, complete cds
9084	22143	35689	7.6	6.0E-99	AF080255.1	NT	Homo sapiens lodeslar protein mRNA, complete cds
9123	22202	35744	0.59	6.0E-99	11431994	NT	Homo sapiens Inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
9123	22202	35745	0.59	6.0E-99	11431994	NT	Homo sapiens Inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
10858	24039	37674	3.15	6.0E-99	11526289	NT	Homo sapiens B3H interacting domain death agonist (BID), mRNA
11742	23928	37553	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
11742	23928	37554	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
2022	15163	28268	1	5.0E-99	Y11365.1	NT	H. sapiens IMPA gene, exon 8
4886	17821	30809	1.81	5.0E-99	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S9A2 to TCRBV12S2 region
12502	25346		2.49	5.0E-99	BE890177.1	EST_HUMAN	601613167F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
8618	21597		4.95	3.0E-99	M95588.1	NT	Human E2A/HLA fusion protein (E2A/HLP) mRNA, complete cds
1268	14428		7.26	2.0E-99	AW274792.1	EST_HUMAN	xp00908.x1 NCL CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI NON-MUSCLE ISOFORM (HUMAN);
3331	16504	29522	1.4	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4665	17800	30787	1.82	2.0E-99	AF095703.1	NT	Homo sapiens short chain L3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7851	20906	34410	0.76	2.0E-99	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8804	21983	35523	10.79	2.0E-99	W23507.1	EST_HUMAN	zb46406.r1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
9353	22428	35986	0.75	2.0E-99	R78254.1	EST_HUMAN	y181b09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145625 5'
11367	24428	38085	3.16	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
12081	25051	38767	1.64	2.0E-99	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
325	13559	26571	1.49	1.0E-99	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
390	13596	26632	1.75	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
1452	14605	27684	3.61	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1587	14739	27819	1.16	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1587	14739	27820	1.16	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1980	15123	28224	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1980	15123	28225	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
3154	16329	29339	0.93	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4498	17639	30621	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4499	17639	30622	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6943	20258	33684	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6943	20266	33695	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7289	25842	33827	0.81	1.0E-99	X88022.1	NT	H.sapiens EG-AP gene exon 2
8400	22474		0.75	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC61309), mRNA
8720	22785	36356	1.7	1.0E-99	AW340174.1	EST_HUMAN	h02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
11403	24464	38128	2.56	1.0E-99	7427514	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN:
11403	24464	38129	2.56	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11462	24521	38191	1.88	1.0E-99	5901979	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11659	24738	38429	2.83	1.0E-99	AB023222.1	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11988	24981	38687	2.45	1.0E-99	11417191	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12257	25193		4.52	1.0E-99	AF240786.1	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
1	13241	26241	1.7	1.0E-100	AL163247.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2	13241	26241	2.91	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
70	13307	26329	1.62	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047
70	13307	26330	1.62	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
89	13324	26353	0.82	1.0E-100	AW275237.1	EST_HUMAN	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
173	13397	26425	0.89	1.0E-100	AL163206.2	NT	x178b11.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3'
327	13541	26573	1.84	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C008
353	13564	26592	1.87	1.0E-100	T05087.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
450	13846		2.24	1.0E-100	AF003528.1	NT	EST02975 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBGR32
502	13897		5.88	1.0E-100	X80631.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
522	13716	26742	1.21	1.0E-100	BE180909.1	EST_HUMAN	G porilla DNA for ZNF80 gene homolog
1044	14210	27268	4.57	1.0E-100	7661685	NT	RC3-HT0625-040500-022-509 HT0625 Homo sapiens cDNA
1577	14730		1.3	1.0E-100	AW207555.1	EST_HUMAN	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1581	14733	27814	1.86	1.0E-100	AI200857.1	EST_HUMAN	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2315	15447		1.14	1.0E-100	D83349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2507	15634	28754	1.41	1.0E-100	X62468.1	NT	H.sapiens mRNA for IFN-gamma (pKG-O)
2771	15886	28096	2.5	1.0E-100	11418978	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
3083	16259		6.55	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4326	17469	30456	1.87	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4351	17494	30474	2.28	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5202	18323	31291	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5202	18323	31292	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5404	18608	31578	1.74	1.0E-100	BF244218.1	EST_HUMAN	601883164FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5'
5625	18819	31893	0.76	1.0E-100	AW075983.1	EST_HUMAN	xa82701.x1 NCI_CGAP_OML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb.X12433
5818	19008	32314	1.45	1.0E-100	AU118182	EST_HUMAN	PROTEIN PHPS1-2 (HUMAN);
5854	19054	32361	1.78	1.0E-100	AF135116.1	NT	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5960	19146	32461	0.85	1.0E-100	X14690.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6292	19465	32817	0.9	1.0E-100	4557568	NT	Human mRNA for plasma inter-alpha-1-hs-glycin inhibitor heavy chain h(3)
6292	19465	32818	0.9	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6826	19788	33174	5.62	1.0E-100	AU140214.1	EST_HUMAN	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6824	19977	33384	1.36	1.0E-100	R10887.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6808	20223	33653	1.77	1.0E-100	7382479	NT	Y38c08.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:129134 3'
6882	20210	33636	1.02	1.0E-100	AA498841.1	EST_HUMAN	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6882	20210	33639	1.02	1.0E-100	AA498841.1	EST_HUMAN	ae33b06.r1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
7026	20162	33583	1.18	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
7026	20162	33584	1.18	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
7033	20169	33581	6.2	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-b05 TN0048 Homo sapiens cDNA
8729	21809	35345	3.93	1.0E-100	BF103853.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0048 Homo sapiens cDNA
8766	21845		5.59	1.0E-100	AL163203.2	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9216	22294	35837	0.47	1.0E-100	AU116951.1	EST_HUMAN	601647357FT NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
9216	22294	35838	0.47	1.0E-100	AU116951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9433	22507	36073	3.86	1.0E-100	AB040518.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9510	22776		1.65	1.0E-100	A1972388.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9533	21076	34588	2.28	1.0E-100	AW98661.1	EST_HUMAN	Human sapiens mRNA for KIAA1485 protein, partial cds
							w37q09.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element MER22 repetitive element ;
							PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9887	22736			0.84	AU12720.1	EST_HUMAN	AU12720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9782	22872	36400		2.17	AB046846.1	NT	Homo sapiens mRNA for KIAA1828 protein, partial cds
9782	22822	36401		2.17	AB046846.1	NT	Homo sapiens mRNA for KIAA1828 protein, partial cds
10048	23086	36687		1.81	AW630487.1	EST_HUMAN	h83c11.y1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868396 5'
10048	23086	36688		1.81	AW630487.1	EST_HUMAN	h83c11.y1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868396 5'
10048	23086	36689		1.81	AF347518.1	EST_HUMAN	602020554F1 NC1_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4166186 5'
10688	23721	37327		0.84	BF347518.1	EST_HUMAN	Homo endogenous retrovirus HERV-K, pol gene
10782	23815			1.35	Y10391.1	NT	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
10986	24076	37708		6.64	BF327282.1	EST_HUMAN	H.sapiens CD97 gene exon 4
11584	24610	38300		1.55	AF11170.3	NT	H.sapiens CD97 gene exon 4
11584	24610	38301		1.55	X94633.1	NT	H.sapiens CD97 gene exon 4
11635	24715	38405		3.91	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11635	24715	38406		3.91	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11685	13241	26241		3.07	AF11170.3	NT	Homo sapiens chromosome 21 segment HS21C047
11977	24982			2.21	AF286286.1	NT	Homo sapiens oligin-like protein (GLP) gene, complete cds
12128	25108	38812		1.93	AF131034.1	NT	Homo sapiens class gene, exon 12
12177	25137	38832		7.59	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12312	26037			1.78	BF446549.1	EST_HUMAN	7q88H03.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to TR.Q21997 Q21997
12493	26341	32063		4.97	B1545732.NT	EST_HUMAN	COSMID R151.[2] TR:Q9UA08 ;
12754	25500	32033		1.31	11418123.NT	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
13195	25778	31835		6.91	11417974.NT	NT	Homo sapiens KIAA0003 gene product (KIAA0003). mRNA
79	13315	26342		0.92	11417974.NT	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
79	13315	26343		0.92	11417974.NT	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
79	13315	26343		0.92	11417974.NT	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13887	26919		1.4	AB007915.2	NT	Homo sapiens mRNA for KIAA0448 protein, partial cds
722	13904	26945		6.12	7110734.NT	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
722	13904	26946		6.12	7110734.NT	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
792	13971	27023		1.37	7857454.NT	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
876	14052	27117		1.35	4503914.NT	NT	Homo sapiens phosphoribosylglycanamide formyltransferase, phosphoribosylglycanamide synthetase,
948	14121	27182		0.95	Z20956.1	EST_HUMAN	phosphoribosylglycanamide synthetase (GART) mRNA
1008	14180	27243		6.07	BF681218.1	EST_HUMAN	phosphoribosylglycanamide synthetase heavy chain gene
1077	14243	27298		1.39	A1221878.1	EST_HUMAN	Homo sapiens of cardiac alpha-myosin heavy chain gene
1634	14767	27849		1.44	1.0E-101	NT	80215647AF1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:1843336 3'
					1.0E-101	EST_HUMAN	qg89d09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
					1.0E-101	EST_HUMAN	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1814	14767	27850	1.44	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1785	14934	28028	1.57	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1785	14934	28029	1.57	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1698	15140	28247	2.07	1.0E-101	4602996	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1), mRNA
2116	16254	28373	2.76	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160600-016-H09 ST0281 Homo sapiens cDNA
2425	16062	28580	1.2	1.0E-101	5728892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2680	15800	28917	4.82	1.0E-101	X72893.1	NT	H. sapiens EWS gene, exon 5
2802	15916	29025	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2802	15916	29026	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3020	16196		20.15	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3273	18447	29407	2.97	1.0E-101	4885270	NT	Homo sapiens gemme-dilamyltransferase 1 (GGT1), mRNA
3313	16486		2.3	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862086 5'
3468	16835	29654	1.82	1.0E-101	AW965556.1	EST_HUMAN	EST377623 IMAGE resequences, MAGI Homo sapiens cDNA
3487	15916	29025	3.69	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3487	15916	29026	3.58	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3981	17138	30142	3.81	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5147	18269	31239	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5147	18269	31240	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5248	18369	31336	0.6	1.0E-101	BE612554.1	EST_HUMAN	601452087F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3855761 5'
5248	18369	31337	0.6	1.0E-101	BE612554.1	EST_HUMAN	601452087F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3855761 5'
5433	18633	31611	1.94	1.0E-101	AW965139.1	EST_HUMAN	EST377212 IMAGE resequences, MAGI Homo sapiens cDNA
6128	19305	32645	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6126	19305	32646	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6834	19987	33396	0.96	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7423	20500		1.26	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7473	20548	34019	4.22	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3), mRNA, alternative splice form 4, partial cds
7473	20548	34020	4.22	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3), mRNA, alternative splice form 4, partial cds
7645	20714	34192	7.65	1.0E-101	AW008475.1	EST_HUMAN	w55f12.X1 NCL CGAP Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7749	20809		1.99	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3349901 5'
7900	20952	34459	6.54	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
8097	21179	34696	0.74	1.0E-101	BE278821.1	EST_HUMAN	601121621F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3345869 5'
8097	21179	34697	0.74	1.0E-101	BE278821.1	EST_HUMAN	601121621F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3345869 5'
8245	21327	34843	1.6	1.0E-101	BF029174.1	EST_HUMAN	601784696F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3996837 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21598	35132	0.71	1.0E-101	AW630070.1	EST_HUMAN	h74g10.y1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8517	21598	35133	0.71	1.0E-101	AW630070.1	EST_HUMAN	h74g10.y1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9212	22290	35832	1.1	1.0E-101	AA036800.1	EST_HUMAN	ZK2908.1 Soares_pregnanter uterus_NHPU Homo sapiens cDNA clone IMAGE:471998 5' similar to PIR-S54640 S54640 YD9335.03c protein - yeast;
9331	22596	36167	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9631	22596	36168	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9661	21103	34619	17.36	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9661	21103	34620	17.36	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9676	22638	36209	19.41	1.0E-101	8845492.1	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9659	22993	36593	3.36	1.0E-101	BE519687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9659	22993	36594	3.36	1.0E-101	BE519687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10068	23136	36737	0.88	1.0E-101	10863360.1	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10620	23654	37284	1.94	1.0E-101	11429127.1	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10656	23690	37299	4.37	1.0E-101	AI570293.1	EST_HUMAN	h77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10656	23690	37300	4.37	1.0E-101	AI570293.1	EST_HUMAN	h77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10771	23604	37426	0.83	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10771	23604	37427	0.83	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
11371	24432	38089	1.31	1.0E-101	AB020626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
12059	25040	38748	1.85	1.0E-101	AI908168.1	EST_HUMAN	RC-BT163-290489-085 BT163 Homo sapiens cDNA
12059	25040	38749	1.85	1.0E-101	AI908168.1	EST_HUMAN	RC-BT163-290489-085 BT163 Homo sapiens cDNA
12738	25489		2.24	1.0E-101	BE163587.1	EST_HUMAN	QV3-HT0460-230200-101-403 HT0460 Homo sapiens cDNA
12793	25529		12.79	1.0E-101	AW939051.1	EST_HUMAN	QV1-DT0088-240200-085-a01 DT0088 Homo sapiens cDNA
40	13278	26284	0.61	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4IK230) mRNA, complete cds
331	13562	26889	4.57	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
635	13820	26844	0.61	1.0E-102	BE262470.1	EST_HUMAN	601108222F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
796	13975	27028	1.06	1.0E-102	4557534.1	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1141	14306	27362	1.9	1.0E-102	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete proviral segment
1297	14493	27518	2.05	1.0E-102	11437146.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1297	14493	27519	2.05	1.0E-102	11437146.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1450	14603	27881	355.9	1.0E-102	BE408447.1	EST_HUMAN	601296882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2383	15514	28642	1.91	1.0E-102	AI124698.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-96 ;
2383	15514	28643	1.91	1.0E-102	AI124698.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-96 ;
3090	16266		0.74	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3133	16309	29322	1.47	1.0E-102	7651979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3203	16378	29387	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3203	16378	29388	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4347	17490	30472	1.74	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4533	17571	30655	2.57	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343982 5'
5224	18348	31316	1.28	1.0E-102	R66488.1	EST_HUMAN	X32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
5487	18586	31704	1.8	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5687	19057		6.87	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5905	19094	32408	3.25	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5905	19094	32409	3.25	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5912	19100	32414	0.81	1.0E-102	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6422	19591	32956	2.81	1.0E-102	AI459826.1	EST_HUMAN	af2009.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52 ;
7227	20080	33507	0.7	1.0E-102	AW451843.1	EST_HUMAN	U1-H-B13-ajl-4-10-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736835 3'
7266	20369	33823	0.91	1.0E-102	BE729323.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7314	20396	33858	1.02	1.0E-102	BE388106.1	EST_HUMAN	601277216F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
7429	20506	33977	1.5	1.0E-102	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7510	20584	34057	8.03	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7802	20858	34350	2.61	1.0E-102	AV710739.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CUAARD03 5'
8418	21499	35031	3.85	1.0E-102	BE763051.1	EST_HUMAN	Q13-NT0025-210600-236-H08 NT0025 Homo sapiens cDNA
8691	21771	35301	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'
8691	21771	35302	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'
8802	21881	35419	0.81	1.0E-102	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9131	22210	35754	1.2	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9131	22210	35755	1.2	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9481	22538	36102	0.84	1.0E-102	AV755842.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD06 5'
9522	22587	36155	2	1.0E-102	T70393.1	EST_HUMAN	yc13d07.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:67021 5'
9522	22587	36156	2	1.0E-102	T70393.1	EST_HUMAN	yc13d07.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:67021 5'
9611	22666	36237	3.11	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM400309 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10563	23628		0.64	1.0E-102	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10647	23681	37291	0.67	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10647	23681	37292	0.67	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10687	23720	37325	3.26	1.0E-102	AJ905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10687	23720	37326	3.26	1.0E-102	AJ905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10748	23761	37394	1.5	1.0E-102	AA970786.1	EST_HUMAN	cn57h04.s1 Soares_NFL T_GBC S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to
11323	24386	38030	1.37	1.0E-102	BE997468.1	EST_HUMAN	SW/CAV2_HUMAN P51636 CAVEOLIN-2 [1];
11327	24390	38035	2.44	1.0E-102	4507822	NT	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3824166 5'
11327	24390	38036	2.44	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11600	24633	38337	1.47	1.0E-102	AA868675.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11690	24683	38376	2.47	1.0E-102	BF358243.1	EST_HUMAN	ak49h10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409347 3'
12009	24694	38699	2.83	1.0E-102	U41302.1	NT	RC8-E70072-150600-011-F01 E70072 Homo sapiens cDNA
12182	25142		5.68	1.0E-102	AL163280.2	NT	Human chromosome 16 creatine transporter (SLC9A8) and (CDM) paralogous genes, complete cds
12775	25517	32000	5.07	1.0E-102	AW300862.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
12831	25553	32015	1.25	1.0E-102	11419159	NT	XK07C12.x1 NCI_CGAP_C020 Homo sapiens cDNA clone IMAGE:2666038 3'
71	13308	26331	0.85	1.0E-103	BE908158.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4), mRNA
71	13308	26332	0.85	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
102	13336	26385	6.24	1.0E-103	D87078.2	NT	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
213	13436	26466	0.84	1.0E-103	5453793	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
1004	14175	27234	74.34	1.0E-103	AJ278348.1	NT	Homo sapiens nucleolar protein (KKEID repeat) (NOP56) mRNA
1272	14428	27500	7.08	1.0E-103	BE877541.1	EST_HUMAN	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE) gene
1626	14778	27803	3.51	1.0E-103	AF012872.1	NT	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1964	15107	28207	1.02	1.0E-103	7657692	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2031	15172	28280	0.95	1.0E-103	4502428	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2031	15172	28281	0.95	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2379	15510	28638	1.95	1.0E-103	AU134691.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2623	15648	28772	1.84	1.0E-103	AF060568.1	NT	AU134691 PLACE1 Homo sapiens cDNA clone IMAGE:1009665 5'
2665	15805	28921	1	1.0E-103	N32770.1	EST_HUMAN	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3137	16313		2.76	1.0E-103	BE744722.1	EST_HUMAN	yw91d08.s1 Soares_placenta_80c5weeks_2NBP18c9W Homo sapiens cDNA clone IMAGE:256569 3'
3487	16634	29653	5.33	1.0E-103	AW286245.1	EST_HUMAN	60157313F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
							UI-H-BW0-ajh-h-11-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733165 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3528	16691	26700	0.95	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3850	17010		5.46	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3894	17053	30053	0.9	1.0E-103	AA485683.1	EST_HUMAN	ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element :
3933	17092	30080	1.54	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4110	17264	30264	4.63	1.0E-103	T236883.1	EST_HUMAN	seg340 b4-HB3MA-Cd109+10-Bio Homo sapiens cDNA clone b4-HB3MA-Cd109+10-Bio-7 3'
5326	18438		0.63	1.0E-103	AA451616.1	EST_HUMAN	zx43b04.r1 Soares, total_fetus_Nb2HF8_6w Homo sapiens cDNA clone IMAGE:789199 5' similar to
6056	19238	32563	0.9	1.0E-103	BF699527.1	EST_HUMAN	TR:G282352 G292352 COLLAGEN CHAIN RH :
6063	19245	32571	1.67	1.0E-103	AF176995.1	EST_HUMAN	602186023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
6397	19556	32926	0.8	1.0E-103	11435053	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6397	19556	32927	0.8	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6587	19748	33130	0.84	1.0E-103	AW854568.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6587	19748	33131	0.84	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6725	25831	33273	1.15	1.0E-103	AA781442.1	EST_HUMAN	aj26603.s1 Soares, testis_NHT Homo sapiens cDNA clone 1391452 3'
6768	19924	33318	0.91	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6859	20011	33422	1.66	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6859	20011	33423	1.66	1.0E-103	AI590071.1	EST_HUMAN	Q13769 ANONYMOUS. ;
6987	18506	31521	1.77	1.0E-103	5032282	NT	tm58b05.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6987	18506	31522	1.77	1.0E-103	5032282	NT	Q13769 ANONYMOUS. ;
7108	18535	31490	1.04	1.0E-103	11431100	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS238, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7178	20310	33753	0.98	1.0E-103	AJ289880.1	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7375	20454	33919	1.88	1.0E-103	AW965776.1	EST_HUMAN	Homo sapiens KIAA0861 gene (partial), X13 gene and LZTFL1 gene
7486	20553	34032	3.6	1.0E-103	BE748158.1	EST_HUMAN	EST377849 MAGC resequences, MAGC Homo sapiens cDNA
7851	21001	34511	4	1.0E-103	AI590071.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3638545 5'
7851	21001	34512	4	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
							Q13769 ANONYMOUS. ;
							Q13769 ANONYMOUS. ;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8484	21565	35101	0.59	1.0E-103	T31080.1	EST_HUMAN	EST27193 Human Brain Homo sapiens cDNA 5' end similar to None
8822	21901	35440	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8822	21901	35441	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8900	21979	35518	1.34	1.0E-103	BF109244.1	EST_HUMAN	7100603.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525964 3' similar to SW-PTNF HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1:
9307	22383	35934	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9307	22383	35935	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9349	22425	35980	0.97	1.0E-103	AA591089.1	EST_HUMAN	nd13c02.s1 NCL_CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:U02426 26S PROTEASE SUBUNIT 4 (HUMAN);
10263	23298	36896	2.04	1.0E-103	Z37970.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10304	23339	36944	2.07	1.0E-103	AW963576.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
10443	23478	37083	10.79	1.0E-103	AI878956.1	EST_HUMAN	au51904.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:O15046 O15046 KIAA0338:
10878	23963	37591	1.52	1.0E-103	BE549706.1	EST_HUMAN	7041103.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
10871	24051	37684	9.5	1.0E-103	AI792759.1	EST_HUMAN	0102006.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING:
11072	24147	37785	2.45	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11072	24147	37786	2.45	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11083	24157	37794	2.4	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11083	24157	37795	2.4	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11656	24735	38426	2.67	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
11731	23917	37542	4.1	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11968	24653		1.71	1.0E-103	AB024750.1	NT	Homo sapiens TSA305 gene, exon 16
12044	25025	38730	2.26	1.0E-103	BE644611.1	EST_HUMAN	7668e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.13 MER29 repetitive element;
12178	25138		3.4	1.0E-103	AF224698.1	NT	Homo sapiens marinosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12209	25162		1.22	1.0E-103	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12414	25293	32083	1.71	1.0E-103	AB011369.1	NT	Homo sapiens gene for AF-6, complete cds
243	13465	26494	2.46	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564H1072 5'
243	13465	26495	2.46	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1937	15090	28182	1.92	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2287	15400	28528	33.29	1.0E-104	AA132975.1	EST_HUMAN	z022c06.s1. Straglene colon (#937204) Homo sapiens cDNA clone IMAGE:587626 3' similar to
2277	15409	28540	4.55	1.0E-104	BE744628.1	EST_HUMAN	gb:Z14116_mn1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2442	15570	28698	9.73	1.0E-104	BF334221.1	EST_HUMAN	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928438 5'
2442	15570	28699	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2508	15633	28763	2	1.0E-104	5031670	NT	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2634	16111	29125	17.99	1.0E-104	M34671.1	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2983	16159		2.15	1.0E-104	Y11151.1	NT	Human lymphocytic antigen CD59/ME43 mRNA, complete cds
3337	16610	29626	0.99	1.0E-104	AU133928.1	EST_HUMAN	H.sapiens gene encoding phenylpyruvate tautomerase II
3478	16945		2.33	1.0E-104	AA319436.1	EST_HUMAN	AU133928 OVARC1 Homo sapiens cDNA clone OVARC1009838 5'
3690	16852	29860	0.65	1.0E-104	AB033102.1	NT	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3690	16852	29861	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4053	17209	30219	0.71	1.0E-104	AB032998.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4248	17394	30383	0.71	1.0E-104	F11746.1	EST_HUMAN	Homo sapiens mRNA for KIAA1276 protein, partial cds
4498	17636	30618	33.95	1.0E-104	X02761.1	NT	HSC1A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4732	17867	30849	1.2	1.0E-104	AF231920.1	NT	Human mRNA for fibronectin (FN precursor)
4732	17867	30850	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
6061	19243	32567	1.05	1.0E-104	U43379.1	NT	Homo sapiens chromosome 21, unknown mRNA
6081	19243	32568	1.05	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6108	19288	32623	0.93	1.0E-104	AB017332.1	NT	Human Down Syndrome region of chromosome 21 DNA
6596	19756	33142	8.5	1.0E-104	A1768797.1	EST_HUMAN	Homo sapiens a1x3 mRNA for Aurora/Plp1-related kinase 3, complete cds
6596	19756	33143	8.5	1.0E-104	A1768797.1	EST_HUMAN	wf03b12.x1 NCL_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR.Q14145 Q14145
6788	19841	33339	0.74	1.0E-104	7708512	NT	KIAA0132 PROTEIN, contains element LTR7 repetitive element
6942	20255	33692	3.39	1.0E-104	BE314182.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element
6942	20255	33693	3.39	1.0E-104	BE314182.1	EST_HUMAN	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51736), mRNA
7373	20452	33917	2.01	1.0E-104	11426572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7788	21875	35414	0.87	1.0E-104	BF509244.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
9398	22443	36004	2.41	1.0E-104	BF448230.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9463	22820	36082	0.46	1.0E-104	AA682308.1	EST_HUMAN	U1H-B14-aw-b-09-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086176 3'
9494	22841		1.03	1.0E-104	T74219.1	EST_HUMAN	ncat16g11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9515	22880	36146	5	1.0E-104	AF091395.1	NT	q88b05.s1 Soares fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9515	22880	36147	5	1.0E-104	AF091395.1	NT	yc63f02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22440 5'
							Homo sapiens Trio isoform mRNA, complete cds
							Homo sapiens Trio isoform mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9841	21084	34597	4.14	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080600-249-F07 HT0619 Homo sapiens cDNA
9841	21084	34598	4.14	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080600-249-F07 HT0619 Homo sapiens cDNA
9856	22994	36589	0.92	1.0E-104	AW103848.1	EST_HUMAN	x376d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9856	22994	36589	0.92	1.0E-104	AW103848.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
9855	22994	36590	0.92	1.0E-104	AW103848.1	EST_HUMAN	x376d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
10153	23180	36787	0.49	1.0E-104	AF113514.1	NT	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
10298	23333	36837	3.15	1.0E-104	BE791713.1	EST_HUMAN	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10298	23333	36838	3.15	1.0E-104	BE791713.1	EST_HUMAN	601681503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10611	23645	37253	1.49	1.0E-104	AV728070.1	EST_HUMAN	601681503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10657	23691	37301	4.47	1.0E-104	AU130765.1	EST_HUMAN	AV728070 HT0619 Homo sapiens cDNA clone HT0619
10757	23790	37407	0.54	1.0E-104	AA931321.1	EST_HUMAN	AU130765 HT0619 Homo sapiens cDNA clone NT2P3001398 5'
10774	23807	37430	0.54	1.0E-104	AA931321.1	EST_HUMAN	6006a10.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1565370 3'
10774	23807	37430	0.54	1.0E-104	AA931321.1	EST_HUMAN	6006a10.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1565370 3'
10774	23807	37430	0.54	1.0E-104	AA931321.1	EST_HUMAN	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
10774	23807	37430	0.54	1.0E-104	AA931321.1	EST_HUMAN	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
10774	23807	37430	0.54	1.0E-104	AA931321.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11577	24632	38310	44.86	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11577	24632	38311	44.86	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11611	24603	38350	4.1	1.0E-104	BF684288.1	EST_HUMAN	802141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
12082	25082	38768	48.12	1.0E-104	11434726	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5), mRNA
13073	25702		1.32	1.0E-104	BE333892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658676 5'
289	15981	28541	2.57	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
438	13238	28238	6.69	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
607	13798	28815	2.51	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
607	13798	28816	2.51	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1865	15011	28118	10.24	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1979	15122	28223	2.39	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2283	15396	28524	3.08	1.0E-105	AA318399.1	EST_HUMAN	EST20609 Spleen I Homo sapiens cDNA 5' and similar to autoimmune antigen Ku, p70/p80 subunit
2298	15529		1.18	1.0E-105	BE891766.1	EST_HUMAN	801434191F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919511 5'
2784	15900		0.88	1.0E-105	AA584608.1	EST_HUMAN	801434191F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:1100285 3'
3071	16247		2.79	1.0E-105	AJ229041.1	NT	no10d05.s1 NCI CGAP Phet1 Homo sapiens cDNA clone IMAGE:1100285 3'
3432	16600	29618	0.88	1.0E-105	7304922	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
3432	16600	29619	0.86	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4213	17362	30350	2.23	1.0E-105	AW061688.1	EST_HUMAN	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
							EST373761 IMAGE: resequences, MAGG Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5053	18181		5.34	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5259	18378	31344	1.08	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5445	18645	31623	1.18	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5513	18711		1.12	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7045	20098	33513	1.44	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7045	20098	33514	1.44	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7121	18547	31458	3.78	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7121	18547	31459	3.78	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7167	20300	33743	0.72	1.0E-105	AW951634.1	EST_HUMAN	EST363689 MAGC resequences, MAGB Homo sapiens cDNA
7436	20513	33986	0.72	1.0E-105	BE902610.1	EST_HUMAN	601677279F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960019 5'
8043	21126	34847	0.93	1.0E-105	X12556.1	NT	Human mRNA for dhl proto-oncogene
8217	21299	34820	11.05	1.0E-105	T05087.1	EST_HUMAN	EST02875 Fetal brain, Striatum (cat#38206) Homo sapiens cDNA clone HFBGR32
8592	21673	35211	1.53	1.0E-105	AW007194.1	EST_HUMAN	SW:ACSA, PENCH P36333 ACETYL-COENZYME A SYNTHETASE, 1
9128	22207	35750	0.82	1.0E-105	AW840817.1	EST_HUMAN	RC1-CN0008-070100-011-e05 CN0008 Homo sapiens cDNA
9250	22327	35874	2.51	1.0E-105	AW016879.1	EST_HUMAN	UI-H-B10p-abb-b-12-Q.UJ.at NCL_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9404	22478	36041	0.83	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9404	22478	36042	0.83	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9767	22764	36333	0.75	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
9767	22764	36334	0.75	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11173	24243	37879	4.82	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11505	24564	38241	1.42	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for a6(V) collagen, exon 31
11559	24614	38293	1.85	1.0E-105	7705936	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11887	24875	38572	2.52	1.0E-105	AW027554.1	EST_HUMAN	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11972	24957	38659	1.48	1.0E-105	BF430921.1	EST_HUMAN	w7407.x1 Soares_thymus_NHFT Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
12111	25091	38794	1.3	1.0E-105	AF218896.1	NT	P87892 PROTEASE 1
155	13380		0.88	1.0E-106	AF503208.1	EST_HUMAN	7o18c10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P87880 P97880
210	13433	26464	5.14	1.0E-106	AI565085.1	EST_HUMAN	RIN1:
555	13748	28774	1.89	1.0E-106	AW995556.1	EST_HUMAN	Homo sapiens attractin precursor (ATRIN) gene, exon 8
820	13807	28828	0.8	1.0E-106	J00146.1	NT	UI-HF-BNO-akt-g-07-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
621	13907	28828	1.13	1.0E-106	J00146.1	NT	UI-HF-BNO-akt-g-07-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
1554	14707	27787	8.84	1.0E-106	AF145712.1	NT	q78c01.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2218008 3'
							EST377629 MAGC resequences, MAGI Homo sapiens cDNA
							Human dihydrofolate reductase pseudogene (psl-hd1)
							Human dihydrofolate reductase pseudogene (psl-hd1)
							Homo sapiens soluble neuropilin-1 mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1736	14885	27978	7.83	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1757	14906	28000	1.33	1.0E-106	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1846	14992	28093	5.51	1.0E-106	AA527448.1	EST_HUMAN	ng41c05.s1 NC1_CGAP_C03 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element LTR3 repetitive element
1846	14992	28084	5.51	1.0E-106	AA527448.1	EST_HUMAN	ng41c05.s1 NC1_CGAP_C03 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element LTR3 repetitive element
2191	15326	28451	1.94	1.0E-106	BE144288.1	EST_HUMAN	MR0-HT0165-140200-008-310 HT0165 Homo sapiens cDNA
2391	15522	28651	3.62	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2574	15699	28821	2.19	1.0E-106	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2667	15768	28804	1.93	1.0E-106	U64675.2	NT	Homo sapiens sperm membrane protein BS-83 mRNA, complete cds
2699	15790	28906	2.01	1.0E-106	BE280201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2815	15929	29041	8.05	1.0E-106	A1276526.1	EST_HUMAN	q176h10.x1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1978307 3'
2866	14617	27700	1.84	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2866	14617	27701	1.84	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2939	16116	29128	1.18	1.0E-106	BE384296.1	EST_HUMAN	601272675F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
3007	16182	29204	5.7	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3007	16182	29205	5.7	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3248	16422	29438	2.5	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3248	16422	29439	2.5	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3461	16628	29646	1.04	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3527	16692	29701	1.07	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3527	16692	29702	1.07	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4149	17301	30283	9.2	1.0E-106	AW074650.1	EST_HUMAN	EST386875 MAGe resequences, MAGN Homo sapiens cDNA
4149	17301	30284	9.2	1.0E-106	AW074650.1	EST_HUMAN	EST386875 MAGe resequences, MAGN Homo sapiens cDNA
4723	17858	30840	2.27	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-310 HT0165 Homo sapiens cDNA
5485	18684	31701	2.95	1.0E-106	AA781155.1	EST_HUMAN	al24609.s1 Scores_NHT Homo sapiens cDNA clone 1391225 3' similar to gb.X12433 PROTEIN PHPS1-2 (HUMAN)
5976	19161	32480	0.95	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5976	19161	32481	0.95	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6026	19209	32529	0.61	1.0E-106	AA434168.1	EST_HUMAN	zvw28d12.s1 Scores ovary tumor NHT Homo sapiens cDNA clone IMAGE:770615 3'
6116	19296	32631	1	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6116	19296	32632	1	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
8227	19402	32762	8.39	1.0E-106	BF079574.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285067 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6336	19507	32864	0.81	1.0E-106	BE997112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6526	19507	32864	0.66	1.0E-106	BE997112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6549	18711	33087	15.91	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6549	19711	33086	15.91	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
7628	20601	34075	5.89	1.0E-106	AA663779.1	EST_HUMAN	aa72e07.s1 Stratagene scizho brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X065873
7582	20654	34130	4.17	1.0E-106	11429617	NT	KINESIN HEAVY CHAIN (HUMAN);
7672	20738	34216	1.64	1.0E-106	BE282722.1	EST_HUMAN	Homo sapiens XPMC2 protein (LOC57109), mRNA
7787	20843	34335	8.06	1.0E-106	11425503	NT	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
7787	20843	34336	8.06	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7894	21044	34556	0.8	1.0E-106	AU116850	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
8173	21255	34776	3.62	1.0E-106	BE741408.1	EST_HUMAN	AU116850 HEMBA1 Homo sapiens cDNA clone HEMBA1000129 5'
8173	21255	34777	3.62	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8368	21449	34972	2.21	1.0E-106	A1523066.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8830	21909	35447	0.84	1.0E-106	BE387950.1	EST_HUMAN	aa88a07.x1 Barslead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233
8830	21909	35448	0.84	1.0E-106	BE387950.1	EST_HUMAN	CALGRANULIN B (HUMAN);
8903	21982	35522	2.77	1.0E-106	A1654123.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3504493 5'
9252	22329	35876	0.83	1.0E-106	AW638631.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3504493 5'
9348	22424	35978	2.34	1.0E-106	AA825307.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
9348	22424	35979	2.34	1.0E-106	AA825307.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
9486	22543	36106	0.77	1.0E-106	A1750447.1	EST_HUMAN	Q05084 68 KD ISLET CELL AUTOANTIGEN;
9629	22684	36255	1.94	1.0E-106	A1479569.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
9629	22684	36256	1.94	1.0E-106	A1479569.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
10269	23241	36832	0.9	1.0E-106	BE389234.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
10269	23241	36832	0.9	1.0E-106	BE389234.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
10269	23241	36832	0.9	1.0E-106	BE389234.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
10269	23241	36832	0.9	1.0E-106	BE389234.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
10446	23481	37088	10.7	1.0E-106	AA604417.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
10446	23481	37089	10.7	1.0E-106	AA604417.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
10482	23527	37136	1.83	1.0E-106	AW383269.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10497	23532	37141	0.66	1.0E-106	11439432	NT	Homo sapiens multimerin (MMRN), mRNA
10497	23532	37142	0.66	1.0E-106	11439432	NT	Homo sapiens multimerin (MMRN), mRNA
10678	23712	37320	0.65	1.0E-106	AL039886.1	EST_HUMAN	DKFZp434F0712.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434F0712.5'
10807	23840	37464	4.26	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11135	24207	37832	4.81	1.0E-106	BF032755.1	EST_HUMAN	801453481F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
11135	24207	37833	4.81	1.0E-106	BF032755.1	EST_HUMAN	801453481F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
11317	24380	38025	2.06	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11317	24380	38026	2.06	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11694	24692	38383	1.35	1.0E-106	BE257385.1	EST_HUMAN	801103219F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3349997 5'
11837	24826	38514	1.89	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-802 BN0192 Homo sapiens cDNA
11837	24826	38515	1.89	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-802 BN0192 Homo sapiens cDNA
12263	25946	32059	1.97	1.0E-106	BE864488.1	EST_HUMAN	ih05h11.xt NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861844 5'
12484	25338	32060	1.97	1.0E-106	BE864488.1	EST_HUMAN	801433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12484	25338	32060	1.97	1.0E-106	BE864488.1	EST_HUMAN	801433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12717	25477		3.71	1.0E-106	BE865005.1	EST_HUMAN	RC1-C10249-090800-024-005 C10249 Homo sapiens cDNA
244	13466		4.52	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudocytosomal region, segment 1/2
276	13493		0.9	1.0E-107	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
697	13922		1.03	1.0E-107	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
647	13832	26858	2.34	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
836	14014	27069	1.02	1.0E-107	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
908	14084	27149	1.38	1.0E-107	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
891	14163	27223	9.71	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1307	14463	27631	1.08	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1600	14753	27836	3.81	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1791	14940	28033	5.42	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
1887	15031	28138	1.52	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1887	15031	28139	1.52	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2282	16414	28846	3.77	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2435	15563	28691	4.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
2435	15563	28692	4.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
3072	16248	29268	6.14	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
3072	16248	29269	6.14	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
3169	16344	29352	2.9	1.0E-107	5902087	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3931	17090	30087	4.89	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5742	18935	32235	0.84	1.0E-107	AW969038.1	EST_HUMAN	EST381115 MAGE resequences, MAGK Homo sapiens cDNA
5986	19171	32493	2.71	1.0E-107	BE667469.1	EST_HUMAN	601442558F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846494 5'
7520	20593	34067	1.33	1.0E-107	AW503913.1	EST_HUMAN	UHF-BNO-alf-c-08-0-JL1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3079310 5'
7520	20593	34068	1.33	1.0E-107	AW503913.1	EST_HUMAN	UHF-BNO-alf-c-08-0-JL1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3079310 5'
7698	20763	34247	1.36	1.0E-107	AI765078.1	EST_HUMAN	WHSB04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
7909	20981	34467	0.59	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7909	20981	34468	0.59	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6597	22729	36239	0.99	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
10889	23973	37604	1.92	1.0E-107	BE168728.1	EST_HUMAN	QV1-HT0516-140300-107-c10 H0516 Homo sapiens cDNA
10944	24028	37682	2.96	1.0E-107	AI392850.1	EST_HUMAN	ig10d06.x1 NCI_CGAP_CL1.1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1
11183	24258	37894	1.58	1.0E-107	L49141.1	NT	P05095 ALPHA-ACTININ 3, NON MUSCULAR
11202	24271	37907	2.3	1.0E-107	BF668511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11603	24656	38341	3.91	1.0E-107	BE540650.1	EST_HUMAN	602123963F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11676	23904	37528	4.29	1.0E-107	11419701	NT	60106668F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11676	23904	37527	4.29	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
12322	26100		7.14	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
13211	25780	31920	1.24	1.0E-107	BE798189.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
977	14160	27210	1.72	1.0E-108	BE293042.1	EST_HUMAN	2845e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
1294	14450	27515	2.41	1.0E-108	Y18000.1	NT	THR repetitive element
2140	15276	28398	1.02	1.0E-108	BF026728.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
2407	15538	28665	12.11	1.0E-108	AI686040.1	EST_HUMAN	Homo sapiens NF2 gene
2407	15538	28666	12.11	1.0E-108	AI686040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2498	16626	28746	11.96	1.0E-108	BE206694.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
3025	16201	29224	0.84	1.0E-108	6006979	NT	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
3430	16599	28614	0.84	1.0E-108	AF032897.1	NT	PROTEOGLYCAN II PRECURSOR (HUMAN);
3430	16598	28615	0.64	1.0E-108	AF032897.1	NT	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
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							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4273	17418	30406	1.57	1.0E-108	AW664438.1	EST_HUMAN	h12et1.1x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872060 3' similar to SW:3BP1_MOUSE
4647	17763	30765	2.62	1.0E-108	U72861.1	NT	P55194 SH3-BINDING PROTEIN 3BP-1.1
4647	17763	30766	2.62	1.0E-108	U72861.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4927	18057	31040	3.37	1.0E-108	7661979	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
5037	18165	31141	0.63	1.0E-108	AW504799.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5083	18191	31166	3.18	1.0E-108	AJ008005.1	NT	UHF-BNO-ah-e-04-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5'
5596	18791	31839	1.24	1.0E-108	AW384094.1	EST_HUMAN	Homo sapiens PSN1 gene, alternative transcript
5644	18838	31916	2.56	1.0E-108	BE869016.1	EST_HUMAN	RCO-HT0372-241189-031-c03 HT0372 Homo sapiens cDNA
5644	18838	31917	2.56	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
6049	19232	32644	0.66	1.0E-108	AF012623.1	NT	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
6125	19304	32644	0.74	1.0E-108	BF334651.1	EST_HUMAN	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6287	19441	32789	6.14	1.0E-108	AF264717.1	NT	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6287	19441	32790	6.14	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6392	19581	32821	1.22	1.0E-108	AJ133269.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6489	19304	32644	1.09	1.0E-108	BF334651.1	EST_HUMAN	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6753	19909	33302	0.64	1.0E-108	AF016706.1	NT	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6753	19909	33303	0.64	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7308	20390	33860	4.52	1.0E-108	11431857	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7597	20667	34143	2.12	1.0E-108	4758333	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
7646	20715	34193	1.32	1.0E-108	BE252607.1	EST_HUMAN	Homo sapiens delta-8 fatty acid desaturase (FADS2) mRNA
7674	20739	34218	0.73	1.0E-108	BF528912.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354064 5'
7674	20739	34219	0.73	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5'
8264	21336	34910	1.72	1.0E-108	AF083500.1	NT	602043384F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5'
8306	21388	34911	0.61	1.0E-108	AW408694.1	EST_HUMAN	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8306	21388	34911	0.61	1.0E-108	AW408694.1	EST_HUMAN	UHF-BMO-ade-a-12-0-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3082878 5'
9247	22324	35869	0.77	1.0E-108	AF203977.1	NT	UHF-BMO-ade-a-12-0-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3082878 5'
9287	22363	35912	0.46	1.0E-108	N44974.1	EST_HUMAN	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
10847	23880	37500	1.08	1.0E-108	11428155	NT	y35h10.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR.A45773
							A45773 kelch protein, long form - fruit fly
							Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10904	21037	34549	2.09	1.0E-108	BE535227.1	EST_HUMAN	601058789F1 NIH_MGC. 10 Homo sapiens cDNA clone IMAGE:3445361 5'
11066	18501	31537	2.67	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Gdgl-associated microtubule-binding protein (GMAP-210)
11319	24382	38027	1.35	1.0E-108	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
11549	24005	38283	3.46	1.0E-108	AW966185.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo sapiens cDNA
11605	24658	38343	1.71	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAE03 5'
11605	24658	38344	1.71	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAE03 5'
11652	24731		2.77	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11688	15538	28665	2.99	1.0E-108	A1686040.1	EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
11688	15538	28666	2.99	1.0E-108	A1686040.1	EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
11712	24752	38446	1.72	1.0E-108	D63539.1	NT	Homo sapiens COL4A6 gene for $\alpha 6(V)$ collagen, exon 23
12499	25344	32064	4.15	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12940	25618		5.09	1.0E-108	BF346356.1	EST_HUMAN	602018571F1 NCI_CGAP Brn67 Homo sapiens cDNA clone IMAGE:4154297 5'
43	13281	26287	1.01	1.0E-109	AW803116.1	EST_HUMAN	IL2-UM0077-280400-079-D06 UM0077 Homo sapiens cDNA
68	13303	26326	1.17	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
226	13447	26475	3.34	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
235	13456	26482	2.77	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
479	13674	26705	2.28	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
611	13800	26820	14.77	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1037	14205	27262	1.62	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1229	14389	27451	8.5	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1230	14389	27451	6.38	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1573	14726	27806	0.89	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC. 15 Homo sapiens cDNA clone IMAGE:2989636 5'
1573	14726	27807	0.89	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC. 15 Homo sapiens cDNA clone IMAGE:2989636 5'
1923	15066	28170	2.3	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2314	15448	28580	5.46	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2326	15457	28589	3.65	1.0E-109	Y11723.1	NT	Homo sapiens SNF3/INI1 gene, exon 6
2687	15907	28923	19.35	1.0E-109	A1022328.1	EST_HUMAN	ow95a01.x1 Scores: fetal_liver_spleen, 1NFLS, S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197.002197 CIRCULATING CATHODIC ANTIGEN. ;
2687	15907	28924	19.35	1.0E-109	A1022328.1	EST_HUMAN	ow95a01.x1 Scores: fetal_liver_spleen, 1NFLS, S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197.002197 CIRCULATING CATHODIC ANTIGEN. ;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2888	15808	28925	2.88	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3125	16301	28314	3.37	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC
3475	16642	29661	2.08	1.0E-109	AW893192.1	EST_HUMAN	FINGER PROTEIN ZNF43
3475	16642	29662	2.08	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-180400-150-110 NN0009 Homo sapiens cDNA
3606	16770	29785	1.1	1.0E-109	AF240688.1	NT	CM3-NN0009-180400-150-110 NN0009 Homo sapiens cDNA
3945	17104		1.31	1.0E-109	BE146144.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
4284	17409	30395	4.35	1.0E-109	AI655417.1	EST_HUMAN	MR0-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
4524	17683	30650	2.67	1.0E-109	4504206	NT	ts98a08.x1 NCL_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:553A2.8
4722	17857	30839	1.7	1.0E-109	7682083	NT	CE16100 ;
5165	18287	31252	0.72	1.0E-109	BE293673.1	EST_HUMAN	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
5165	18287	31252	0.72	1.0E-109	BE293673.1	EST_HUMAN	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5361	18564	31480	0.67	1.0E-109	AU137282.1	EST_HUMAN	601185922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5374	18577	31445	0.92	1.0E-109	BF673718.1	EST_HUMAN	601185922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5428	18628	31604	2.92	1.0E-109	5174622	NT	AU137282 PLACE1 Homo sapiens cDNA clone PLACE1006159 5'
5724	18917		1.23	1.0E-109	BE179356.1	EST_HUMAN	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
6050	25817	32556	1.23	1.0E-109	BF370688.1	EST_HUMAN	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6119	18917		1.41	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6721	19878	33289	0.85	1.0E-109	A1221385.1	EST_HUMAN	CM1-UT0038-060900-399-h07 UT0038 Homo sapiens cDNA
6907	20222	33651	0.69	1.0E-109	11024711	NT	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6907	20222	33652	0.69	1.0E-109	11024711	NT	qg86h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
7389	20487	33933	0.67	1.0E-109	AB046811.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7738	20799	34288	3.75	1.0E-109	11432574	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7740	20801	34290	4.91	1.0E-109	BF182707.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF-1), mRNA
7740	20801	34291	4.91	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8368	21447	34970	1.35	1.0E-109	AL049784.1	NT	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8480	21561	35098	1.39	1.0E-109	AW749130.1	EST_HUMAN	Novel human gene mapping to chromosome 13
8857	21838		2.84	1.0E-109	AA077498.1	EST_HUMAN	PM0-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
8932	22011	35549	4.36	1.0E-109	BE787540.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8932	22011	35550	4.36	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9177	22555	35797	0.57	1.0E-109	BE145672.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9439	22513	36077	1.05	1.0E-109	H84860.1	EST_HUMAN	IL0-HT0205-071199-142-p01 HT0205 Homo sapiens cDNA
							ys90g08.r1 Soares retina N255HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491
							A53491 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPINY ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9550	22615	36184	0.64	1.0E-109	BE397068.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9550	22615	36185	0.64	1.0E-109	BE397068.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9685	22734	36304	1.37	1.0E-109	F06804.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-10012
11013	24092	37730	1.8	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11013	24092	37731	1.8	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11046	24123	37757	19.68	1.0E-109	BF694831.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
11387	24448	38109	1.57	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
11651	24730	38422	2.18	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11693	24891	38382	4.5	1.0E-109	W16510.1	EST_HUMAN	z008b12.r1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat;
11884	24872	38569	1.64	1.0E-109	BE045560.1	EST_HUMAN	ht2305.x1 NCI_CGAP_LU24 Homo sapiens cDNA clone IMAGE:2955989 3' similar to TR:Q9Z124 Q9Z124
11948	24834	38638	1.5	1.0E-109	AL119824.1	EST_HUMAN	YGR163W MRNA HOMOLOGUE, COMPLETE CDS. ;
11984	24869	38673	1.31	1.0E-109	11418618	NT	DKFZp761t1124_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761t1124 5'
12126	25106	38810	2.26	1.0E-109	AB007892.1	NT	Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA
12387	15457	28589	2.32	1.0E-109	Y17123.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
12636	15457	28589	3.2	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12782	25508	32036	8.36	1.0E-109	AB011398.1	NT	Homo sapiens SNF5/INI1 gene, complete cds
3	13242	26242	1.4	1.0E-110	7549804	NT	Homo sapiens calcitonin receptor-like type II (DIO2), transcript variant 2, mRNA
38	13276	26281	3.96	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
38	13276	26282	3.96	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
112	13242	26242	1.83	1.0E-110	7549804	NT	Homo sapiens deiodinase, calcitonin, type II (DIO2), transcript variant 2, mRNA
305	13621	26555	1.31	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
540	13733	26757	1.04	1.0E-110	U84550.1	NT	Human dyatrobrexin (DTN) gene, exon 20
1207	14369	27429	0.89	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1308	14464	27532	1.02	1.0E-110	AB032283.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1973	15116	28217	1.51	1.0E-110	BE379477.1	EST_HUMAN	601237549F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609693 5'
2118	15256		1.66	1.0E-110	BF508996.1	EST_HUMAN	U1H-B14-acb-05-Q-U1 s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2903	16081		7.19	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3196	16331		1.48	1.0E-110	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3264	16438	29457	2.66	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3264	16438	29458	2.66	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4320	17463	30449	1.09	1.0E-110	M15918.1	NT	Human autimmune antigen small nuclear ribonucleoprotein E pseudogene

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4758	17893	30872	2.04	1.0E-110	AI017213.1	EST_HUMAN	ou32b10.x1 Sources_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to SW:NI21_RAT P62391 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4777	17912	30897	3.01	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5088	18216		2.28	1.0E-110	7862441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5409	18611	31583	2.23	1.0E-110	BE299408.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3026538 5'
5843	19033	32339	0.78	1.0E-110	BE621089.1	EST_HUMAN	601493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'
5860	19050	32358	8.61	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5860	19050	32357	8.61	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6858	25835	33421	5.43	1.0E-110	IM55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7179	20311	33754	0.59	1.0E-110	BE281496.1	EST_HUMAN	601106388F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
7261	20334	33782	0.85	1.0E-110	U08898.1	NT	Human GS2 gene, exon 2
7261	20334	33783	0.85	1.0E-110	U08898.1	NT	Human GS2 gene, exon 2
7477	20552	34025	0.78	1.0E-110	AI560286.1	EST_HUMAN	Int2d08.X1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN P50549 ETS TRANSLOCATION VARIANT 1 ;
7593	20655	34131	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCE01 5'
7593	20655	34132	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCE01 5'
7613	20683	34159	2.87	1.0E-110	AB020675.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds
7743	20804	34293	0.96	1.0E-110	AU137923.1	EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
9536	22801	36174	1.09	1.0E-110	BE302594.1	EST_HUMAN	ba68f01.Y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905561 5' similar to TR:O77258 O77258
9777	22817	36395	2.46	1.0E-110	AW83394.1	EST_HUMAN	EG-114D9.2 PROTEIN.;
10529	23564	37171	3.38	1.0E-110	11432732	NT	QV2-L.T0053-020400-119-e04 LT0053 Homo sapiens cDNA
10986	24065	37700	3.2	1.0E-110	Y12337.1	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
11209	24278	37916	3.64	1.0E-110	BE794357.1	EST_HUMAN	Hi sapiens mRNA for myotonic dystrophy protein kinase like protein
11209	24278	37917	3.64	1.0E-110	BE794357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11608	24661	38347	1.89	1.0E-110	MT0051.1	NT	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11728	23914	37539	1.7	1.0E-110	AA446529.1	EST_HUMAN	Human insulin receptor mRNA, complete cds
12311	25164		2.47	1.0E-110	BE897218.1	EST_HUMAN	zw67g02.r1 Sources_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816
12341	25246		2.86	1.0E-110	AW062268.1	EST_HUMAN	G1145816 FKBP54 ;
12594	25400		2.86	1.0E-110	AB011399.1	NT	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12748	26113		6.01	1.0E-110	BF364546.1	EST_HUMAN	IL0-BT0163-0-0089-094-g10 BT0163 Homo sapiens cDNA
13071	15256		1.16	1.0E-110	BF508868.1	EST_HUMAN	Homo sapiens gene for AF-6, complete cds
179	13402		11.82	1.0E-111	U43701.1	NT	PI43-NN1082-140800-008-f12 NN1082 Homo sapiens cDNA
							U1-H-B14-acc-b-05-Q-U1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
							Human ribosomal protein L23a mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
201	13424	28455	1.64	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
793	13934		1.99	1.0E-111	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
762	13943	26989	4.13	1.0E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
950	14123	27185	2.5	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
4286	17431	30419	1.15	1.0E-111	7661569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4449	17588	30570	4.59	1.0E-111	K02268.1	NT	Human enkephalin B (enkb) gene, exon 4 and 3' flank and complete cds
5593	18788	31835	0.75	1.0E-111	AA151017.1	EST_HUMAN	z47607.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5593	18788	31836	0.75	1.0E-111	AA151017.1	EST_HUMAN	z47607.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
6749	18941	32242	0.88	1.0E-111	BE887809.1	EST_HUMAN	601443690F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847655 5'
5962	19052	32359	0.66	1.0E-111	U119969.1	NT	Human two-handed zinc finger protein ZEB mRNA, partial cds
6156	19332	32678	2.09	1.0E-111	A1344679.1	EST_HUMAN	q09912.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1817574 3' similar to gb:M28893 RAS-RELATED PROTEIN RAL-A (HUMAN);
6818	19671	33379	0.96	1.0E-111	AL040762.1	EST_HUMAN	DKFZP434C1815.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434C1815 5'
6845	20258	33697	1.31	1.0E-111	AW294648.1	EST_HUMAN	U1-H-BWO-01-R-03-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729525 3'
7605	20675	34149	3.04	1.0E-111	BF386228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
7704	20769	34254	0.7	1.0E-111	A1761228.1	EST_HUMAN	w168d01.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIIA5 (HUMAN);
7791	20847	34340	0.83	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8286	21368	34898	0.8	1.0E-111	AA278888.1	EST_HUMAN	zs78g03.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
8286	21368	34899	0.8	1.0E-111	AA278888.1	EST_HUMAN	zs78g03.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
8383	21464	34989	0.63	1.0E-111	U66533.1	NT	Homo sapiens protein x 0007 (LOC51185), mRNA
8435	21516	35047	3.56	1.0E-111	U66533.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
8878	21957	35492	0.96	1.0E-111	AK024453.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8975	22064	35597	0.64	1.0E-111	BF214902.1	EST_HUMAN	Homo sapiens mRNA for FLJ00045 protein, partial cds
9008	22087	35708	8.43	1.0E-111	X17033.1	NT	601847132F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4078303 5'
9085	22164	35709	15.93	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9085	22164	35709	15.93	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9289	22365	35914	3.37	1.0E-111	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9518	22583	36152	0.54	1.0E-111	BF333210.1	EST_HUMAN	QV2-BT0817-270900-398-c06 BT0817 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10355	23390	37000	1.56	1.0E-111	AA504160.1	EST_HUMAN	aa58902.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gbL09235
10383	23418		1.04	1.0E-111	D10083.1	NT	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10479	23514	37127	5.56	1.0E-111	AA131248.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
10995	24074	37707	1.34	1.0E-111	AW293467.1	EST_HUMAN	Z31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
11299	24355	38006	3.29	1.0E-111	U68159.1	NT	UI-HBW0-alc-4-07-0-UI.s1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730276 3'
12167	25130	38828	4.07	1.0E-111	11417901	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
12741	25492	32029	4.72	1.0E-111	AV708482.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12881	25888	31855	4.82	1.0E-111	W22562.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAOB08.5'
13041	18504	31539	1.27	1.0E-111	AB035356.1	NT	72C9 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
623	13808	26829	2.77	1.0E-112	4501854	NT	Homo sapiens mRNA for neurixin 1-alpha protein, complete cds
625	13810	26831	4.84	1.0E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
625	13810	26832	4.84	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
649	13834	26860	1.82	1.0E-112	BF509039.1	EST_HUMAN	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
649	13834	26861	1.82	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-aot-g-04-0-UI.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1028	14197	27255	33.06	1.0E-112	AF157623.1	NT	UI-H-B14-aot-g-04-0-UI.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1087	14253	27308	1.49	1.0E-112	F52742	SWISSPROT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1718	14868	27658	7.1	1.0E-112	7682125	NT	ZINC FINGER PROTEIN 135
1718	14868	27659	7.1	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1863	15009	28115	1.11	1.0E-112	AF248540.1	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2577	15703	28823	2.83	1.0E-112	BE86859.1	EST_HUMAN	Homo sapiens intercalin 2 (SH3D1B) mRNA, complete cds
3147	16323		0.76	1.0E-112	4504116	NT	Homo sapiens intercalin 2 (SH3D1B) mRNA, complete cds
3444	16812	29630	0.61	1.0E-112	AB28511.1	EST_HUMAN	801442874F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848658 5'
3990	17147	30153	0.63	1.0E-112	BE076073.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4726	17861	30843	0.68	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4875	18007	30890	5.87	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4875	18007	30891	5.87	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5784	18976	32282	36.7	1.0E-112	NA6046.1	EST_HUMAN	Y39307.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5'
6201	19376	32727	1.33	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6273	19447	32795	0.66	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-als-g-08-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6273	19447	32796	0.66	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-als-g-08-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6379	19548	32804	0.93	1.0E-112	BE741666.1	EST_HUMAN	UI-HF-BR0p-als-g-08-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3948557 5'
6688	19749	33132	0.7	1.0E-112	BF672815.1	EST_HUMAN	601594717F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293420 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6773	19928	33323	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6773	19928	33324	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6981	20209	33637	1.51	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270821 5'
7305	20387	33847	0.68	1.0E-112	AL043298.1	EST_HUMAN	DKFZp434M0523_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434M0523 5'
7491	20566	34037	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7491	20566	34038	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8387	21488	34995	1.79	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
9158	22236	35781	2.64	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9158	22238	35782	2.64	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
10097	23135	36796	2.37	1.0E-112	BF111413.1	EST_HUMAN	7130907.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to
11017	24086	37735	16.73	1.0E-112	AW683327.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
11103	24175	37810	1.31	1.0E-112	T63967.1	EST_HUMAN	Yd86d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
11103	24175	37811	1.31	1.0E-112	T63967.1	EST_HUMAN	SP:C40H1.1 CE00109 OVARIAN PROTEIN;
11191	24260	37896	3.14	1.0E-112	AJ249900.1	NT	SP:C40H1.1 CE00109 OVARIAN PROTEIN;
11359	24421	38077	2.24	1.0E-112	BE280479.1	EST_HUMAN	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11428	24489	38153	2.26	1.0E-112	AI792603.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
11428	24489	38154	2.26	1.0E-112	AI792603.1	EST_HUMAN	FUSED TOES;
11460	24519	38188	4.76	1.0E-112	AW377670.1	EST_HUMAN	qk24c08.y6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362
12096	25076	38783	1.66	1.0E-112	AI792603.1	EST_HUMAN	FUSED TOES;
12096	25076	38784	1.66	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362
12727	25484		1.31	1.0E-112	AF106666.1	NT	FUSED TOES;
781	13942	26987	6.82	1.0E-113	AI365586.1	EST_HUMAN	PM0-CT0237-141089-001-H02 CT0237 Homo sapiens cDNA
751	13942	26988	6.82	1.0E-113	AI365586.1	EST_HUMAN	qk24c08.y6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362
965	14138	27199	2.93	1.0E-113	IM11965.1	NT	FUSED TOES;
1572	14725	27805	3.23	1.0E-113	AI365586.1	EST_HUMAN	qk24c08.y6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362
							FUSED TOES;
							Homo sapiens adenylylucinate lyase gene, complete cds
							ac95601.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
							ac95601.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
							Human X-linked phosphoglycerate kinase gene, exon 8
							ac95601.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1983	15894	28240	1.63	1.0E-113	AF240776.1	NT	Homo sapiens aIF4E-transporter mRNA, complete cds
2161	15297	28422	1.49	1.0E-113	BF515218.1	EST_HUMAN	U1H-BW1-ant1-03-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082878 3'
3200	16375	29385	2.06	1.0E-113	AJ223848.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5178	18300	31263	36.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5178	18300	31264	36.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5359	25930		2.4	1.0E-113	BE760858.1	EST_HUMAN	Homo sapiens activating transcription factor B (B-ATF), mRNA
5610	18805	31870	6.37	1.0E-113	AU127214.1	EST_HUMAN	601469468F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5045	19228	32562	3.54	1.0E-113	AU140291.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
6072	19264	32563	1.02	1.0E-113	AF016535.1	NT	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
							Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
							Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
6195	19371	32722	2.57	1.0E-113	11525737	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6285	19458	32808	0.8	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6285	19458	32810	0.8	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6446	19613	32976	0.88	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6446	19613	32977	0.88	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7474	20549	34021	0.63	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
7474	20549	34022	0.63	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
9093	22172	35717	0.5	1.0E-113	8922819	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
9286	22372	36921	2.91	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827554 5'
9286	22372	36922	2.91	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827554 5'
9801	22656		0.82	1.0E-113	BE772987.1	EST_HUMAN	RC1-FT0134-280600-021-d02 FT0134 Homo sapiens cDNA
10036	23074	36674	1.27	1.0E-113	11429367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10256	23291	36888	1.01	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10256	23291	36889	1.01	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10842	23878	37495	0.47	1.0E-113	AW500519.1	EST_HUMAN	U1HF-BN0-ak3-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5'
11385	24446	38107	1.89	1.0E-113	AW500519.1	EST_HUMAN	U1HF-BN0-ak3-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
							h81a09.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968176 5' similar to TR:O60327 O60327
							KIAA0584 PROTEIN;
11396	24457	38119	5.42	1.0E-113	AW630291.1	EST_HUMAN	h81a09.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968176 5' similar to TR:O60327 O60327
11396	24457	38120	5.42	1.0E-113	AW630291.1	EST_HUMAN	KIAA0584 PROTEIN;
11540	24596	38272	2.91	1.0E-113	BE202968.1	EST_HUMAN	KIAA0584 PROTEIN;
59	13297	26314	0.75	1.0E-114	Y17151.2	NT	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5'
							Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
59	13297	26315	0.75	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCG3)
59	13297	26316	0.75	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCG3)
662	13848	26876	7.46	1.0E-114	T70551.1	EST_HUMAN	yd15c01.g1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1098	14261	27318	2.54	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1341	14497	27569	4.65	1.0E-114	7657529	NT	Homo sapiens ribodol tumor deletion region protein 1 (RTDR1), mRNA
1673	14825	27909	1.9	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient 1 (S. cerevisiae) 3 (MCM3), mRNA
1708	14858	27945	5.08	1.0E-114	6678073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2145	15281	28406	2.52	1.0E-114	BE171984.1	EST_HUMAN	MF0-HT0558-250200-002-007 HT0559 Homo sapiens cDNA
2330	15462	28595	0.99	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2665	13283	28291	0.6	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2865	13283	28291	0.6	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3201	16376	28386	2.6	1.0E-114	X04066.1	EST_HUMAN	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3240	18414	28429	1.03	1.0E-114	BF206374.1	NT	601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4124	17278	30275	3.27	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4570	17649	30637	0.7	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Reo) mRNA, complete cds
5282	18401	31370	1.1	1.0E-114	AW294203.1	EST_HUMAN	UH-B12-aho-d-01-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726424 3'
5516	18714	31727	1.68	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5516	18714	31728	1.68	1.0E-114	4506880	NT	(TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5712	18905	32200	0.9	1.0E-114	9257201	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
7224	20068		0.71	1.0E-114	AB041533.1	NT	Homo sapiens HCMOG T-1 mRNA for sperm antigen, complete cds
7388	20466	33931	1.09	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7388	20466	33932	1.09	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7434	20511	33983	8.2	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7434	20511	33984	8.2	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
8075	21157	34675	1.94	1.0E-114	4557630	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8360	21441	34963	1.85	1.0E-114	AB03139.1	EST_HUMAN	qy68a06.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8360	21441	34964	1.85	1.0E-114	AB03139.1	EST_HUMAN	qy68a06.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8898	21977	35516	2.99	1.0E-114	AB03041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
8966	22045	35569	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8966	22045	35569	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9384	22459	36022	0.87	1.0E-114	BF109832.1	EST_HUMAN	7169g12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to
9514	22669		1.3	1.0E-114	AW327455.1	EST_HUMAN	TR:Q9JHN6 Q9JHN6 TRANSMEMBRANE PROTEIN 2 ;
9692	21104	34621	2.67	1.0E-114	AF077754.1	NT	gq03f05.x1 NIH_MGC 2 Homo sapiens cDNA clone IMAGE:2846744 5'
9748	22812		1.36	1.0E-114	M13535.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
10343	23378	36089	1.02	1.0E-114	BE870004.1	EST_HUMAN	Human ceruloplasmin mRNA
10364	23399	37010	1.11	1.0E-114	AL163227.2	NT	601449762F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3853500 5'
10762	23785	37415	1.18	1.0E-114	BE171984.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
							MF0-HT0559-260200-002-d07 HT0559 Homo sapiens cDNA
11027	24106						ba73g12.y1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206.40S
11466	24525	38197	4.31	1.0E-114	BE302666.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
11466	24525	38198	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
11842	24831	38522	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
11842	24831	38523	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
12843	26187		4.63	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12936	25616	31975	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12936	25616	31976	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
24	13262	26264	3.06	1.0E-115	4756111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
132	13358	26391	1.09	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
136	13362		18.42	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
303	13619	26552	2.02	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-508 UM0094 Homo sapiens cDNA
549	13742	26766	1.68	1.0E-115	AI339206.1	EST_HUMAN	q0601.x1 NCL CGAP_GCA Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
549	13742	26767	1.68	1.0E-115	AI339206.1	EST_HUMAN	q0601.x1 NCL CGAP_GCA Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
809	13988	27041	3	1.0E-115	5174702	NT	TTF-J INTERACTING PEPTIDE 5;
809	13988	27042	3	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
811	13990	27044	15.24	1.0E-115	4503794	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1590	14742	27823	1.15	1.0E-115	AF229180.1	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1590	14742	27824	1.15	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1888	15032	28140	1.31	1.0E-115	U78027.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
2142	15278	28400	1.13	1.0E-115	BE745469.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
							601679338F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928632 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2142	15278	28401	1.13	1.0E-115	BE745489.1	EST_HUMAN	601578838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2150	15286	28411	1.1	1.0E-115	AB007802.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2374	15505	28631	1.11	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
2912	15090		1.03	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-155-508 UM0094 Homo sapiens cDNA
3184	16359	29365	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3184	16359	29366	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3561	16726	29742	1.8	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4163	17305	30289	4.2	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4521	17660	30847	2.49	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4557	17695	30974	4.28	1.0E-115	4768279	NT	Homo sapiens EPHA4 (EPHA4) mRNA
4797	17832	30918	2.88	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4797	17832	30919	2.86	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5028	18155	31132	2.99	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5028	18155	31133	2.99	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5044	18172	31149	1.01	1.0E-115	Y19215.1	NT	Homo sapiens putative pshHBC pseudogene for hair keratin, exons 1 to 9
5304	18421	31391	1.23	1.0E-115	4504658	NT	Homo sapiens Interleukin 1 receptor, type I (IL1R1) mRNA
5347	18460	31425	0.92	1.0E-115	AB018311.1	NT	Homo sapiens mRNA for KIAA0788 protein, partial cds
5463	18663	31642	2.8	1.0E-115	AW970335.1	EST_HUMAN	EST382416 MAGE sequences, MAGK Homo sapiens cDNA
5540	18737	31754	0.97	1.0E-115	BF685387.1	EST_HUMAN	602119346F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278738 5'
5659	18853	32139	1.74	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5659	18853	32137	1.74	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5808	18998	32304	1.15	1.0E-115	A1828799.1	EST_HUMAN	af64g01 x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:U7807
5808	18998	32305	1.15	1.0E-115	A1828799.1	EST_HUMAN	af64g01 x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:U7807
6391	19560	32919	0.68	1.0E-115	11426786	NT	DYNAMIN-1 (HUMAN);
6391	19560	32920	0.68	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6525	19690	33064	9.49	1.0E-115	11426038	NT	Homo sapiens sperm surface protein (HSS), mRNA
6658	19817	33204	1.68	1.0E-115	7661883	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
6658	19817	33205	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7074	20127	33543	0.75	1.0E-115	T86774.1	EST_HUMAN	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7428	20505	33975	1.24	1.0E-115	A1076598.1	EST_HUMAN	y88b08.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:115098 5' similar to SP-DPOG_YEAST P15801 DNA POLYMERASE GAMMA;
7428	20505	33976	1.24	1.0E-115	A1076598.1	EST_HUMAN	o231a06.x1 Soares fetal spleen 1NPLS Homo sapiens cDNA clone IMAGE:1676914 3'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7246	20329	33775	1	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: hta3) Homo sapiens cDNA clone DKFZp434O0127 5'
7778	20833	34324	4.7	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7790	20846	34339	0.72	1.0E-118	L46590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cde
8189	21241	34781	1.95	1.0E-118	BE78123.1	EST_HUMAN	801469159F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872247 5'
8577	21668	35188	7	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8577	21668	35189	7	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8583	21684	35204	1.1	1.0E-118	AA443024.1	EST_HUMAN	z89807.r1 Soares_NHMFU_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8583	21684	35205	1.1	1.0E-118	AA443024.1	EST_HUMAN	z89807.r1 Soares_NHMFU_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8873	21952	36488	0.94	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8873	21952	36489	0.94	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8918	21997	35537	1.94	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9236	22313	35855	5.15	1.0E-118	BE263134.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9266	22343	35894	0.55	1.0E-118	AL048474.2	EST_HUMAN	801144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
9792	22832	36411	1.07	1.0E-118	7657016	NT	DKFZp596K1824_r1 586 (synonym: hula1) Homo sapiens cDNA clone DKFZp596K1824
10541	23578	37184	1.23	1.0E-118	BE736213.1	EST_HUMAN	Homo sapiens hypodermal protein (DJ328E19.G1.1), mRNA
10541	23578	37185	1.23	1.0E-118	BE736213.1	EST_HUMAN	Homo sapiens hypodermal protein (DJ328E19.G1.1), mRNA
10586	23621	37228	1.75	1.0E-118	BF195407.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641803 5'
10752	23785	37389	0.59	1.0E-118	AW286351.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641803 5'
11555	24610	38290	3.75	1.0E-118	AA315007.1	EST_HUMAN	7n17608.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW_ZP3A_HUMAN
11855	24843	38539	2.92	1.0E-118	BE908876.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR :
11855	24843	38540	2.92	1.0E-118	BE908876.1	EST_HUMAN	U1H-BW0-alc-a-07-Q-U1.s1 NCI_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2729772 3'
12071	25052	38761	1.81	1.0E-118	BE218235.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
776	13956	27007	2.46	1.0E-119	AF170492.1	NT	801499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3801563 5'
1052	18028	27284	0.93	1.0E-119	7705607	NT	801499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3801563 5'
1987	15129	28232	2.98	1.0E-119	AB023147.1	NT	h39a06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175474 3' similar to TR:Q922H4
3171	16348	29353	1.01	1.0E-119	8922203	NT	Q922H4 G PROTEIN-COUPLED RECEPTOR LGRA.1
3312	16485		2.17	1.0E-119	AA816760.1	EST_HUMAN	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4063	17219	30227	1.22	1.0E-119	4504116	NT	Homo sapiens CGI-105 protein (LOC61011), mRNA
5453	18653	31632	3.96	1.0E-119	AU133399.1	EST_HUMAN	Homo sapiens mRNA for KIAA0930 protein, partial cds
							Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
							on10605.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:Q04F0.2
							CE01214.1
							Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
							AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001891 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6468	18698	31645	16.48	1.0E-119	M8914.1	NT	Human neurofibromin (NF1) gene, complete cds
5470	18670	31650	3.29	1.0E-119	BE636121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5550	18747	31782	1.61	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDH603 5'
5707	18900	32194	0.86	1.0E-119	AL134603.1	EST_HUMAN	DKFZp762M0710.1_1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
5707	18900	32195	0.86	1.0E-119	AL134603.1	EST_HUMAN	DKFZp762M0710.1_1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6255	19429	32775	6.7	1.0E-119	AI150703.1	EST_HUMAN	qb77c09.x1 Soares_fetal_NHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
6414	19583	32944	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
8414	19583	32945	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6481	19628	32989	1.22	1.0E-119	AI476732.1	EST_HUMAN	fm23f10.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2157451 3'
6589	19750	33133	2.39	1.0E-119	X06292.1	NT	Human c-fes/fps proto-oncogene
6801	19761	33149	4.01	1.0E-119	AW974193.1	EST_HUMAN	EST386296 IMAGE resequences, MAGM Homo sapiens cDNA
7588	20640	34116	1.09	1.0E-119	BE786614.1	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'
8862	21241	35476	0.93	1.0E-119	BE615160.1	EST_HUMAN	601280564F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:362526 5'
9667	22866	36592	0.46	1.0E-119	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
10111	23149	36750	0.96	1.0E-119	11036843	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10311	23348	36952	0.61	1.0E-119	AI149796.1	EST_HUMAN	qf43a11.x1 Soares_fetal_NHT Homo sapiens cDNA clone IMAGE:1752764 3' similar to TR:Q13458
10452	23487	37095	2.29	1.0E-119	AA463124.1	EST_HUMAN	Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO. ;
10722	23756	37361	1.13	1.0E-119	AJ297701.1	NT	aa3205r1 NCI_CGAP_G031 Homo sapiens cDNA clone IMAGE:814977 5'
10766	23799	37420	0.77	1.0E-119	11425837	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10768	23799	37421	0.77	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10844	23877	37497	0.59	1.0E-119	BE561967.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10849	23882	37502	0.73	1.0E-119	AB032261.1	NT	601347190F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687887 5'
11308	24373	38015	1.58	1.0E-119	AJ297701.1	NT	Homo sapiens Scd mRNA for stearyl-CoA desaturase, complete cds
11308	24373	38016	1.58	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11479	24538		6.62	1.0E-119	BF566571.1	EST_HUMAN	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
12490	26098		5.48	1.0E-119	AW847919.1	EST_HUMAN	602166072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
12845	25882		3.03	1.0E-119	X89211.1	NT	RC3-CT0212-240999-011-f03 CT0212 Homo sapiens cDNA
247	13468	26500	0.68	1.0E-120	AB018301.1	NT	H. sapiens DNA for endogenous retroviral like element
312	13528	26561	0.97	1.0E-120	AF248540.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
1066	14232	27290	2.74	1.0E-120	AF248540.1	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1066	14232	27291	2.74	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1456	14608	27689	3.26	1.0E-120	N44873.1	EST_HUMAN	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
							yy40g12.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:273766 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1631	14783	27869	11.19	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1849	14995	28098	8.58	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2174	15309	28437	1.83	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2174	15309	28438	1.83	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3382	13328	28581	1.81	1.0E-120	4507334	NT	Homo sapiens synaptobrianin 1 (SYNJ1), mRNA
4477	17617	30598	2.05	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4477	17617	30599	2.05	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4784	17919	30906	3.11	1.0E-120	AF089463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4784	17919	30907	3.11	1.0E-120	AF089463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5853	19043	32349	16.08	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5853	19043	32350	16.08	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
7746	20806	34295	1.84	1.0E-120	D34619.1	NT	Human TEXAS1 gene for thromboxane synthase, exon 7
8078	21160	34677	1.38	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8078	21160	34678	1.38	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8527	21608	35147	2.31	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183333 5'
8599	21680	35218	0.9	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8599	21680	35219	0.9	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8603	21684	35221	1.94	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8603	21684	35222	1.84	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8847	21727	35264	1.31	1.0E-120	AB007934.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
9701	22750	36319	4.67	1.0E-120	BE392102.1	EST_HUMAN	601307730F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5'
9701	22750	36320	4.67	1.0E-120	BE392102.1	EST_HUMAN	601307730F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5'
9946	22885	36578	3.54	1.0E-120	BF306841.1	EST_HUMAN	601888950F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122878 5'
9946	22885	36578	3.54	1.0E-120	BF306841.1	EST_HUMAN	601888950F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122878 5'
9962	23001	36597	6.7	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
9979	23018	36612	1.02	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10066	23134		0.55	1.0E-120	AI904151.1	EST_HUMAN	CM-BT043-080299-075 BT043 Homo sapiens cDNA
10281	23316	36916	3.4	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11391	24452	38115	8.66	1.0E-120	BE286387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
11625	24705	38387	2.12	1.0E-120	BE667819.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11625	24705	38388	2.12	1.0E-120	BE667819.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
12687	25436	32049	1.42	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
75	13311	26337	0.62	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
389	13595	26631	1.35	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
742	16020	28964	1.31	1.0E-121	6032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF/SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2023	15164	28269	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107MD (INPP4A), splice variant a, mRNA
2023	15164	28270	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107MD (INPP4A), splice variant a, mRNA
2169	15304	28431	1.22	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2643	15766	28880	1.07	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150286 5'
2643	15766	28881	1.07	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150286 5'
3150	16325	29336	5.8	1.0E-121	Y19208.1	NT	Homo sapiens HBB3 gene for hair keratin, exons 1 to 9
3150	16325	29337	5.8	1.0E-121	Y19208.1	NT	Homo sapiens HBB3 gene for hair keratin, exons 1 to 9
3626	16790	29807	1.23	1.0E-121	AB037759.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3626	16790	29808	1.23	1.0E-121	AB037759.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3768	16929	29934	8.25	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4450	17500	30571	1.76	1.0E-121	A1263294.1	EST_HUMAN	q67601.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
5091	18219	31189	3.42	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
5382	18584	31453	0.84	1.0E-121	BE222250.1	EST_HUMAN	hu0808.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5679	18873	32161	0.73	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6757	19913	33308	0.64	1.0E-121	M91463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
7028	20164		0.96	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
7102	18529	31463	0.79	1.0E-121	AW898985.1	EST_HUMAN	RC3-NN0066-270400-011-02 NN0066 Homo sapiens cDNA
7102	18529	31484	0.79	1.0E-121	AW898985.1	EST_HUMAN	RC3-NN0066-270400-011-02 NN0066 Homo sapiens cDNA
8123	21203	34725	1.07	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8127	21209	34729	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8127	21209	34730	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
10062	23100	36702	1.02	1.0E-121	AW563858.1	EST_HUMAN	iso5g05.v1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ;
10062	23100	36703	1.02	1.0E-121	AW563858.1	EST_HUMAN	iso5g05.v1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ;
11015	24094	37733	3.45	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
11023	24102	37740	1.94	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
11211	24280	37919	5.74	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11243	24312	37950	1.93	1.0E-121	N59624.1	EST_HUMAN	y74c01.s1 Scarsa fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'
278	13496	26526	2.64	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
346	13557	26585	2.33	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
368	13577	26810	2.66	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
905	14080	27146	3.34	1.0E-122	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN), mRNA, complete cds
1247	14406	27468	5.19	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1728	14878	27669	18.7	1.0E-122	AF187706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1750	14899	27995	1.61	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1750	14899	27996	1.61	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1857	15003	28110	6.92	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896356 5'
2560	15685	28810	7.43	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2560	15685	28811	7.43	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2801	16080	29096	4.87	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4971	18100	31078	3.81	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5104	18232		1.41	1.0E-122	AW504645.1	EST_HUMAN	UI-HF-BNO-all-a-03-Q-U1T NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
5681	18875	32164	1.2	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6896	18875	32164	6.8	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7363	20442	33904	0.64	1.0E-122	AA868671.1	EST_HUMAN	ak48106.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1408339 3'
8996	22075	35614	0.6	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
9228	22306	35849	1.17	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LGL2), mRNA
9524	22589	36159	0.96	1.0E-122	A1359618.1	EST_HUMAN	qy32h07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1
9524	22589	36160	0.96	1.0E-122	A1359618.1	EST_HUMAN	qy32h07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1
10338	23373	36983	0.64	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dBl (proto-oncogene)
11233	24302	37839	2.12	1.0E-122	AW955834.1	EST_HUMAN	EST3787904 MAGE resequences, MAGD Homo sapiens cDNA
11667	24744	38436	1.83	1.0E-122	AB024088.1	NT	Homo sapiens gene for B120, exon 10
12231	25178		5.28	1.0E-122	11418187	NT	Homo sapiens phosphonormylase 1 (PNMT), mRNA
789	13968	27019	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
789	13968	27020	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1038	14206	27263	6.18	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment H521C049
1047	14213	27270	3.36	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1267	14424	27491	3.83	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 6-kinase, type II, beta (PIP6K2B) mRNA, and translated products

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1267	14424	27492	3.83	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2035	15178	28286	0.94	1.0E-123	11422479	NT	Homo sapiens similar to sex comb on midleg (Drosophila)-like 2 (H. sapiens) (LOC63782), mRNA
2166	15301	28427	3.21	1.0E-123	M55418.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28428	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28429	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2389	15520		4.21	1.0E-123	7705862	NT	Homo sapiens RAB8-like protein (LOC51209), mRNA
3322	16495	29512	0.71	1.0E-123	6912617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5563	18760	31769	1.82	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5583	18760	31800	1.62	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5699	18893	32185	1.78	1.0E-123	BE798748.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6598	19768	33146	1.93	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7143	20278	33718	0.91	1.0E-123	H53198.1	EST_HUMAN	Y84603.1 Source fetal liver spleen 1NF5 Homo sapiens cDNA clone IMAGE:202444 5' similar to SP-YAK1 YEAST P14680 PROTEIN KINASE YAK1;
7156	20290	33733	1.39	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7344	20424	33887	0.71	1.0E-123	U56258.1	NT	Human HRAVO/INr-CAM precursor (HRAVO/INr-CAM) gene, complete cds
7562	20634	34109	0.83	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA
7820	20875	34374	1.31	1.0E-123	11436439	NT	Homo sapiens Z'-5-oligoadenylate synthetase 2 (OAS2), mRNA
7829	20884	34386	2.22	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3609162 5'
7838	20891	34393	0.6	1.0E-123	11437202	NT	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA
7975	21025	34538	0.6	1.0E-123	N35841.1	EST_HUMAN	Y889411.1 Source melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein kinase PkPa - Phycomyces blakesleeanus;
7975	21025	34539	0.6	1.0E-123	N35841.1	EST_HUMAN	Y889411.1 Source melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein kinase PkPa - Phycomyces blakesleeanus;
8100	21182	34701	0.79	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8100	21182	34702	0.79	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8732	21812		0.7	1.0E-123	AW371924.1	EST_HUMAN	RC4-BT0311-251169-012-a07 BT0311 Homo sapiens cDNA
9569	22711	36279	2.07	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9705	22784	36325	18.77	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
12020	25004	38705	4.91	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
12020	25004	38708	4.91	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
12114	25094	38798	2.71	1.0E-123	AW460931.1	EST_HUMAN	UI-H-B13-ali-f-10-0-UI.st1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'
12114	25094	38799	2.71	1.0E-123	AW460931.1	EST_HUMAN	UI-H-B13-ali-f-10-0-UI.st1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
279	13497	26927	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
279	13497	26928	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
285	13503		1.49	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
498	13593	26725	2.26	1.0E-124	AL103240.2	NT	Homo sapiens chromosome 21 segment HS21G046
709	13891	26926	4	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
709	13891	26927	4	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
777	13957	27008	3.72	1.0E-124	AF195694.1	NT	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
831	14009	27065	2.06	1.0E-124	4507500	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
927	14102	27165	2.67	1.0E-124	7705446	NT	Human putative ribosomal protein S1 mRNA
1343	14499	27572	0.68	1.0E-124	11419092	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1377	14532	27605	6.42	1.0E-124	AF274892.1	NT	Homo sapiens hypothetical protein (HSPC088), mRNA
1377	14532	27606	6.42	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
1898	15004	28111	4.06	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2123	15289	28379	2.16	1.0E-124	BE879524.1	EST_HUMAN	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2528	15653	28777	0.98	1.0E-124	AB024069.1	NT	Homo sapiens mRNA for nuclear RNA-helicase (noH81 gene)
3579	16744	29761	1.08	1.0E-124	S78684.1	NT	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
3739	16900	29904	1.24	1.0E-124	X13794.1	NT	Homo sapiens gene for B120, exon 11
4006	17153	30170	0.64	1.0E-124	4507500	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4179	17329	30321	0.69	1.0E-124	4504116	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4187	17337	30330	0.98	1.0E-124	4504116	NT	Homo sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined ODS)
4866	17999	30983	2.51	1.0E-124	AB024069.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5050	18178		15.32	1.0E-124	M18178.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5205	18326	31296	0.74	1.0E-124	AW963390.1	EST_HUMAN	Homo sapiens gene for B120, exon 11
5412	18614	31598	10.49	1.0E-124	8922337	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5789	18981	32284	1.2	1.0E-124	4506786	NT	EST:7375463 IMAGE resequences, MAGH Homo sapiens cDNA
6008	19193	32511	6.89	1.0E-124	BF596135.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6296	19471	32826	0.8	1.0E-124	AV711283.1	EST_HUMAN	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6663	19725	33103	1.12	1.0E-124	11420654	NT	602124544F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
7162	20286	33728	3.15	1.0E-124	Y11717.1	NT	AV711283 Cu Homo sapiens cDNA clone CUAAD707 5'
7287	20370	33824	0.94	1.0E-124	BE271286.1	EST_HUMAN	Homo sapiens ubiquitin specific protease 8, X chromosome (Drosophila fat facets related) (USP9X), mRNA
							Mmusculus mRNA for hoxa3 gene.
							600643771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966885 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7287	20370	33825	0.94	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2986585 5'
7725	20789	34278	2.38	1.0E-124	AA630331.1	EST_HUMAN	ac0805.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:859897 3'
8453	21634	35084	2.73	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8657	21737	35277	1.24	1.0E-124	AW612108.1	EST_HUMAN	hg54a09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
8657	21737	35278	1.24	1.0E-124	AW612108.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.;
9363	22438	35956	0.88	1.0E-124	AI799864.1	EST_HUMAN	hg54a09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
9363	22438	35997	0.88	1.0E-124	AI799864.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.;
9691	22740	36309	1.72	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2321428 3'
9691	22740	36310	1.72	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9808	22848	36426	7.77	1.0E-124	AI767133.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9808	22848	36427	7.77	1.0E-124	AI767133.1	EST_HUMAN	wf93f02.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
10075	23113	36717	1.46	1.0E-124	AW503755.1	EST_HUMAN	UIHF-BN0-alk-b-0-q-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078848 5'
11302	24388	38009	1.87	1.0E-124	U64776.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
11617	24698	38356	3.9	1.0E-124	AW665663.1	EST_HUMAN	h05c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2880906 3'
11761	23947	37575	2.18	1.0E-124	AI446455.1	EST_HUMAN	YKRS PROTEIN.;
11761	23947	37576	2.18	1.0E-124	AI446455.1	EST_HUMAN	YKRS PROTEIN.;
12310	13891	26926	4.6	1.0E-124	AA397551.1	EST_HUMAN	Z81b04.t1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
12310	13891	26927	4.6	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
12780	25522	32004	1.99	1.0E-124	AB028016.1	NT	Z81b04.t1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
13080	26038	31680	2.36	1.0E-124	11417862	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
13080	26038	31681	2.36	1.0E-124	11417862	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
329	13543		7.32	1.0E-125	AB032898.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
439	13239	26239	4.69	1.0E-125	BE743922.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
681	13847	26874	2.02	1.0E-125	AI110656.1	EST_HUMAN	Homo sapiens mRNA for KIAA1172 protein, partial cds
681	13847	26875	2.02	1.0E-125	AI110656.1	EST_HUMAN	50157981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926655 5'
746	13927	26888	2.42	1.0E-125	AF284750.1	NT	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
							Homo sapiens ALR-like protein mRNA, partial cds
							Z453c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1023	14194	27252	1.54	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1177	14340	27394	1.73	1.0E-125	7682270	NT	Homo sapiens KIAA0744 gene product: histone deacetylase 7 (KIAA0744), mRNA
1707	18045	27949	1.44	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1854	15000	28106	5.91	1.0E-123	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1854	15000	28107	5.91	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2433	15561	28687	4.81	1.0E-126	AA011278.1	EST_HUMAN	201g09.r1 Soares_fetal_liver_spleen_1NF.LS_S1 Homo sapiens cDNA clone IMAGE:428368 5'
2573	15698	28820	0.96	1.0E-125	AA042813.1	EST_HUMAN	2k53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
2661	15783	28898	2.34	1.0E-125	4504636	NT	gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2661	15783	28899	2.34	1.0E-125	4504636	NT	Homo sapiens inhibin, alpha (INH) mRNA
3661	17119	30123	1.33	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens inhibin, alpha (INH) mRNA
4672	17507	30796	1.82	1.0E-125	11425114	NT	2k53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
4672	17507	30797	1.82	1.0E-125	11425114	NT	gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4739	17674	30857	0.85	1.0E-125	BE315412.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5877	19067	32375	0.65	1.0E-125	BF683845.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140798 5'
5894	19179	32501	1.39	1.0E-125	11436448	NT	602139874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'
6013	19197	32514	1.2	1.0E-125	BE175169.1	EST_HUMAN	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6054	19238	32561	3.53	1.0E-125	BE692660.1	EST_HUMAN	QV2-HT0577-010500-165-308 HT0577 Homo sapiens cDNA
6096	19277	32606	0.85	1.0E-125	AI079904.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6412	19591	32942	0.72	1.0E-125	BE738056.1	EST_HUMAN	tu67c07.x1 NCI_CGAP_Gaa4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP:04509.2
6711	19869	33259	3.71	1.0E-125	BE662526.1	EST_HUMAN	CE01854
6711	19869	33260	3.71	1.0E-125	BE662526.1	EST_HUMAN	601305670F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640097 5'
7207	20072	33483	4.06	1.0E-125	X03427.1	NT	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7207	20072	33484	4.06	1.0E-125	X03427.1	NT	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7700	20765	34249	1.56	1.0E-125	BE278823.1	EST_HUMAN	Homo sapiens GF-II gene, exon 5
7933	20983	34491	0.59	1.0E-126	11425572	NT	Homo sapiens GF-II gene, exon 5
8743	21622	35357	1.49	1.0E-125	U90288.1	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8743	21622	35358	1.49	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9318	22394	35645	4.15	1.0E-125	BE181840.1	EST_HUMAN	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9318	22394	35646	4.15	1.0E-125	BE181840.1	EST_HUMAN	QV1-HT0638-070500-191-312 HT0638 Homo sapiens cDNA
							QV1-HT0638-070500-191-312 HT0638 Homo sapiens cDNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9581	22723	36293	1.06	1.0E-125	AI565968.1	EST_HUMAN	tr52b03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089
10670	23704	37313	0.72	1.0E-125	BE794576.1	EST_HUMAN	HYPOTHETICAL PROTEIN;
10712	23745	37351	1.06	1.0E-125	AB002298.1	NT	601590345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944531 5'
10921	24004	37639	3.03	1.0E-125	AF043458.1	NT	Human mRNA for KIAA0300 gene, partial cds
11091	24165	37802	1.34	1.0E-125	11425670	NT	Homo sapiens IREL gene, exon 5
11357	24419	38076	2.42	1.0E-125	AL040855.1	EST_HUMAN	Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), mRNA
11401	24482	38126	3.35	1.0E-125	AB014587.1	NT	DKFZp434N2414.1 r1 434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434N2414 5'
11538	24594	38303	1.63	1.0E-125	R81450.1	EST_HUMAN	Homo sapiens mRNA for KIAA0667 protein, partial cds
11568	24623	38303	2.13	1.0E-125	7669505	NT	Y15a12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:37663 5'
11575	24630	38309	5.32	1.0E-125	AF026029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11686	24685	38375	2.27	1.0E-125	AW812688.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
11793	24763	38479	4.71	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g08 BT0569 Homo sapiens cDNA
11793	24763	38480	4.71	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
795	13974	27027	2.16	1.0E-128	4768007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
798	13977	27030	1.74	1.0E-128	M61936.1	NT	Human laminin B1 chain gene, exon 20
942	14116	27175	1.53	1.0E-126	X68735.1	NT	H. sapiens gene for alpha1-antichymotrypsin, exon 3
2863	15785	28900	4.55	1.0E-128	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3140	16316	29329	8.12	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
3140	16316	29330	8.12	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
3719	16860	29685	0.87	1.0E-126	X53941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3745	16906	29910	2.52	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4908	18038	31026	1.08	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4908	18038	31027	1.08	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4956	18088	31062	1.81	1.0E-126	N34078.1	EST_HUMAN	yK78c03.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:267650 5'
5820	19010	32316	0.88	1.0E-126	T86998.1	EST_HUMAN	ya52b12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:65527 3'
6382	19532	32891	2.91	1.0E-128	AA460075.1	EST_HUMAN	z66e03.r1 Soares fetal fetus Nb2HF8_gw Homo sapiens cDNA clone IMAGE:796444 5' similar to
6419	19588	32951	4.33	1.0E-126	AB040958.1	NT	TR-G1145880 G1145880 TITIN ;
6419	19588	32952	4.33	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7669	20735	34212	0.9	1.0E-126	AF257737.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7669	20735	34213	0.9	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 8 (DNAH9) mRNA, complete cds
8062	21144	34662	0.73	1.0E-126	AB037715.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8062	21144	34663	0.73	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	21259	34781	2.42	1.0E-126	X16609.1	NT	Human mRNA for ankyrin (variant 2.1)
8377	21458	34982	0.8	1.0E-126	AA483368.1	EST_HUMAN	ne74b12.s1 NCJ CGAP_Ev1 Homo sapiens cDNA clone IMAGE:908983 similar to SW:TS66_HUMAN
10000	23038	36829	0.57	1.0E-126	4506424	NT	P88066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR ;
11098	24172	37807	2.01	1.0E-126	BF683176.1	EST_HUMAN	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
11806	24766	38494	2.2	1.0E-126	BE261860.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298240 5'
12823	18500	31538	6.48	1.0E-126	BE743922.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
176	13400	26429	2.92	1.0E-127	AB024597.1	NT	601577981F1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:3926685 5'
176	13400	26430	2.92	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	26429	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	26430	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
284	13502	26535	2.14	1.0E-127	D87676.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
284	13502	26536	2.14	1.0E-127	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
904	14079	27145	1.17	1.0E-127	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
938	14113	27174	4.81	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1728	14876	27987	2.22	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2127	15263	28382	1.97	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2127	15263	28383	1.97	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2273	15406	28635	17.46	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L28 (RPL28) mRNA
2418	15547	28675	3.12	1.0E-127	AF245505.1	NT	Homo sapiens adiclin mRNA, complete cds
2674	15794	28911	21.46	1.0E-127	X12881.1	NT	Human mRNA for cytochrome 18
3781	16942	29948	0.61	1.0E-127	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
3913	17072	30070	0.7	1.0E-127	AW161297.1	EST_HUMAN	eu80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ; contains element MER22 repetitive element ;
4232	17379	30368	0.59	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4368	17511	30491	24.93	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4368	17511	30492	24.93	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4618	17755	30737	0.83	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 reductase metabolizing protein P450RAI-2 mRNA, complete cds
4725	17860	30842	6.74	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4765	17990		2.69	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4795	17930	30916	4.36	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5824	19014	32320	1.57	1.0E-127	W03547.1	EST_HUMAN	za01a10.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291288 5' similar to SW:PIPB6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5854	19044	32351	0.91	1.0E-127	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5923	19110	32423	4.18	1.0E-127	X85764.1	NT	H sapiens NOS2 gene, exon 6
6291	19464	32816	2.23	1.0E-127	X84060.1	NT	H sapiens TGF11 gene, exon 3-6
6451	19618	32981	5.73	1.0E-127	4504778	NT	H sapiens integrin, beta 8 (ITGB8) mRNA
6797	19852	33352	1.09	1.0E-127	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7208	20073	33485	0.81	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
7884	21014	34525	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7964	21014	34526	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7973	21023	34536	0.63	1.0E-127	BF77355.1	EST_HUMAN	602151232F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4292575 5'
8088	22167	35713	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8088	22167	35714	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9840	22880	36462	3.73	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9840	22880	36463	3.73	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10077	23115	36718	0.86	1.0E-127	A128832.1	EST_HUMAN	gm84h09.x1 NCJ_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1896449 3'
10551	23586	37194	0.99	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11426	24487	38150	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H sapiens) (LOC63184), mRNA
11426	24487	38151	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H sapiens) (LOC63184), mRNA
11927	24913	38614	1.55	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3919917 5'
11927	24913	38615	1.55	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3919917 5'
12539	13400	26429	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12539	13400	26430	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12763	25507	32037	1.74	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13170	26044		1.84	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
472	13667	26700	1.66	1.0E-128	BE366617.1	EST_HUMAN	601276127F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3618822 5'
1178	14342	27399	0.96	1.0E-128	4758031	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (GSPG2) mRNA
1179	14342	27397	0.96	1.0E-128	4758031	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (GSPG2) mRNA
2132	15268	28387	18.07	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2132	15268	28388	18.07	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2283	15415	28547	37.91	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2516	15642		1.11	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3481	16948	29664	1.17	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4766	17821	30903	7.27	1.0E-128	11428673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5682	18956	32139	0.76	1.0E-128	X89539.1	NT	H sapiens gene for Inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6548	19710	33086	1.5	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7070	20123	33538	6.26	1.0E-128	BF224346.1	EST_HUMAN	7q86b10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
8746	21824	35360	0.67	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8745	21824	35361	0.67	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10341	23376	36987	1.29	1.0E-128	AA639108.1	EST_HUMAN	ns04a11.r1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338
10949	24031	37666	3.54	1.0E-128	11426254	NT	CHROMOSOME SEGREGATION GENE HOMOLOG CAS.1
10957	24038	37673	3.61	1.0E-128	AA926559.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
11210	24278	37818	1.98	1.0E-128	BE887554.1	EST_HUMAN	om68h08.s1 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X64941 CYCLIN-
12402	25282		4.26	1.0E-128	AW955290.1	EST_HUMAN	DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
124	13621	26663	1.93	1.0E-129	S37722.1	NT	EST367360 MAGe sequences, MAGC Homo sapiens cDNA
426	13621	26663	1.66	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1756	14906	27099	3.74	1.0E-129	AL096880.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1761	14910	28004	1.66	1.0E-129	AF240786.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1761	14910	28004	1.66	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1894	15037	28145	1.66	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2838	15952	29058	4.07	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 78 (expressed in testis) (ZNF78), mRNA
2838	15952	29058	2.83	1.0E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2838	15952	29059	2.93	1.0E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
3198	16373	29380	1.43	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3198	16373	29381	1.43	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3198	16373	29382	1.43	1.0E-129	Q14586	SWISSPROT	ZINC FINGER PROTEIN HZF10
4279	17424	30413	2.37	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4395	17539	30517	2.32	1.0E-129	AW765254.1	EST_HUMAN	CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYAS
							Cardiomyopathy associated gene 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4395	17538	30518	2.32	1.0E-128	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to OMYA5
6216	19391	32739	3.77	1.0E-129	AJ008345.1	NT	Cardiomyopathy associated gene 5
6654	19813	33201	0.61	1.0E-129	BE88934.1	EST_HUMAN	Homo sapiens KVLQ11 gene
7277	20360	33814	3.98	1.0E-128	AJ008345.1	NT	601513881F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915350 5'
7340	20420	33882	4.03	1.0E-128	11420850	NT	Homo sapiens KVLQ11 gene
7697	20762	34245	1.04	1.0E-129	AF041056.1	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
7697	20762	34246	1.04	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8513	21594		3.57	1.0E-129	AB014634.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
10284	23319	36920	1.03	1.0E-128	11437282	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10284	23319	36921	1.03	1.0E-128	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10730	23763	37370	0.52	1.0E-128	AI198117.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10730	23763	37371	0.52	1.0E-128	AI198117.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11497	24555	38230	3.32	1.0E-129	AA625526.1	EST_HUMAN	q140408.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840
11578	20420	33882	5.01	1.0E-128	11420850	NT	MITOGEN INDUCIBLE GENE MIG-2;
12387	25273		4.28	1.0E-128	H83155.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIG-2;
12817	25544		1.97	1.0E-129	AL120739.1	EST_HUMAN	q140408.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840
78	13314	26341	1.01	1.0E-130	7705530	NT	MITOGEN INDUCIBLE GENE MIG-2;
1187	14359	27418	0.64	1.0E-130	AB037835.1	NT	SP:B48150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN;
1700	14852	27939	22.97	1.0E-130	BE275192.1	EST_HUMAN	q149c05.r1 Scarses fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:199112 5' similar to
1700	14852	27940	22.97	1.0E-130	BE275192.1	EST_HUMAN	DKFZp762K171_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5'
2040	15181		2.63	1.0E-130	X04092.1	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
2830	15944		7.23	1.0E-130	AJ010230.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
2943	16120	29132	1.36	1.0E-130	BE664219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2943	16120	29133	1.36	1.0E-130	BE664219.1	EST_HUMAN	601121895F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
3668	16831	29842	1.03	1.0E-130	AF240598.1	NT	601121895F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
3864	16120	29132	6.31	1.0E-130	BE664219.1	EST_HUMAN	601121895F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
3864	16120	29133	6.31	1.0E-130	BE664219.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH), mRNA, complete cds
4047	17203	30213	1.8	1.0E-130	AW503580.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4184	17334	30326	0.91	1.0E-130	M97710.1	NT	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4660	17796	30782	9.77	1.0E-130	AW843993.1	EST_HUMAN	UI-HF-BND-aky-g-06-o-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
							Human T-cell receptor (V alpha 22.1, J alpha RPLM4265-variant, C alpha 1) mRNA
							CM4-CN0045-1802005-511-102 CN0045 Homo sapiens cDNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5208	18328	31300	1.49	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
5208	18328	31301	1.49	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
6860	20188	33612	1.03	1.0E-130	AW843875.1	EST_HUMAN	GM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6860	20188	33613	1.03	1.0E-130	AW843875.1	EST_HUMAN	GM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6876	20203	33630	0.85	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7404	20482	33949	1.85	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7608	20680	34052	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 8 (DNAH9) mRNA, complete cds
7808	20580	34053	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8881	21890		0.53	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
9019	22098	35698	2.08	1.0E-130	AW969242.1	EST_HUMAN	EST368312 MAGE resequences, MAGD Homo sapiens cDNA
9415	22489	36054	1.82	1.0E-130	AB03736.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
10137	23175		0.63	1.0E-130	AW103454.1	EST_HUMAN	x38a08.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595874 3'
4	13243	26243	2.52	0.0E+00	AA228128.1	EST_HUMAN	zr58c04.r1 Scores_NhHMPu S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	13243	26244	2.52	0.0E+00	AA228128.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
8	13246	26248	1.14	0.0E+00	4885136	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
18	13254	26254	3.34	0.0E+00	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
16	13254	26255	3.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13261	26262	3.17	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13261	26263	3.17	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
27	13265	26267	8	0.0E+00	AF141349.1	NT	Homo sapiens DCRR1 mRNA, partial cds
35	13273	26277	0.62	0.0E+00	5802997	NT	Homo sapiens beta-tubulin mRNA, complete cds
37	13275	26280	0.89	0.0E+00	M88800.1	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
41	13279	26285	4.6	0.0E+00	6857825	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
58	13296	26312	1.77	0.0E+00	Y17151.2	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
58	13296	26313	1.77	0.0E+00	Y17151.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
60	13298	26317	1.45	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	13298	26318	1.45	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	13298	26319	9.83	0.0E+00	L16558.1	NT	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
63	13301	26322	16.36	0.0E+00	AW069534.1	EST_HUMAN	Human ribosomal protein L7 (RPL7) mRNA, complete cds
63	13301	26323	16.36	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC cr48e07 3'
67	13304	26327	2.48	0.0E+00	M60676.1	NT	cr48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC cr48e07 3'
							Human von Willebrand factor pseudogene corresponding to exons 23 through 34

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
69	13308		23.72	0.0E+00	M60878.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
77	13313	26339	2.1	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	13313	26340	2.1	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26339	1.06	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26340	1.06	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
83	13318	26346	0.62	0.0E+00	AA953770.1	EST_HUMAN	on89s04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563870 3' similar to SW:TMOD_HUMAN P28289 TROPOMODULIN.;
84	13319	26347	16.96	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
85	13320	26347	12.3	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
94	13326	26336	23.92	0.0E+00	5016098	NT	Homo sapiens actin, beta (ACTB) mRNA
97	13332	26359	40.86	0.0E+00	U89277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
103	13339	26366	2.4	0.0E+00	AI114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
104	13340	26367	0.9	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
110	13343	26371	0.68	0.0E+00	X91213.1	NT	H.sapiens nrx1 gene (exon 2)
118	13350	26377	0.68	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99561 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.;
119	13350	26377	1.58	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99561 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.;
120	15980	26378	1.92	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270017 5'
120	15980	26379	1.92	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270017 5'
123	13353	26384	1.63	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
133	13359	26392	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
133	13359	26393	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
141	13009	26647	1.9	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
143	13367	26400	0.7	0.0E+00	T56945.1	EST_HUMAN	yy83g04.r2 Stralagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
143	13367	26401	0.7	0.0E+00	T56945.1	EST_HUMAN	yy83g04.r2 Stralagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
157	13382		12.8	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
161	13388	26416	2.06	0.0E+00	BF036881.1	EST_HUMAN	601460376F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
163	13388		98.39	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
166	13391	26419	12.6	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit I gene, complete cds; and unknown genes
168	13393	26420	1.03	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
169	13393	26420	0.79	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
170	13394	26421	2.4	0.0E+00	W73973.1	EST_HUMAN	z62605.t1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346201 5' similar to gb:X16282 cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
171	13395	26422	0.79	0.0E+00	BE162632.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
171	13395	26423	0.79	0.0E+00	BE162632.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
172	13396	26424	4.73	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
175	13399	26427	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
175	13399	26428	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
185	13407	26435	6.75	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
185	13407	26435	6.75	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
185	13407	26436	6.75	0.0E+00	BE018970.1	EST_HUMAN	CE22631.1
190	13412	26439	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
190	13412	26439	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
190	13412	26440	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26441	1.88	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26441	1.88	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26442	1.68	0.0E+00	AB018327.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
199	13422	26453	57.89	0.0E+00	D50659.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
204	13427	26458	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
204	13427	26459	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
208	13429	26461	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSI3-2 protein mRNA, complete cds
208	13429	26461	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSI3-2 protein mRNA, complete cds
208	13429	26462	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSI3-2 protein mRNA, complete cds
216	16007	26469	12	0.0E+00	AI587308.1	EST_HUMAN	iq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN (HUMAN);
216	16007	26469	12	0.0E+00	AI587308.1	EST_HUMAN	iq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN (HUMAN);
218	13440	26470	12	0.0E+00	AI587308.1	EST_HUMAN	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
218	13440	26472	1.93	0.0E+00	AF195558.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
221	13443		11.48	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
222	13444		6.53	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
228	13450	26478	1.48	0.0E+00	AB018294.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
228	13450	26478	1.34	0.0E+00	AB018294.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
230	13451	26478	2.02	0.0E+00	6878444	NT	Mus musculus testis-specific protein, Y-encoded-like (TspY), mRNA
237	13459	26483	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
237	13459	26484	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
237	13459	26485	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
245	13467	26496	1.17	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
245	13467	26497	1.17	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
248	13469	26501	7.54	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
250	13471		3.79	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
257	13476	26507	4.65	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
259	13478	26510	1.22	0.0E+00	X89772.1	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
267	13486		5.95	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
280	13498	26529	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
280	13498	26530	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
282	13500	26532	1.9	0.0E+00	7709028	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
283	13510		0.96	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
284	13511	26545	1.2	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
294	13511	26546	1.2	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
295	13512		1.41	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 GT0031 Homo sapiens cDNA
304	13520	26553	5.65	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
304	13520	26554	5.65	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
315	13531	26564	6.16	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
316	13532	26565	4.28	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
317	15010		8.13	0.0E+00	4505728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
318	13533		1.42	0.0E+00	AA480002.1	EST_HUMAN	zrl8c06.r1 Scarsa_NHMPu_S1 Homo sapiens cDNA clone IMAGE:753994 5'
319	13534	26566	19.55	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
320	13534	26566	24.65	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
324	13538	26570	1.59	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
337	13560	26579	1.15	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (B1B AND CNC HOMOLOG 1) (HA2303)
337	13560	26580	1.15	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (B1B AND CNC HOMOLOG 1) (HA2303)
338	13551	26581	4.14	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
339	13551	26581	1.82	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
354	13565	26593	4.38	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (MLLT4) mRNA
355	13566	26594	0.74	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
358	13569	26598	4.58	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
361	13572	26603	0.96	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
366	13576	26807	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
366	13578	26808	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
367	16011	26809	2.53	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
366	13578	26811	1.01	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
372	13561	26815	1.59	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
373	13562	26816	2	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
374	13562	26816	1.43	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
376	13564	26818	0.99	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
387	13593	26829	3.37	0.0E+00	AU134983.1	EST_HUMAN	AU134983 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
398	13635	26873	7.56	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
399	13636	26874	1.08	0.0E+00	A1863014.1	EST_HUMAN	qy61h05.x1 NCI_CGAP Brn25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb.X54199
404	13601	26836	1.32	0.0E+00	AW764180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
407	13603	26839	2.24	0.0E+00	4503680	NT	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA
408	13604	26840	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
408	13604	26841	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
409	13605	26842	2.18	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
410	13606	26843	1.42	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
411	13607	26845	1.98	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
412	13608	26846	2.55	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
413	13609	26847	2.14	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
414	13610	26848	0.96	0.0E+00	X74870.1	NT	H sapiens gene for RNA pol II largest subunit, exons 23-29
414	13610	26849	0.96	0.0E+00	X74870.1	NT	H sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26848	1.07	0.0E+00	X74870.1	NT	H sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26849	1.07	0.0E+00	X74870.1	NT	H sapiens gene for RNA pol II largest subunit, exons 23-29
419	13614	26877	18.46	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
433	13233	26233	1.49	0.0E+00	R17795.1	EST_HUMAN	yp09a02.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:31652 5'
441	13637	26875	1.39	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
442	13638	26876	3.85	0.0E+00	4506728	NT	phosphoribosylmethyltransferase synthetase (GART) mRNA
443	13639	26876	2.82	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
444	13640	26877	17.7	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
444	13640	26878	17.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
445	13641	26679	4.23	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
457	13652		1.45	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
459	13654	26692	4.44	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
464	13659		0.75	0.0E+00	BE284447.1	EST_HUMAN	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
480	13675	26706	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
480	13675	26707	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
486	13680	26715	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
486	13680	26716	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
496	13691	26722	4.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26723	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26724	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
509	13700	26729	4.25	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
509	13702	26731	1.81	0.0E+00	AU132898	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
516	13710	26737	1.66	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
517	16014	26738	1.7	0.0E+00	AW938825.1	EST_HUMAN	PM0-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
620	13713	26740	1.82	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
521	13714	26741	0.95	0.0E+00	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
525	13718		1.9	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
532	13725	26751	4.43	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
539	16015	26755	1.57	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
544	13737	26761	1.15	0.0E+00	BF028003.1	EST_HUMAN	60176458F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3696998 5'
550	13743	26768	1.57	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
553	13746	26771	8.39	0.0E+00	5006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
554	13747	26772	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
554	13747	26773	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
558	13749	26775	0.73	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26776	0.63	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26777	0.63	0.0E+00	8923831	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
562	13754		4.82	0.0E+00	AF003528.1	NT	UH-B1-ach-h04-0-U1.s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
570	13762	26785	1.39	0.0E+00	AW136324.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
580	13772		5.31	0.0E+00	D10083.1	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCORF1), nuclear gene
596	13789	26810	1.85	0.0E+00	5174742	NT	encoding mitochondrial protein, mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
612	13801		7.14	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
615	13804	26824	1.87	0.0E+00	BF104898.1	EST_HUMAN	g01822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
617	13806	26826	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
617	13806	26827	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26828	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26827	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13808	26826	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13808	26827	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
624	13809	26830	0.64	0.0E+00	4501854	NT	Homo sapiens acyl-Coenzyme A carboxylase beta (ACACB), mRNA
629	13814	26836	1.93	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
629	13814	26837	1.93	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
639	13824	26847	2.19	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
641	13826	26850	0.93	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1385 protein, partial cds
643	13828	26851	1.99	0.0E+00	8606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13829	26852	2.34	0.0E+00	8606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13829	26853	2.34	0.0E+00	8606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
646	13830	26854	0.98	0.0E+00	8606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
645	13830	26855	0.98	0.0E+00	8606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
652	13838	26865	1.42	0.0E+00	AA394486.1	EST_HUMAN	z60c07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
656	13842	26869	6.57	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
660	13846	26872	4.28	0.0E+00	W79811.1	EST_HUMAN	z515b04.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to
660	13846	26873	4.28	0.0E+00	W79811.1	EST_HUMAN	z515b04.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to
663	13849	26876	3.58	0.0E+00	4885526	NT	g5-A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
670	13856	26885	2.16	0.0E+00	6006003	NT	g5-A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
672	13858	26888	1.25	0.0E+00	5031624	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
675	13861	26892	1.88	0.0E+00	U05235.1	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
679	13865	26896	1.07	0.0E+00	AF108389.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
679	13865	26896	1.07	0.0E+00	AF108389.1	NT	Homo sapiens neutral amino acid transporter (ASCT1) gene, exon 8
679	13865	26896	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCaS3 (NCX1) mRNA, complete cds
685	13870	26901	5.11	0.0E+00	4826947	NT	Homo sapiens sodium/calcium exchanger isoform NaCaS3 (NCX1) mRNA, complete cds
685	13870	26902	5.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
691	16018		1.8	0.0E+00	X67147.1	NT	Human endogenous retrovirus PHE-1 (ERV9)
700	13883	26916	3.92	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
705	13888	26920	4.94	0.0E+00	AB023012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
715	13897	26935	3.83	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
727	13909	26949	13.13	0.0E+00	AA614537.1	EST_HUMAN	np-0401.61 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129833 3' similar to gb:X57952 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
731	13913	26953	6.4	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
731	13913	26954	6.4	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
741	13923	26963	1.35	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
747	13928	26968	4.82	0.0E+00	AF284730.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
747	13928	26970	4.82	0.0E+00	AF284730.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
749	13930	26973	9.17	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
755	13938	26981	2.26	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D00778 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
775	13956	27005	1.19	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
775	13956	27006	1.19	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
778	13958	27009	8.92	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
778	13958	27010	8.92	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
781	13981	27011	0.98	0.0E+00	AB037790.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
782	13982	27012	2.07	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
784	16022	27014	2.98	0.0E+00	D30812.1	NT	Homo sapiens mRNA for repressor protein, partial cds
785	13994	27015	3.55	0.0E+00	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3849803 5'
790	13969	27021	4.04	0.0E+00	R48915.1	EST_HUMAN	Y89908.1 Soares breast 2NDHBT Homo sapiens cDNA clone IMAGE:154046 5'
791	13970	27022	2.85	0.0E+00	5032088	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
800	13979	27031	1.84	0.0E+00	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
803	13983	27035	3.01	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
815	13994	27048	1.24	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
815	13994	27049	1.24	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
820	13998	27053	2.74	0.0E+00	X88772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
824	14003	27057	3.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
824	14003	27058	3.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
829	14007	27064	13.47	0.0E+00	5174478	NT	Homo sapiens perlecanin (PCNT) mRNA
830	14008		11.09	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
847	14025	27065	1.65	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
848	14028	27066	2.46	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	14028	27068	1.84	0.0E+00	4557858	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNK1) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
856	14033	27094	2.19	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
856	14033	27095	2.19	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
857	14034	27098	1.45	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
862	14039	27101	2.85	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
866	14042	27108	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
866	14042	27107	1.37	0.0E+00	4507500	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
873	14049		2.07	0.0E+00	AF027163.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
877	14053	27118	5.27	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
877	14053	27119	5.27	0.0E+00	AB028942.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
878	14054	27120	11.32	0.0E+00	4507162	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
878	14055	27121	4.03	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
880	14056	27122	3.87	0.0E+00	4508728	NT	Homo sapiens ribosomal protein for KIAA0910 protein, partial cds
884	14060	27125	1.54	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
884	14060	27126	1.54	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
885	14061	27127	1.82	0.0E+00	AA53272.1	EST_HUMAN	nj86d07.31 NCJ CGAP_P10 Homo sapiens cDNA clone IMAGE:397453
885	14061	27128	1.82	0.0E+00	AA53272.1	EST_HUMAN	nj86d07.31 NCJ CGAP_P10 Homo sapiens cDNA clone IMAGE:397453
886	14062		8.41	0.0E+00	BF877894.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915.5
890	14066	27128	1.4	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
890	14066	27130	1.4	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27131	2.54	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27132	2.54	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27132	2.54	0.0E+00	7657213	NT	Homo sapiens chromsome 21 segment HS21C003
914	14089	27155	0.98	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
921	14096	27160	1.93	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
921	14096	27161	1.93	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
931	14108	27170	2.7	0.0E+00	AL163203.2	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
941	14115		9.08	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
943	14115		9.89	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
944	14117	27178	1.42	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds
945	14118	27177	0.69	0.0E+00	S69384.1	NT	protein G inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
945	14118	27178	0.69	0.0E+00	S69384.1	NT	protein G inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
945	14118	27179	0.69	0.0E+00	S69384.1	NT	protein G inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
946	14119	27180	1.82	0.0E+00	Z20656.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds
949	14122	27183	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
949	14122	27184	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
973	14146	27205	0.93	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
974	14147	27206	9.11	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
975	14148	27207	0.79	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
976	14149	27208	1.24	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
976	14149	27209	1.24	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
984	16027	27216	3.95	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
984	16027	27217	3.95	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
986	14158	27219	14.34	0.0E+00	7557266	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
997	14168	27229	1.76	0.0E+00	AB030568.1	NT	Homo sapiens mRNA for PSP24, complete cds
1006	14177	27236	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1006	14177	27237	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1006	14177	27238	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1008	14179	27241	2.02	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1008	14179	27242	2.02	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1017	14188	27249	3.97	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
1029	14199	27257	1.07	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1030	14200	27258	5.81	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1031	14200	27258	9.09	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1034	14203		4	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1035	14203		29.59	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1039	14207	27264	0.96	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1040	14207	27264	4.66	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1041	14207	27264	1.3	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1042	14208	27265	1.18	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1045	14211	27268	2.11	0.0E+00	7661685	NT	Homo sapiens DKFZP666M0122 protein (DKFZP666M0122), mRNA
1049	14216	27272	1.27	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1051	14217		1.39	0.0E+00	AA458890.1	EST_HUMAN	aa86g07.s1 Stratagene fetal retina 037202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PR98 HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;
1054	14220	27277	2.43	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1054	14220	27278	2.43	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1055	14221	27279	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1055	14221	27280	0.67	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1058	14224		3.27	0.0E+00	8922833	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
1072	14238	27285	1.51	0.0E+00	4758669	NT	Homo sapiens heat shock 70kD protein B5 (mortalin-2) (HSPA9B) mRNA
1090	14255	27310	1.51	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH5) mRNA
1090	14255	27311	1.51	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH5) mRNA
1094	14259	27315	2.74	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1094	14259	27316	2.74	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1095	14260	27317	13.57	0.0E+00	AJ248622.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1097	14262		0.82	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1099	14264	27321	2.81	0.0E+00	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1099	14271	27330	2.04	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1106	14285	27340	1.91	0.0E+00	BE005208.1	EST HUMAN	MR0-BN0116-200300-003-H08 BN0115 Homo sapiens cDNA
1143	14308	27364	3.82	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1143	14308	27365	3.82	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1155	14319	27373	0.82	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1155	14319	27374	0.82	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1156	14320	27375	9.35	0.0E+00	4508712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1156	14322	27377	1.2	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1161	14325	27380	3.95	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1163	14327	27381	19.6	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1164	14328	27382	4.52	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1164	14328	27383	4.52	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1168	14331	27386	1.44	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1169	14332	27387	0.71	0.0E+00	XG6828.1	NT	H. sapiens ART4 gene
1169	14332	27388	0.71	0.0E+00	XG6828.1	NT	H. sapiens ART4 gene
1170	14332	27389	1.15	0.0E+00	AI147690.1	EST HUMAN	qb22d10.x1 Soares_pregnant_uterus NBHPU Homo sapiens cDNA clone IMAGE:1697011 3'
1172	14335	27391	1.62	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1181	14344	27400	1.22	0.0E+00	4758081	NT	Homo sapiens chondrolectin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1181	14344	27401	1.22	0.0E+00	4758081	NT	Homo sapiens chondrolectin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1182	14345	27402	1.32	0.0E+00	9966844	NT	Homo sapiens chondrolectin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1195	14357	27415	2.19	0.0E+00	7305076	NT	Homo sapiens chondrolectin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1195	14357	27416	2.19	0.0E+00	7305076	NT	Homo sapiens chondrolectin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1198	14360	27419	1.09	0.0E+00	AB037835.1	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1205	14367	27428	8.64	0.0E+00	4567887	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
							Homo sapiens keratin 18 (KRT18) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1236	14395		1.28	0.0E+00	7657336	NT	Homo sapiens mutL (E. coli) homolog 3 (MLH3), mRNA
1250	14409	27471	0.94	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1264	14413	27475	2.89	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1264	14413	27476	2.89	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1265	14414	27477	3.33	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1265	14414	27478	2.46	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1275	14432	27503	4.86	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1275	14432	27504	1.67	0.0E+00	AF109718.1	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1276	14433	27504	0.69	0.0E+00	4503098	NT	Homo sapiens prefoldin 4 (PFND4), mRNA
1286	14442	27510	0.69	0.0E+00	4505740	NT	Homo sapiens NF2 gene
1295	14451		1.38	0.0E+00	Y18000.1	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1303	14459	27525	29.86	0.0E+00	4505718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1310	14466	27534	2.86	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9), mRNA, complete cds
1316	14472	27538	1.53	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1316	14472	27539	1.53	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1328	14485	27552	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS), mRNA
1328	14485	27553	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS), mRNA
1328	14485	27554	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS), mRNA
1329	14486		2.16	0.0E+00	AF096156.1	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1339	18034	27566	1.2	0.0E+00	7657529	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1339	18034	27567	1.2	0.0E+00	7657529	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1345	15991	27573	1.4	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1346	14501	27574	1.86	0.0E+00	5803145	NT	Homo sapiens zinc finger protein 9 (RNFB), mRNA
1347	14502	27575	0.83	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 9 (RNFB), mRNA
1349	14504	27576	1.7	0.0E+00	Y07829.2	NT	Homo sapiens zinc finger protein 9 (RNFB), mRNA
1350	14505	27577	1.55	0.0E+00	5803146	NT	Homo sapiens zinc finger protein 9 (RNFB), mRNA
1351	14506	27578	0.71	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 9 (RNFB), mRNA
1353	14508	27580	4.44	0.0E+00	AB011149.1	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1354	14509	27581	1.34	0.0E+00	7681955	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1355	14510	27582	4.99	0.0E+00	7661985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1356	14511	27583	3.83	0.0E+00	8687387	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1356	14511	27584	3.83	0.0E+00	8687387	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1368	14522	27597	1.36	0.0E+00	IM14123.1	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1429	14583	27656	1.02	0.0E+00	BE257955.1	EST_HUMAN	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1429	14583	27657	1.02	0.0E+00	BE257955.1	EST_HUMAN	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA

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1440	14593	27688	1.03	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cyndromatosis cyld gene
1449	14602	27680	13.57	0.0E+00	6042206	NT	RAN, member RAS oncogene family-Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1457	14610	27690	0.97	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1457	14510	27691	0.97	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1459	14612	27694	1.99	0.0E+00	7705585	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1459	14612	27695	1.99	0.0E+00	7705585	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1462	14615	27697	29.09	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1471	14625	27709	4.93	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-fucosyltransferase (alpha1-6FucT) gene, exon 7
1490	14643	27724	4.2	0.0E+00	AL132599.1	NT	Novel human gene on chromosome 20
1491	14644	27726	1.37	0.0E+00	AL13764.1	NT	Novel human gene mapping to chromosome 1
1495	14648	27730	1.73	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1498	14651	27733	8.24	0.0E+00	6912457	NT	Homo sapiens calcitriol binding protein 1 (KIAA0330), mRNA
1500	14653	27735	2.28	0.0E+00	7681965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1500	14653	27736	2.28	0.0E+00	7661983	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1501	14654	27742	3.74	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1507	14660	27743	6.62	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1507	14660	27743	6.62	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1541	14693	27772	2.61	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1555	14708	27788	2.68	0.0E+00	AA481172.1	EST_HUMAN	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51896), mRNA
1562	14715	27792	27.8	0.0E+00	AF023860.1	NT	ae34a03.r1 NCI_QGAP_GCB1 Homo sapiens cDNA clone IMAGE:815115 5'
1562	14715	27793	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1584	14717	27796	1.55	0.0E+00	AW976097.1	EST_HUMAN	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1584	14717	27797	1.55	0.0E+00	AW976097.1	EST_HUMAN	EST388208 MAGE resequences, MAGN Homo sapiens cDNA
1565	14718	27798	1.03	0.0E+00	D10884.1	NT	EST388208 MAGE resequences, MAGN Homo sapiens cDNA
1557	14720		3.2	0.0E+00	U76027.1	NT	Bovine mRNA for neurocalcin
1558	14721	27801	26.69	0.0E+00	4505404	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1558	14721	27802	26.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1570	14723	27804	3.85	0.0E+00	7682405	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1571	14724		9.78	0.0E+00	7656972	NT	Homo sapiens KIAA0857 protein (KIAA0857), mRNA
1576	14729	27810	64.77	0.0E+00	M89478.1	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1578	14731	27811	0.97	0.0E+00	4507720	NT	Human transglutaminase mRNA, complete cds
1578	14731	27812	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1578	14731	27812	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA

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1579	16042		32.23	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1580	14732	27813	27.68	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1592	14746	27828	1.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1592	14745	27829	1.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1594	14747	27830	13.85	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1602	14758		3.25	0.0E+00	D00333.1	NT	human c-yes-2 gene
1611	14764	27844	11.38	0.0E+00	Z83738.1	NT	H. sapiens IH2B/c gene
1612	14765	27845	2.55	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1612	14765	27846	2.55	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1613	14766	27847	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1613	14766	27848	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1616	16043	27851	2.1	0.0E+00	AB040005.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1616	14770	27852	1.88	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1620	14772	27855	6.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1620	14772	27856	6.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1622	14774	27857	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1622	14774	27858	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1624	14776	27860	1.53	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1639	14791	27876	6.26	0.0E+00	H28973.1	EST_HUMAN	y076c05 s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:163848 3'
1648	14801	27887	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1648	14801	27888	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1648	14807	27886	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1688	14820	27903	1.66	0.0E+00	AW44637.1	EST_HUMAN	U1-H-B13-ajw-c-04-Q-U1 st NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1698	14850	27936	2.12	0.0E+00	BE144364.1	EST_HUMAN	MFO-H10166-191199-004-b11 HT0168 Homo sapiens cDNA
1698	14850	27937	2.12	0.0E+00	BE144364.1	EST_HUMAN	MFO-H10166-191199-004-b11 HT0168 Homo sapiens cDNA
1702	14854	27941	1.3	0.0E+00	A1768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to
1703	14855	27942	1.71	0.0E+00	4758513	NT	TR-Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. ;
1704	14856	27943	2.8	0.0E+00	AF057177.1	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1708	14859	27947	2.1	0.0E+00	M29580.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1708	14859	27948	2.1	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1710	14861	27950	64.4	0.0E+00	4557887	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1711	14862	27951	2.42	0.0E+00	7657085	NT	Homo sapiens keratin 18 (KRT18) mRNA
1714	14865	27954	1.08	0.0E+00	BE222374.1	EST_HUMAN	Hu11d05.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147
							MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1714	14865	27955	1.08	0.0E+00	BE22374.1	EST_HUMAN	h11405.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:095147 O95147
1716	14866	27957	3.2	0.0E+00	4557610	NT	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1719	14869	27960	4.3	0.0E+00	H30132.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1719	14869	27961	4.3	0.0E+00	H30132.1	EST_HUMAN	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1721	14871		0.97	0.0E+00	A1149880.1	EST_HUMAN	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1722	14872	27963	10.28	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1722	14872	27964	10.28	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1725	14875	27976	21.3	0.0E+00	5031748	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1734	14883	27978	6.13	0.0E+00	8923841	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1737	14886	27979	1.63	0.0E+00	5453855	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1741	14890	27983	1.95	0.0E+00	M75980.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1741	14890	27984	1.95	0.0E+00	M75980.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1744	14893	27988	1.11	0.0E+00	4828973	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1747	14896	27990	2.54	0.0E+00	M75980.1	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1747	14896	27991	2.54	0.0E+00	M75980.1	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1751	14900	27997	6.57	0.0E+00	AB026542.1	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1753	14902		2.64	0.0E+00	S94400.1	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1762	14911	28006	5.29	0.0E+00	4557538	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1764	14933	28027	3.33	0.0E+00	AF273841.1	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1826	15047		41.98	0.0E+00	4506718	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1830	14978	28073	3.2	0.0E+00	4557556	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1830	14978	28074	3.2	0.0E+00	4557556	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1833	14980	28078	2.47	0.0E+00	U63963.1	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1837	16048	28083	7.55	0.0E+00	4505332	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1839	14985	28085	1.7	0.0E+00	AA113030.1	EST_HUMAN	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1850	14936	28099	24.06	0.0E+00	U14967.1	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1852	14938	28102	9	0.0E+00	AB002331.1	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1853	14966	28103	24.99	0.0E+00	4502264	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1853	14966	28104	24.99	0.0E+00	4502264	NT	gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1853	14999	28105	24.89	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1870	15015	28124	3.11	0.0E+00	4504628	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1870	15015	28125	3.11	0.0E+00	4504628	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1881	15025	28131	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1881	15025	28132	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1892	15036	28143	1.84	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1892	15036	28144	1.84	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1895	15038	28146	3.59	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1895	15038	28147	3.59	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1896	15039	28148	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1896	15039	28149	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1899	15042	28152	2.3	0.0E+00	AW207280.1	EST_HUMAN	U1H-B11-efn-4-07-0-U1.s1 NCJ CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1899	15042	28153	2.3	0.0E+00	AW207280.1	EST_HUMAN	U1H-B11-efn-4-07-0-U1.s1 NCJ CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1924	15087	28171	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1924	15087	28172	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1943	15086	28187	1.04	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0128-200300-012-034 BN0128 Homo sapiens cDNA
1972	15115	28215	1.82	0.0E+00	7657380	NT	Homo sapiens nuclear protein (NP220), mRNA
1972	15115	28216	1.82	0.0E+00	7657380	NT	Homo sapiens nuclear protein (NP220), mRNA
1975	15118	28218	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1975	15118	28219	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1981	15124	28226	1.29	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1985	15128		1.84	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1986	16051	28230	57.92	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1986	16051	28231	57.92	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1991	15133	28238	3.19	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1991	15133	28239	3.19	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1994	15135	28241	2.41	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1998	15137		8.39	0.0E+00	AF240786.1	NT	Human topoisomerase I pseudogene 1
2001	15142		5.28	0.0E+00	M55632.1	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
2003	16052	28248	1.84	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2009	15145	28250	1.3	0.0E+00	BE018066.1	EST_HUMAN	b573f11.yt NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 6'
2011	15151	28255	1.69	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2011	15151	28255	1.69	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2024	15165		1.04	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
2026	15167	28272	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2026	15167	28273	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2027	15168	28274	12.98	0.0E+00	4826633	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2027	15168	28275	12.98	0.0E+00	4826633	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2037	15178	28288	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2037	15178	28289	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2043	15184	28293	1.93	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2043	15184	28294	1.93	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2045	15186	28295	3.24	0.0E+00	AW193024.1	EST_HUMAN	x09601.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2876813 3'
2045	15186	28296	3.24	0.0E+00	AW193024.1	EST_HUMAN	x09601.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2876813 3'
2046	15187	28297	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2046	15187	28298	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2048	15189	28300	1.53	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2049	15190	28301	1.09	0.0E+00	Z47556.1	NT	H sapiens genes for semenogelin I and semenogelin II
2049	15190	28302	1.09	0.0E+00	Z47556.1	NT	H sapiens genes for semenogelin I and semenogelin II
2056	15197	28311	5.04	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2078	15218	28337	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2078	15218	28338	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2109	15247	28368	1.53	0.0E+00	8394546	NT	Homo sapiens chromosome 21 open reading frame 7 (YGB1), mRNA
2112	15250	28370	0.98	0.0E+00	7706742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2117	15255	28374	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2117	15255	28375	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
							Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2119	15267	28376	1.02	0.0E+00	4503648	NT	
2121	15258	28378	57.63	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLAGE4 Homo sapiens cDNA clone PLACE400321 5'
2122	14612	27694	0.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2122	14612	27695	0.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2124	15260	28380	2.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2124	15260	28381	2.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2126	15262		3.79	0.0E+00	7657469	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2128	15264		1.48	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cAMP-specific, rod, alpha (PDE6A), mRNA
2129	15265	28384	2.9	0.0E+00	Z42398.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02
2131	15267		2.38	0.0E+00	A1244247.1	EST_HUMAN	q98008.X1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element.
2136	15272	28393	4.37	0.0E+00	BE877225.1	EST_HUMAN	601485148F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2138	15274	28395	2.25	0.0E+00	BF315325.1	EST_HUMAN	601802604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2138	15274	28396	2.25	0.0E+00	BF315325.1	EST_HUMAN	601802604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2144	15280	28404	3.9	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2144	15280	28405	3.9	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2152	15288	28414	3.43	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2152	15288	28415	3.43	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2153	15289	28416	1.11	0.0E+00	AJ207709.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 1
2158	15294	28420	1.18	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2162	15298	28423	1.94	0.0E+00	BE500995.1	EST_HUMAN	7a34602.X1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:3220610 3' similar to SW:DTD_HUMAN
2182	15317		3.17	0.0E+00	BE767964.1	EST_HUMAN	P50443 SULFATE TRANSPORTER
2183	15318		1.26	0.0E+00	AF018953.1	NT	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2185	15320	28446	4.84	0.0E+00	BF027582.1	EST_HUMAN	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2188	15321	28447	1.5	0.0E+00	BE072624.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2188	15323	28448	1.29	0.0E+00	AF240786.1	NT	PM0-BT0547-270300-004-F04 BT0547 Homo sapiens cDNA
2190	15325	28450	3.41	0.0E+00	AW752708.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2192	15327	28452	6.48	0.0E+00	A1804640.1	EST_HUMAN	IL3-CT0215-271095-022-G10 CT0219 Homo sapiens cDNA
2192	15327	28453	6.48	0.0E+00	A1804640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2225	15359		1.08	0.0E+00	7657252	NT	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2249	15382		1.52	0.0E+00	L14787.1	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA
2259	15392	28518	1.26	0.0E+00	BE274696.1	EST_HUMAN	Human DNA-binding protein mRNA, 3' end
2261	15394	28521	0.94	0.0E+00	D97695.1	NT	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346888 5'
2262	15395	28522	23.12	0.0E+00	AV738288.1	EST_HUMAN	Human mRNA for KIAA0244 gene, partial cds
2262	15395	28523	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBD08 5'
2264	15397	28525	2.57	0.0E+00	AA931691.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBD08 5'
2268	15401	28529	24.38	0.0E+00	BF344434.1	EST_HUMAN	0332601.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2269	15402	28530	40.14	0.0E+00	BE748809.1	EST_HUMAN	602014829F1 NCL CGAP_Brm4 Homo sapiens cDNA clone IMAGE:4150734 5'
							601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2272	15405	28533	5.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2272	15405	28534	5.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2278	16059	28539	4.06	0.0E+00	BF313617.1	EST_HUMAN	601900281F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128822 5'
2278	15411	28542	3.13	0.0E+00	BE018750.1	EST_HUMAN	bb84e02.v1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-J-RELATED PROTEIN ;
2281	15413	28544	1.68	0.0E+00	AA042813.1	EST_HUMAN	gb-X65887_cds1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb-X65887_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2281	15413	28545	1.68	0.0E+00	AA042813.1	EST_HUMAN	gb-X65887_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2289	15421	28553	3.06	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2289	15421	28554	3.06	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2290	15422	28555	3.72	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2290	15422	28556	3.72	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2295	15427	28558	2.34	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2296	15428	28561	1.02	0.0E+00	AA282261.1	EST_HUMAN	xt2b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2313	15445	28579	7.92	0.0E+00	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2320	15452	28584	2.63	0.0E+00	BE895281.1	EST_HUMAN	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2327	15459	28592	3.44	0.0E+00	BE805663.1	EST_HUMAN	601433625F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2331	15463	28598	1.51	0.0E+00	BE805663.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2331	15463	28597	1.51	0.0E+00	BE805663.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2333	15484	28599	1.83	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2375	15506	28632	4.35	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2375	15506	28633	4.35	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2376	15507	28634	2.67	0.0E+00	A1078404.1	EST_HUMAN	ox28c07.x1 Soares_fetal_liver_spleen_TNLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2378	15509	28636	2.95	0.0E+00	AA428001.1	EST_HUMAN	zt78a11.r1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2378	15509	28637	2.95	0.0E+00	AA428001.1	EST_HUMAN	zt78a11.r1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2380	15511	28639	1.82	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157339 5'
2385	15516	28645	1.33	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2385	15516	28646	1.33	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2386	15517	28647	2.34	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2393	15524	28653	2.36	0.0E+00	BE978095.1	EST_HUMAN	7122a02.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94939 O94939 KIAA0957 PROTEIN ;
2396	15527	28655	5.46	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHK42) gene, exon 32
2397	15528	28656	2.6	0.0E+00	A1625542.1	EST_HUMAN	y57c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2399	15530	28657	1.5	0.0E+00	AB011393.1	NT	Homo sapiens gene for AF-4, complete cds
2402	15533	28659	2.22	0.0E+00	7662401	NT	Homo sapiens KIAA00952 protein (KIAA00952), mRNA
2402	15533	28660	2.22	0.0E+00	7662401	NT	Homo sapiens KIAA00952 protein (KIAA00952), mRNA
2405	15536	28663	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2405	15536	28664	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2424	15553	28679	3.04	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1), mRNA
2428	15556	28683	3.56	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2429	15557	28684	9.82	0.0E+00	BE794028.1	EST_HUMAN	60186843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2430	15558	28684	3.96	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2431	15559	28685	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2431	15559	28686	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2432	15560		7.14	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4), and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 8 (CYP3A5) gene, partial cds
2434	15562	28688	10.61	0.0E+00	AU118082	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28689	10.61	0.0E+00	AU118082	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28690	10.61	0.0E+00	AU118082	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2452	15580		1.03	0.0E+00	BE814424.1	EST_HUMAN	MR0-BN0070-090600-028-d12 BN0070 Homo sapiens cDNA
2483	15612	28735	1.14	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2487	15614		4.63	0.0E+00	A1042035.1	EST_HUMAN	ox00502.x1 Soeres NIHMPu S1 Homo sapiens cDNA clone IMAGE:1660583 3' similar to TR:008662
2489	15616	28737	0.94	0.0E+00	8923620	NT	O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ;
2492	15619		1.35	0.0E+00	BE895633.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2503	15630		2.22	0.0E+00	AB005622.1	EST_HUMAN	601433608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2505	15632	28752	6.05	0.0E+00	6006002	NT	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2510	15636	28756	1.99	0.0E+00	D85606.1	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA
2510	15636	28757	1.99	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2520	15646	28769	2.42	0.0E+00	AF106275.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2524	15649	28773	0.96	0.0E+00	BF345274.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2530	15655	28780	3.64	0.0E+00	5729771	NT	802018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
2538	15663	28786	1.02	0.0E+00	U13666.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2538	15663	28787	1.02	0.0E+00	U13666.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2539	15664	28788	28.11	0.0E+00	BF569144.1	EST_HUMAN	Human G protein-coupled receptor (GPR1) gene, complete cds
2547	15672	28796	4.18	0.0E+00	AW466922.1	EST_HUMAN	602184568T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2550	15675	28798	3.03	0.0E+00	AW601010.1	EST_HUMAN	UI-HF-BP0p-as-c-07-0-UI.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2575	15700		2.02	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2578	15704	28824	7.28	0.0E+00	BE795642.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2579	15135	28241	1.12	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2580	15705	28825	1.44	0.0E+00	BF509482.1	EST_HUMAN	UI-H-B14-azb-b-08-0-UI.1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2583	15708	28827	2.21	0.0E+00	Z32684.2	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
2585	15710		5.17	0.0E+00	5453871	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2587	15712	28830	1.07	0.0E+00	BE910378.1	EST_HUMAN	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2588	15713	28831	2.39	0.0E+00	7657468	NT	Human Sec62 (Sec62) mRNA, complete cds
2589	15714	28832	3.09	0.0E+00	U93239.1	NT	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2605	15720	28838	1.66	0.0E+00	BE986490.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3881371 5'
2606	15722	28842	13.07	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3881371 5'
2608	15722	28843	13.07	0.0E+00	BE875511.1	EST_HUMAN	Homo sapiens adiccan mRNA, complete cds
2609	15723	28844	1.12	0.0E+00	AF245505.1	NT	601084738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2616	15740	28852	1.83	0.0E+00	BE636921.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2623	15746	28860	3.66	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2623	15746	28861	3.66	0.0E+00	AU143277.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987855 5'
2624	15747	28862	1.25	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987855 5'
2624	15747	28863	1.25	0.0E+00	BE292896.1	EST_HUMAN	7a27h12.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:3' similar to TR:O00246 O00246
2625	15748	28864	1.04	0.0E+00	BF223041.1	EST_HUMAN	HYPOTHETICAL 9.3 KD PROTEIN ;
2626	15751	28868	8.3	0.0E+00	AF245505.1	NT	Homo sapiens adiccan mRNA, complete cds
2664	16000	28901	2.18	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2694	16000	28902	2.18	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2695	16786		2.35	0.0E+00	BF613835.1	EST_HUMAN	UI-HBW1-emp-4-12-0-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070831 3'
2675	16795	28912	32.6	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2675	16795	28913	32.6	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2678	16798	28915	2.15	0.0E+00	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2679	15798	28916	2.52	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF2)
2681	15801	28918	8.53	0.0E+00	AB037859.1	NT	mRNA
2682	15802	28919	1.16	0.0E+00	BE786445.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2682	15802	28920	1.16	0.0E+00	BE786445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2682	15802	28920	1.16	0.0E+00	BE786445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2680	15810		2.75	0.0E+00	BE792472.1	EST_HUMAN	601884930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	15919	28935	2.52	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2710	15828			0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2711	15829	28942	1.16	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2715	15833	28943	5.67	0.0E+00	AF173227.1	NT	Homo sapiens mRNA for KIAA0936 protein, partial cds
2716	15834	28943	1.07	0.0E+00	AB011108.1	NT	Homo sapiens NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2718	15838	28946	0.96	0.0E+00	AU133386.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2721	15839	28949	0.96	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2721	15839	28949	1.15	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2721	15839	28950	1.15	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2724	15842	28953	1.66	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-4C7 OT0086 Homo sapiens cDNA
2727	15845	28958	4.83	0.0E+00	BE383165.1	EST_HUMAN	601288714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2728	15846		2.8	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2763	15878	28987	1	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2785	15901		11.99	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2789	15906	29013	4.04	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2791	15907	29015	3.72	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2792	15908	29016	2.32	0.0E+00	AB051828.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2797	15912	29020	11.38	0.0E+00	BE796376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2800	16072	29024	17.3	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2801	15915		3.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2803	15917	29027	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2803	15917	29028	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2804	15918	29029	2.21	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2805	15919		47.74	0.0E+00	AV651086.1	EST_HUMAN	AV651086 GLC Homo sapiens cDNA clone GLCGLD07 3'
2806	15920	29030	5.84	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-108 TN0141 Homo sapiens cDNA
2806	15920	29031	5.84	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-108 TN0141 Homo sapiens cDNA
2810	15924	29034	1.15	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (GDR1) mRNA
2810	15924	29035	1.15	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (GDR1) mRNA
2813	15927	29039	21.96	0.0E+00	BE747193.1	EST_HUMAN	601590903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2814	15928	29040	1.05	0.0E+00	N44974.1	EST_HUMAN	y356h10.1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR-A45773
2816	15930	29042	1.15	0.0E+00	BE176836.1	EST_HUMAN	A45773 kelch protein, long form - fruit fly
2827	15941		1.13	0.0E+00	AL163201.2	NT	RC4-HT0587-170300-072-d11 HT0587 Homo sapiens cDNA
2828	15942	29052	3.19	0.0E+00	BF514110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
							UJH-BW1-amw-e-07-0-UJ.s1 NCJ_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2835	15949		1.67	0.0E+00	4503058	NT	Homo sapiens choroidin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2841	15955	29062	1.08	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2841	15955	29063	1.08	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2842	15956	29064	5.05	0.0E+00	BF077694.1	EST_HUMAN	60208579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2848	15962	29072	1.33	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2852	15966	29075	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2852	15966	29076	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2854	15968		14.75	0.0E+00	AI879163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW-R13A, HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
2857	15971	29081	2.14	0.0E+00	BF530651.1	EST_HUMAN	602071957F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4214679 5'
2858	15972	29082	71.97	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3884642 5'
2860	15974	29083	2.42	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2860	15974	29084	2.42	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2861	15975	29085	64.06	0.0E+00	BE300344.1	EST_HUMAN	600944784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2861	15975	29086	64.06	0.0E+00	BE300344.1	EST_HUMAN	600944784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2867	13415	26444	5.26	0.0E+00	S76830.1	NT	glycoprotein D-Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2870	15982		1.64	0.0E+00	AB033281.1	NT	Homo sapiens BTROP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2876	13933	26978	1.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2876	13933	26979	1.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2880	14230	27287	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dieldrin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2880	14230	27288	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dieldrin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2897	16076	29094	3.73	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2898	16077		1.26	0.0E+00	AF086824.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
2900	16079		1.91	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1627 protein, partial cds
2907	16085	29099	4.25	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2911	16086	29102	6.5	0.0E+00	M80902.1	NT	Human AHNAC nucleoprotein mRNA, 5' end
2914	16092	29104	0.93	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281289-003-e02 HT0343 Homo sapiens cDNA
2914	16092	29105	0.93	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281289-003-e02 HT0343 Homo sapiens cDNA
2916	16094		2.05	0.0E+00	X73428.1	NT	H. sapiens l33 gene for HLH type transcription factor
2918	16096		2.6	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
2919	16097	29108	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2919	16097	29109	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2919	16097	29110	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2921	16099	29111	15.94	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2926	16103	29117	30.49	0.0E+00	D50637.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2926	16103	29118	30.49	0.0E+00	D50637.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2929	16106	29121	3.42	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2930	16107		6.12	0.0E+00	Y10688.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2931	16108		1.13	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2932	16109	29122	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2932	16109	29123	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2944	16121	29134	2.54	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2947	16124	29138	1.19	0.0E+00	AL047598.1	EST_HUMAN	DKFZp596G0821_r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp586G0821
2948	16125	29130	0.96	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2948	16125	29140	0.98	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2949	16126		2.44	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (OSPG4), mRNA
2952	16129	29142	5.16	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2952	16129	29143	5.16	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2958	16135	29151	0.77	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2958	16135	29152	0.77	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2961	16138	29156	2.3	0.0E+00	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
2961	16138	29157	2.3	0.0E+00	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
2962	16139	29159	1.3	0.0E+00	AA215579.1	EST_HUMAN	z96b011.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element
2969	16145		3.99	0.0E+00	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
2972	16148	29167	1.05	0.0E+00	4759279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2974	16150	29170	25.96	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2975	16151		1.15	0.0E+00	AI561002.1	EST_HUMAN	t18407.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2975	16151		1.15	0.0E+00	AI561002.1	EST_HUMAN	t18407.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2977	16153	29174	1.18	0.0E+00	P52740	SWISSPROT	O16247 F44E7.2 PROTEIN ;
2978	16154	29175	1.04	0.0E+00	AF152338.1	NT	ZINC FINGER PROTEIN 132
2984	16170	29187	3.4	0.0E+00	AB033093.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2984	16170	29188	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2984	16170	29188	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2986	16171	29189	6.2	0.0E+00	AD04094.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2985	16171	29190	6.2	0.0E+00	ABO40841.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2986	16174	29193	3.31	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2988	16174	29194	3.31	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2989	16175	29195	4.83	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24)) mRNA
2990	16175	29196	4.83	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24)) mRNA
3003	16178	29199	1.29	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
3003	16178	29200	1.29	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
3011	16187	29211	3.91	0.0E+00	4505084	NT	Q9VLN1 CG17293 PROTEIN ;
3011	16187	29212	3.91	0.0E+00	4505084	NT	Q9VLN1 CG17293 PROTEIN ;
3019	16187	29218	1.51	0.0E+00	4758827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3022	16188	29221	0.98	0.0E+00	AB033034.1	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3024	16200	29223	9.6	0.0E+00	AF106273.1	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3038	16214	29242	1.44	0.0E+00	AI149880.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3045	16221	29243	0.71	0.0E+00	AF231074.1	NT	ql43f09.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752809 3'
3045	16221	29243	0.71	0.0E+00	AF231074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3046	16222	29244	0.82	0.0E+00	4508118	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3047	16223	29245	2.81	0.0E+00	AB004884.1	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3057	16233	29252	1.85	0.0E+00	7662273	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3058	16234	29253	1.92	0.0E+00	AW812526.1	EST_HUMAN	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
3059	16235	29254	2.4	0.0E+00	5729755	NT	hh03f08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2854055 3' similar to TR:O60407 O60407
3059	16235	29255	2.4	0.0E+00	5729755	NT	PAC CLONE DJ116BDT11 FROM T721-P22, COMPLETE SEQUENCE ;
3067	16243	29263	1.17	0.0E+00	AF114488.1	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3067	16243	29263	1.17	0.0E+00	AF114488.1	NT	Homo sapiens intercalin 5 short isoform (ITSN) mRNA, complete cds
3067	16243	29264	1.17	0.0E+00	AF114488.1	NT	Homo sapiens intercalin 5 short isoform (ITSN) mRNA, complete cds
3061	16257	29285	0.61	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
3063	16266	29285	1.29	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
3102	16279	29292	0.88	0.0E+00	4506882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3109	16285	29303	3.33	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPBP2) gene, complete cds
3112	16288	29303	4.9	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA7A), mRNA
3142	16298	29304	4.8	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA7A), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3114	16280		7.27	0.0E+00	AL359403.1	NT	isoform 2 of a novel human mRNA from chromosome 22
3119	16295	29309	1.88	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR63 (CR63) mRNA, partial cds
3122	16298		2.21	0.0E+00	AF198779.1	NT	Homo sapiens transcription factor IGHE enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
3124	16300	29313	3.78	0.0E+00	4504664	NT	Homo sapiens Interleukin 2 receptor, beta (IL2RB) mRNA
3145	16321	29333	3.23	0.0E+00	X03529.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3151	16328		1.92	0.0E+00	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3155	16330	29340	1.75	0.0E+00	AF064599.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3175	16350	29358	4.71	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3178	16351	29357	10.17	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3181	16356	29361	3.92	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3182	16357	29362	1.29	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3187	16362	29368	1.19	0.0E+00	AW188146.1	EST_HUMAN	X92107.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2694733 3' similar to SW-RNP_HYDHY P00677 RIBONUCLEASE PANCREATIC ;
3210	16384	29395	3.61	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3219	16393	29404	20.63	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3222	16396	29407	1.05	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3222	16398	29408	1.05	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3229	16403	29415	25.61	0.0E+00	T94870.1	EST_HUMAN	ye32103.e1 Sitragene lung (#937210) Homo sapiens cDNA clone IMAGE:118453 3' similar to SP-S29539
3244	16418	29433	0.93	0.0E+00	BF243336.1	EST_HUMAN	S29539 BASIC PROTEIN, 29K -;
3246	16419	29434	1.22	0.0E+00	AI968086.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3250	16424	29441	5.36	0.0E+00	X98022.1	NT	wu12110.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516803 3'
3250	16424	29442	5.38	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3252	16426	29444	1.01	0.0E+00	AI685950.1	EST_HUMAN	H. sapiens mRNA for gamma-glutamyltransferase
3282	16436	29455	1.39	0.0E+00	4758827	NT	tu38g09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI
3282	16436	29456	1.39	0.0E+00	4758827	NT	P03987 RAS-LIKE PROTEIN RASD ;
3270	16444	29464	9.58	0.0E+00	4504658	NT	Homo sapiens neurokin III (NKN3) mRNA
3288	16462	29482	4.54	0.0E+00	M28699.1	NT	Homo sapiens neurokin III (NKN3) mRNA
3292	16468	29485	1.92	0.0E+00	4502098	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
							Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3298	16472	29493	0.76	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3298	16472	29494	0.76	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3300	16474	29495	28.49	0.0E+00	AA747483.1	EST_HUMAN	aa87b11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3308	16482	29503	8.38	0.0E+00	AF286588.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3308	16482	29504	8.38	0.0E+00	AF286588.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3320	16493	29510	3.04	0.0E+00	4557590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3326	16498	29517	1.01	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3334	16507		10.18	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
3335	16508						Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3338	16511	29524	0.95	0.0E+00	AF019413.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3346	16511	29527	4.06	0.0E+00	AF055084.1	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3348	16464	29535	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3348	16484	29536	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3363	16535	29549	3.56	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3364	16536	29550	0.95	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3377	16549	29563	1.42	0.0E+00	7687038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3388	16558	29573	0.72	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3401	16571	29586	3.14	0.0E+00	AI592294.1	EST_HUMAN	tr5808.x2 NCL CGAP_Pent1 Homo sapiens cDNA clone IMAGE:2222635 3' similar to SW:RL11_RAT
3404	16574	29589	9.94	0.0E+00	AW955400.1	EST_HUMAN	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3412	16581	29596	2.41	0.0E+00	AF128893.1	NT	EST367470 MAGE resequences, MAGEC Homo sapiens cDNA
3412	16581	29597	2.41	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3413	16582	29598	1.03	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3413	16582	29599	1.03	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3416	16585	29601	1.29	0.0E+00	4502582	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3416	16585	29602	1.29	0.0E+00	4502582	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3419	16588	29604	11.92	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3421	16590	29606	1.02	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
3428	16593	29612	0.79	0.0E+00	BE779039.1	EST_HUMAN	90146495F1 NIH_JMGC_67 Homo sapiens cDNA clone IMAGE:3888246 5'
3441	16609	29627	0.67	0.0E+00	AI632599.1	EST_HUMAN	90146495F1 NIH_JMGC_67 Homo sapiens cDNA clone IMAGE:3888246 5'
3483	16651	29667	10	0.0E+00	AU123664.1	EST_HUMAN	ZINC FINGER PROTEIN 1
3492	16658	29671	1.16	0.0E+00	7706239	NT	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM200735 5'
							Homo sapiens neuroblastoma-amplified protein (LOC51694), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3493	16860	29672	1.26	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1i-a isoform (CACNA1I) mRNA, complete cds
3498	16865		0.94	0.0E+00	AW867015.1	EST_HUMAN	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3511	16877	29687	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3511	16877	29688	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3512	16878	29689	0.92	0.0E+00	4602398	NT	Homo sapiens beaded filament structural protein 1, filenin (BF-SF1) mRNA
							Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3514	16880	29690	2.35	0.0E+00	5803067	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3523	16907	29015	3.08	0.0E+00	AF110763.1	NT	Homo sapiens death receptor 6 (DR6), mRNA
3528	16893	29703	2.46	0.0E+00	7657038	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC incompatibility determinants
3532	16897	29708	5.5	0.0E+00	K02390.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3535	16700	29711	1.38	0.0E+00	7427522	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3538	16703	29714	1.83	0.0E+00	4557746	NT	wp14d10.x1 NCJ_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE ;
3544	16709	29719	4.17	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCJ_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE ;
3544	16709	29720	4.17	0.0E+00	AI935159.1	EST_HUMAN	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3548	16713	29725	1.91	0.0E+00	AJ278120.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3555	16720	29734	5.38	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3555	16720	29735	5.38	0.0E+00	6552332	NT	Human endogenous retrovirus HERV-K10
3560	16725	29741	1.41	0.0E+00	M14123.1	NT	Human MDSTA (AML1/MDST fusion) mRNA, partial cds
3566	16731	29747	5.78	0.0E+00	U43293.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3574	16739	29755	2.57	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3574	16739	29756	2.57	0.0E+00	AF045452.1	NT	Homo sapiens chromosome Z1 unknown mRNA
3582	16747	29765	1.18	0.0E+00	AF231922.1	NT	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3594	16758	29773	3.29	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3594	16758	29774	3.29	0.0E+00	BE304791.1	EST_HUMAN	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3597	16761	29777	1.04	0.0E+00	4928795	NT	TRANSCRIPTION REGULATORY PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3600	16764	29780	0.8	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
							le35g12.x1 Sceres_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3603	16767	29782	0.89	0.0E+00	AI984007.1	EST_HUMAN	O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3621	16785	29801	0.6	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3621	16785	29802	0.6	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3623	16757	29803	0.68	0.0E+00	AA456282.1	EST_HUMAN	z89h04.r Scores_NHhMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3623	16787	29804	0.68	0.0E+00	AA456282.1	EST_HUMAN	z89h04.r1 Scores_NHhMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3630	16794	29811	1.45	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ADBDAH06 5'
3631	16795	29812	4.48	0.0E+00	4506884	NT	Homo sapiens semaphorin II (SEMG2) mRNA
3633	16797		1.17	0.0E+00	AF078968.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3642	16806	29820	1.34	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3644	16807	29821	1.16	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3665	16828	29837	0.97	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3665	16828	29838	0.97	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3667	16830	29841	1.06	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3672	16835		4.28	0.0E+00	AW852217.1	EST_HUMAN	QV0-GT0225-230300-169-ep1 CT0225 Homo sapiens cDNA
3679	16842		1.28	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLC1C) gene, partial cds
3680	16843	29850	7.65	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 5'
3704	16865	29868	0.59	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3704	16865	29869	0.59	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3705	16866		0.99	0.0E+00	4828967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3707	16868	29871	0.76	0.0E+00	AW684693.1	EST_HUMAN	h84g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3707	16868	29872	0.76	0.0E+00	AW684693.1	EST_HUMAN	h84g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3711	16872	29876	0.89	0.0E+00	4826763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3713	16874	29879	0.93	0.0E+00	7662319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3720	16881	29886	0.74	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3720	16881	29887	0.74	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3737	16888	29901	2.36	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3741	16902		6.26	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3757	16918	29920	3.98	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3759	16920	29922	1.06	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
3761	16922	29923	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3761	16922	29924	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3767	16928	29932	32.49	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3767	16928	29933	32.49	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3770	16931	29935	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3770	16931	29936	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3771	16932	29937	0.99	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3771	16932	29938	0.99	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3774	16935	29941	2.4	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281089-005-e05 OT0222 Homo sapiens cDNA
3776	16937	29943	2.37	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3778	16938	29945	1.15	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0756 protein, partial cds
3780	16941	29947	0.74	0.0E+00	O14897	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3782	16943	29949	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3782	16943	29950	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3794	16945	29959	5.42	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-qis-e-12-O-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022.3'
3794	16955	29960	5.42	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-qis-e-12-O-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022.3'
3823	16983	29986	1.04	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3824	16984	29987	1.17	0.0E+00	AA463659.1	EST_HUMAN	ae06g01.1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1] ;
3831	16991	29993	3.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3841	17000	30003	0.83	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3855	17015	30015	5.72	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3859	17019	30018	18.03	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3868	17026	30023	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3868	17025	30024	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3889	17028	30027	8.94	0.0E+00	4505584	NT	Homo sapiens plasminogen activator inhibitor, type II (arginine-serpin) (PAI2), mRNA
3922	17081	30077	1.86	0.0E+00	AF145712.1	NT	Homo sapiens soluble neutrophil-1 mRNA, complete cds
3924	17083		0.73	0.0E+00	AF195058.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3925	17084	30079	2.36	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3928	17087	30083	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3928	17087	30084	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3929	17088	30085	1.74	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3935	17094	30092	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3935	17094	30093	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3936	17095	30094	1.29	0.0E+00	A1377698.1	EST_HUMAN	is62f10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307.3'
3937	17096		1	0.0E+00	AF152496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3938	17097	30095	2.6	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
3940	17099	30096	15.6	0.0E+00	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3942	17101	30098	2.14	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3943	17102	30099	1.78	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3946	17105	30101	1.82	0.0E+00	AF068601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3946	17105	30102	1.82	0.0E+00	AF068601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3951	17109	30107	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3951	17109	30108	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3952	17110	30109	0.9	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3957	17115	30117	6.96	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3957	17115	30118	6.96	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3959	17117	30121	4.85	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3960	17118	30122	1.12	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3963	17121	30124	1.23	0.0E+00	4826763	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3966	17124	30127	1.44	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3967	17125	30128	2.87	0.0E+00	4799171	NT	Homo sapiens SC35-interacting protein 1 (SRP129), mRNA
3969	17127	30130	0.77	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3979	17136	30140	3.22	0.0E+00	AB64727.1	EST_HUMAN	wk01801 x1 NC1 CGAP Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:043340
3980	17137	30141	1.03	0.0E+00	AL163248.2	NT	O43340 R28830_2, contains element P17Y repetitive element;
3983	17140	30145	18.17	0.0E+00	4506742	NT	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3988	17146	30151	1.33	0.0E+00	AL040398.1	EST_HUMAN	DKFZ:434N0413.1 434 (synonym: hhs3) Homo sapiens cDNA clone DKFZ:434N0413 5'
3994	17151	30155	1.9	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3994	17151	30159	1.9	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3996	17153	30161	3.94	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GFRM3) mRNA
3997	17154	30164	2.26	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
4001	17158	30164	0.97	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
4013	17170	30178	2.65	0.0E+00	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4017	17174	30182	1.9	0.0E+00	4595642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4026	17182	30191	6.14	0.0E+00	BF356295.1	EST_HUMAN	RC3-H70860-170800-011-a12 H70860 Homo sapiens cDNA
4028	17184	30193	1.37	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5
4028	17184	30194	1.37	0.0E+00	AW888221.1	EST_HUMAN	Matrix remodeling associated gene 5
4035	17191	30201	3.05	0.0E+00	AF129533.1	NT	Matrix remodeling associated gene 5
4038	17194	30204	1.14	0.0E+00	U86281.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
							Homo sapiens olfactory receptor (OR7-141) gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4038	17194	30205	1.14	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4042	17198	30209	3.47	0.0E+00	BE378902.1	EST_HUMAN	601236986F1 NIH_MGC_24 Homo sapiens cDNA clone IMAGE:3608800 5'
4043	17199	30210	1.2	0.0E+00	BE313146.1	EST_HUMAN	601163727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508743 5'
4051	17207	30217	1.28	0.0E+00	AW580740.1	EST_HUMAN	PM3-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA
4052	17208	30218	1.03	0.0E+00	5360215	NT	Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA
4077	17233	30238	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30239	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30240	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4084	17239	30244	9.31	0.0E+00	AF118195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4084	17239	30245	9.31	0.0E+00	AF118195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4093	17248		3.51	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4095	17250		7.25	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4104	17258	30258	2.93	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C088
4112	17266	30266	2.13	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4127	17281		111.8	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4134	17287		0.89	0.0E+00	AI657076.1	EST_HUMAN	t55g08.x1 NCJ_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:060309 060309 KIAA0563 PROTEIN. ;
4137	17289	30284	1.91	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4138	17290	30285	2.85	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
4157	17308	30304	6	0.0E+00	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
4166	17316		3.22	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor RNA-associated antigenic protein (RNA48 gene)
4177	17327	30318	1.58	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4178	17328	30319	2.68	0.0E+00	AJ27276.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4178	17328	30320	2.88	0.0E+00	AJ27276.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4185	17335	30327	8.33	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4185	17335	30328	8.33	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4194	17344	30337	0.64	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
4202	17351	30343	6.02	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4203	17352	30344	11.98	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4206	17355	30345	1.26	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4207	17356	30346	7.08	0.0E+00	11419287	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4208	17357	30347	4.33	0.0E+00	AL096867.1	NT	Novel human mRNA from chromosome 1, which has similarities to BA72 genes

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4209	17358		0.98	0.0E+00	AA018975.1	EST_HUMAN	ze55e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element;
4218	17367	30358	5.32	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4227	14319	27373	0.7	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4227	14319	27374	0.7	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4234	17381	30369	1.32	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
4234	17381	30370	1.32	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
4236	16796	29812	0.64	0.0E+00	4506884	NT	Homo sapiens semorogelin II (SEMG2) mRNA
4238	17384	30372	0.91	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4238	17384	30373	0.91	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4244	17390	30377	0.85	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4252	17398	30386	5.57	0.0E+00	A1982597.1	EST_HUMAN	wu04404.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4252	17398	30387	5.57	0.0E+00	A1982597.1	EST_HUMAN	wu04404.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4255	17400	30389	1	0.0E+00	BE184866.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4255	17400	30390	1	0.0E+00	BE184866.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4259	17404		5.89	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
4265	17410	30398	2.07	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4272	17417		5.76	0.0E+00	AW675598.1	EST_HUMAN	ba51804.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:TH12_BOVIN
4277	17422	30410	1.12	0.0E+00	AW409788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4278	17423	30411	1.55	0.0E+00	8922468	NT	UI-HF-BM0-adv-c-02-0-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4278	17423	30412	1.55	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4287	17432		2.35	0.0E+00	5174632	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4300	17443	30429	1.07	0.0E+00	AB037739.1	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4309	17452	30438	11.47	0.0E+00	AA401438.1	EST_HUMAN	Homo sapiens mRNA for KIAA1318 protein, partial cds
4309	17452	30439	11.47	0.0E+00	AA401438.1	EST_HUMAN	zu68407.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4312	17455	30443	1.2	0.0E+00	AF157476.1	NT	zu68407.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4338	17481	30461	8.09	0.0E+00	4758199	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4338	17481	30462	8.09	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4345	17488		0.86	0.0E+00	AL163303.2	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4388	17531	30512	5.01	0.0E+00	J02610.1	NT	Homo sapiens chromosome 21 segment HS21C103
							Human apolipoprotein B-100 mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4402	17545	30529	0.81	0.0E+00	AW936889.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4406	16598	28612	0.65	0.0E+00	BE779039.1	EST_HUMAN	601464995F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868246 5'
4410	17552	30537	5	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
4419	17560	30544	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4419	17560	30545	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4420	17561		2.25	0.0E+00	AI188844.1	EST_HUMAN	qcd2306.x1 Soares placenta 8to9weeks 2kbHP8to9W Homo sapiens cDNA clone IMAGE:1724579 3'
4424	17564		4.68	0.0E+00	U14520.1	NT	similar to contains MER20.b2 MER20 repetitive element ; Human CBFA3 (Cbfa3) gene, partial cds
4428	17568	30550	0.96	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL T4) mRNA
4445	17585	30565	0.72	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4445	17585	30566	0.72	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4451	17591	30572	1.08	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4451	17591	30573	1.08	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4460	17600	30578	10.33	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4480	17620		1.06	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (Cx36) gene, complete cds
4490	17630	30611	3.62	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4494	17634	30616	6.28	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4494	17634	30617	6.28	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4500	17640	30623	1.59	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4500	17640	30624	1.59	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4505	17644	30630	10.05	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4505	17644	30631	10.05	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4517	17656	30645	14.1	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4518	17657	30646	1.16	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4519	17658		1.24	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4522	17661	30648	1.2	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1380 protein, partial cds
4553	17691	30671	1.9	0.0E+00	7019456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4564	17702		6.61	0.0E+00	AF185653.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4570	17708	30687	2.78	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4570	17708	30688	2.78	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4574	17711	30694	0.69	0.0E+00	W26179.1	EST_HUMAN	2497 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4574	17711	30695	0.69	0.0E+00	W26179.1	EST_HUMAN	2497 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4591	17728		2.29	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
4610	17747	30726	0.65	0.0E+00	T10233.1	EST_HUMAN	seq1328 b4HB3MA Cc8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4610	17747	30727	0.65	0.0E+00	T10233.1	EST_HUMAN	seq1328 b4HB3MA Cc8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4613	17750		0.89	0.0E+00	M14723.1	NT	Human endogenous retrovirus HERV-K10
4623	17760	30742	27.37	0.0E+00	AW084984.1	EST_HUMAN	xc88e08.x1 NC1_CGAP_Eso2 Homo sapiens cDNA clone IMAGE288646 3' similar to SW:AHNK_HUMAN
4625	18470		2.97	0.0E+00	8051619	NT	Q09668 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4627	17763	30745	1.48	0.0E+00	AF016050.1	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4631	17767		8.47	0.0E+00	AL163207.2	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4633	17769	30750	0.97	0.0E+00	AW381570.1	EST_HUMAN	Homo sapiens chromosome 21, segment HS21C007
4640	17776	30757	1.3	0.0E+00	AJ278120.1	NT	PM1-HT0305-101195-002-c03 HT0305 Homo sapiens cDNA
4640	17776	30758	1.3	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4642	17778	30760	1.08	0.0E+00	4759467	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4643	17779	30761	2.07	0.0E+00	AF108830.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4651	17787	30770	1.02	0.0E+00	S78694.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
4652	17788	30771	1.2	0.0E+00	AF111163.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4652	17788	30772	1.2	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4661	18471	30783	3.19	0.0E+00	6005973	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4686	17801	30788	20.19	0.0E+00	AF208161.1	NT	Homo sapiens zinc finger protein 185 (ZNF185), mRNA
4671	17806	30795	2.17	0.0E+00	AF152337.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4674	17809	30799	2.17	0.0E+00	5464175	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4685	17820	30808	59.97	0.0E+00	4503470	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4693	17828	30814	0.73	0.0E+00	4505016	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4697	17832	30817	1.84	0.0E+00	4503098	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4702	17837	30823	1.03	0.0E+00	4502556	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4707	17842		3.19	0.0E+00	L35485.1	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4709	17844	30826	15.03	0.0E+00	7662091	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4709	17844	30827	15.03	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4724	17859	30841	2.87	0.0E+00	AF143314.1	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4727	17862	30844	11.57	0.0E+00	AJ245418.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
							Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4727	17882	30845	11.57	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein. (G7c gene located in the class III region of the major histocompatibility complex)
4746	17881		1.68	0.0E+00	AA174072.1	EST_HUMAN	2p18g08.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4749	17884		1.96	0.0E+00	7657410	NT	Homo sapiens cdz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4751	17886		3.31	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4752	17887	30868	1.33	0.0E+00	AF184110.1	NT	Homo sapiens chromosome 21 segment HS21C100
4753	17888	30869	4.83	0.0E+00	AL163300.2	NT	Homo sapiens cyclophilin-related protein (NIPT) gene, complete cds
4754	17889		1.95	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4756	17891	30870	0.69	0.0E+00	AF185658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4761	17898	30876	1.06	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4764	17899	30879	31.32	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4764	17899	30880	31.32	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4765	17900	30881	1.42	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4765	17900	30882	1.42	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4766	17901	30883	2.62	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4776	17911	30895	0.96	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4776	17911	30896	0.96	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4781	17915	30902	17.22	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4787	17922	30910	1.93	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0835-160400-142-05 BT0835 Homo sapiens cDNA
4788	17923	30911	1.37	0.0E+00	AA418246.1	EST_HUMAN	z06b07.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767605 3'
4784	17929		1.9	0.0E+00	AF086641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4799	17934	30921	1.3	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4799	17934	30922	1.3	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4800	17935	30923	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4800	17935	30924	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4801	17936	30925	3.06	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4804	17939	30927	2.06	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4804	17939	30928	2.06	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4806	13367	28400	2.93	0.0E+00	T56945.1	EST_HUMAN	ye83g04.r2 Stralagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
4806	13367	28401	2.93	0.0E+00	T56945.1	EST_HUMAN	ye83g04.r2 Stralagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
4810	17943		1.18	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4814	17947	30932	1.13	0.0E+00	BE390050.1	EST_HUMAN	601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5'
4830	17963	30981	0.95	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4830	17963	30952	0.95	0.0E+00	6729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4835	17968	30950	50.79	0.0E+00	M60902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4838	17971	30959	3.07	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4838	17971	30960	3.07	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4842	17975	30965	2.07	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4844	17977	30987	1.05	0.0E+00	7662479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4846	17979	30988	1.73	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4851	17984	30972	1.15	0.0E+00	U07583.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exon 2-10, complete cds
4856	17989	30977	1.29	0.0E+00	AL068857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4872	18005	30987	0.74	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4872	18005	30988	0.74	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4882	18012	30996	1.25	0.0E+00	AF028601.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4886	18016	31000	0.82	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (ADO13), mRNA
4886	18016	31001	0.82	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (ADO13), mRNA
4907	18037	31025	1.29	0.0E+00	AW444637.1	EST_HUMAN	U1-H-B3-ajw-c-04-U1.61 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4911	18041	31031	1.18	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4919	18043		2.01	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4924	18054		1.33	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
4925	18055		0.84	0.0E+00	AW339253.1	EST_HUMAN	x288000x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'
4968	18095		2.87	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4967	18096	31072	1.95	0.0E+00	4505394	NT	Homo sapiens nidogen (enactin) (NID) mRNA
4970	18099	31076	1.09	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4972	18101	31077	0.99	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Buren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4973	18102	31078	1.04	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kalso mRNA, complete cds
4974	18103	31079	4.54	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4976	18105	31081	9.88	0.0E+00	4985048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4977	18106	31082	1	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4982	18111	31088	3.41	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4985	18114	31091	1.35	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1-J81 segments; and Tor-C-alpha gene, exons 1-4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4885	18114	31092	1.35	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1-J61 segments; and Tor-C-alpha gene, exons 1-4
4987	18116	31094	1.3	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4987	18116	31095	1.3	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4990	18119	31098	1.48	0.0E+00	M55582.1	NT	Human collagenase type IV (CLG4) gene, exon 2
4991	18120	31099	2.55	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5000	18129	31104	1.08	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF2)
5007	18136	31110	1.19	0.0E+00	X92841.1	NT	H.sapiens MICA gene
5009	18138	31112	1.32	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
5010	18139	31113	1.39	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5011	18140	31114	2.74	0.0E+00	667648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zlk1), mRNA
5012	18141	31115	1.02	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-col proline-rich) (MGEA6), mRNA
5013	18142	31116	0.94	0.0E+00	BE007935.1	EST_HUMAN	QV0-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
5013	18142	31117	0.94	0.0E+00	BE007935.1	EST_HUMAN	QV0-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
5014	18143	31118	4.26	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DP11) (DSP) mRNA
5016	18145	31120	1.79	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-col proline-rich) (MGEA6), mRNA
5018	18145	31121	1.79	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-col proline-rich) (MGEA6), mRNA
5017	18146	31122	0.98	0.0E+00	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HUMH0XY1), mRNA
5020	18149	31127	11.02	0.0E+00	AF055068.1	NT	Homo sapiens MHC class 1 region
5022	18151		2.46	0.0E+00	4505508	NT	Homo sapiens oploid receptor, delta 1 (OPRD1) mRNA
5023	18152	31130	2.77	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
5036	18164	31140	1.55	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS) mRNA
5040	18168		1.17	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5042	18170	31145	1.14	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
5042	18170	31146	1.14	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
5043	18171	31147	7.67	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5043	18171	31148	7.67	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5049	18177	31154	1.39	0.0E+00	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
5049	18177	31155	1.39	0.0E+00	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
5067	18195	31169	1.26	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5073	18201	31173	0.71	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
5082	18210	31182	1.15	0.0E+00	8922928	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5087	18215		7.66	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
5097	18225	31197	1.25	0.0E+00	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5099	18227		2.87	0.0E+00	BE405663.1	EST_HUMAN	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
5102	18230	31201	4.85	0.0E+00	4758169	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
5110	18238	31205	1.43	0.0E+00	A502866.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5121	18247	31212	2.32	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5121	18247	31213	2.32	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5135	18259	31225	0.72	0.0E+00	AA601246.1	EST_HUMAN	no14609.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.3 similar to TR:E239140
5135	18259	31226	0.72	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN
5135	18259	31227	0.72	0.0E+00	AA601246.1	EST_HUMAN	no14609.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.3 similar to TR:E239140
5139	18262	31229	2.09	0.0E+00	U82871.2	NT	E239140 SPALT PROTEIN
5139	18262	31230	2.09	0.0E+00	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracrin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
5146	13440	26472	0.72	0.0E+00	AF196656.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracrin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
5148	18270		1.09	0.0E+00	4758225	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5160	18282	31247	0.84	0.0E+00	U53586.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5167	18289		1.89	0.0E+00	AL163209.2	NT	Homo sapiens MHC class 1 region
5170	18292		16.96	0.0E+00	D50667.1	NT	Homo sapiens chromosome 21 segment HS21C006
5182	18304	31288	0.92	0.0E+00	4507720	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5196	18318	31287	3.55	0.0E+00	X62988.1	NT	Homo sapiens titin (TTN) mRNA
5197	18319	31288	0.81	0.0E+00	X72791.1	NT	Bacillus amyloliqueficans sacB gene for levansucrase (EC 2.4.1.10)
5213	18334	31305	1.82	0.0E+00	AF240635.1	NT	Human endogenous retrovirus mRNA for gag protein
5213	18334	31306	1.82	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5214	18335	31307	1.18	0.0E+00	5454153	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5232	18354	31322	0.82	0.0E+00	5902055	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5234	18356	31323	4.68	0.0E+00	M10905.1	NT	Homo sapiens ring finger protein (RNF), mRNA
5234	18358	31324	4.68	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5236	18358	31327	0.8	0.0E+00	Y08032.1	NT	Human cellular fibronectin mRNA
5236	18358	31327	0.8	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5250	18371	31338	0.65	0.0E+00	5902091	NT	Homo sapiens solute carrier family 5 (inositol transporters), member 3 (SLC5A3), mRNA
5253	18373	31339	1.91	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
5268	18385	31351	1.2	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5266	18385	31352	1.2	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5267	18386	31353	0.69	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5267	18386	31354	0.69	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5274	18393	31362	1.89	0.0E+00	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
5278	18397	31384	1.03	0.0E+00	AA425183.1	EST_HUMAN	z444f12.r1 Scores_totat_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:772843 5'
5278	18397	31365	1.03	0.0E+00	AA425183.1	EST_HUMAN	z444f12.r1 Scores_totat_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:772843 5'
5280	18408	31375	0.93	0.0E+00	7657442	NT	Homo sapiens protocadherin 11 (PCDH11), mRNA
5294	18412	31378	1.47	0.0E+00	AF155582.1	NT	Homo sapiens core1 UDP-galactose 4-epimerase/alpha-R beta 1,3-galactosyltransferase (C1GALT1) mRNA, complete cds
5297	18472	31382	1.84	0.0E+00	AF167335.1	NT	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP) gene, exon 4
5300	18417	31386	0.94	0.0E+00	S69002.1	NT	AML1-EV1-1+AML1-EV1-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5838 nt]
5301	18418	31387	1.93	0.0E+00	AF009568.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
5301	18418	31388	1.93	0.0E+00	AF009568.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
5303	18420	31390	24.35	0.0E+00	6360213	NT	Homo sapiens glypican 3 (GPC3) mRNA
5306	18423	31393	1.07	0.0E+00	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU16652), mRNA
5319	18435	31405	0.79	0.0E+00	X76060.1	NT	H.sapiens mRNA for YRRM2
5321	18426	29444	0.85	0.0E+00	AI685950.1	EST_HUMAN	tu39g09.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICD1
5328	18441	31410	0.96	0.0E+00	AF245703.1	NT	P03967 RAS-LIKE PROTEIN RASD
5328	18441	31411	0.96	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5333	18446	31414	0.96	0.0E+00	AL163208.2	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5338	18451	31419	110.9	0.0E+00	AF008061.1	NT	Homo sapiens chromosome 21 segment HS21C006
5340	18453	31421	1.06	0.0E+00	AV726632.1	EST_HUMAN	Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds
5344	18457	31423	1.29	0.0E+00	5174632	NT	AV726632 HTC Homo sapiens cDNA clone HTCCGA03 5'
5346	18459	31424	1.18	0.0E+00	4502582	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
5356	18482		2.45	0.0E+00	AF093093.1	NT	Homo sapiens casepase 8, apoptosis-related cysteine protease (CASP8) mRNA
5366	18569	31436	2.17	0.0E+00	AF137286.1	NT	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5366	18569	31437	2.17	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5366	18569	31437	2.17	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5398	18590	31562	1.21	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464084 3'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5391	18593	31565	1.2	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDH13), mRNA
5406	18608	31580	3.52	0.0E+00	BE631080.1	EST_HUMAN	RC3-GN0076-310800-013-503 GN0076 Homo sapiens cDNA
5410	18612	31584	3.5	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5410	18612	31585	3.5	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5418	18619	31594	8.57	0.0E+00	X55163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5418	18619	31595	8.57	0.0E+00	X55163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5499	18598	31714	6.41	0.0E+00	BE676498.1	EST_HUMAN	710c06.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5500	18699	31715	1.7	0.0E+00	BE220763.1	EST_HUMAN	h59e02.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3165184 3' similar to SW:Y054_HUMAN
5501	18700	31716	1.57	0.0E+00	BE794412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0054. ;
5501	18700	31717	1.57	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5502	18701	31718	0.72	0.0E+00	AI189142.1	EST_HUMAN	q404e04.x1 Soares placenta 8to9weeks 2NBHP8to9W Homo sapiens cDNA clone IMAGE:1722702 3' similar to SW:T2D3_DROME P.49846 TRANSCRIPTION INITIATION FACTOR TF1D 85 KD SUBUNIT ;
5506	18705	31721	5.23	0.0E+00	M23908.1	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5510	18709	31724	1.3	0.0E+00	AI791363.1	EST_HUMAN	ch58e03.y5 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512 IG
5520	25806	31732	4.52	0.0E+00	11421038	NT	HEAVY CHAIN PRECURSOR V-J REGION (HUMAN);
5530	18727		4	0.0E+00	BF685982.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4), mRNA
5531	18728	31743	0.78	0.0E+00	AU134405.1	EST_HUMAN	602118028F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276254 5'
5531	18728	31744	0.78	0.0E+00	AU134405.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5537	18734	31751	0.61	0.0E+00	BE538857.1	EST_HUMAN	AU134408 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5546	18743	31777	1.63	0.0E+00	BE292784.1	EST_HUMAN	601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5551	18748	31783	1.65	0.0E+00	BF526328.1	EST_HUMAN	601105381F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2888310 5'
5551	18748	31784	1.65	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272 5'
5570	20121	33535	1.71	0.0E+00	4557364	NT	602071372F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272 5'
5573	18769	31811	1.29	0.0E+00	AB007935.1	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5573	18769	31812	1.29	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5577	18772	31816	8.95	0.0E+00	AF257757.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5577	18772	31817	8.95	0.0E+00	AF257757.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5590	18785	31831	1.34	0.0E+00	D26535.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5590	18785	31832	1.34	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5608	18801	31867	2.01	0.0E+00	11420819	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5612	18806	31873	0.78	0.0E+00	Z38133.1	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
							H.sapiens mRNA for myosin

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5630	18824	31898	0.73	0.0E+00	D61594.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6536) Homo sapiens cDNA clone GEN-418D05 5'
5630	18824	31899	0.73	0.0E+00	D61594.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5'
5633	18827	31903	2.92	0.0E+00	BF529831.1	EST_HUMAN	602042322F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4179988 5'
5633	18827	31904	2.92	0.0E+00	BF529831.1	EST_HUMAN	602042322F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4179988 5'
5638	18832	31908	2.82	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128615 5'
5648	18843	32124	4.23	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5664	18858	32141	0.59	0.0E+00	A1928181.1	EST_HUMAN	w095b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054
5664	18858	32142	0.59	0.0E+00	A1928181.1	EST_HUMAN	w095b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054
5682	18876	32165	1.3	0.0E+00	BE260777.1	EST_HUMAN	O75054 KIAA0466 PROTEIN;
5691	18885	32190	3.95	0.0E+00	AW867316.1	EST_HUMAN	601150252F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3502909 5'
5705	18898	32190	2.49	0.0E+00	BE292889.1	EST_HUMAN	MFO-SN0037-030400-001-r07 SN0037 Homo sapiens cDNA
5705	18898	32191	2.49	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887903 5'
5725	18918	32212	1.7	0.0E+00	11420819	NT	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887903 5'
5725	18918	32213	1.7	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5733	18926	32221	4.16	0.0E+00	AF064254.1	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5733	18926	32222	4.16	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5740	18933	32232	2.64	0.0E+00	AJ224639.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5740	18933	32233	2.64	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5769	18961	32262	1	0.0E+00	A1198515.1	EST_HUMAN	Homo sapiens Surf-5 and Surf-6 genes
5773	18965	32268	7.55	0.0E+00	M85719.1	EST_HUMAN	q194g10.x1 Soares, placenta, 8to9weeks, 2NbHP8to9w Homo sapiens cDNA clone IMAGE:1757730 3'
5780	18972	32277	4.62	0.0E+00	AW405472.1	EST_HUMAN	similar to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR;
5793	18984	32287	1.12	0.0E+00	Z26289.1	NT	EST02238 Fetal brain, Striatogene (cat#936205) Homo sapiens cDNA clone HFBCM48
5804	18994	32298	1.85	0.0E+00	AW361877.1	EST_HUMAN	UHF-BLO-adt-d-02-0-UI-1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5804	18994	32299	1.85	0.0E+00	AW361877.1	EST_HUMAN	H.sapiens isoform 1 gene for L-type calcium channel, exon 14 cdnd 15
5804	18994	32299	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5807	18997	32302	0.59	0.0E+00	AB035266.1	NT	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5807	18997	32303	0.59	0.0E+00	AB035266.1	NT	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5809	18999	32306	1.87	0.0E+00	U36261.1	NT	Homo sapiens mRNA for neurxin II, complete cds
5840	19030	32336	1.02	0.0E+00	AB046861.1	NT	Homo sapiens mRNA for neurxin II, complete cds
5840	19030	32336	1.02	0.0E+00	AB046861.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5840	19030	32336	1.02	0.0E+00	AB046861.1	NT	Homo sapiens mRNA for KIAA1641 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5889	19088	32400	1.49	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5898	19088	32401	1.49	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5906	19085	32410	1.23	0.0E+00	AJ207610.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5928	19114	32427	4.63	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
5933	19119	32430	1.19	0.0E+00	BE791173.1	EST_HUMAN	601584032F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938551 5'
5942	19128	32441	1.1	0.0E+00	8989943	NT	Homo sapiens anilloide-sensitve cation channel 1, neuronal (degeneth) (ACCN1), mRNA
5943	19129	32442	7.24	0.0E+00	BE600082.1	EST_HUMAN	601345141F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3677843 5'
5944	19130	32443	2.46	0.0E+00	10048478	NT	Mus musculus ezonin (Azz), mRNA
5945	19131	32444	3.08	0.0E+00	U86981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5945	19131	32445	3.08	0.0E+00	U86981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5965	19151	32468	2.96	0.0E+00	BF339835.1	EST_HUMAN	602036272F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4184321 5'
5968	19154	32469	0.92	0.0E+00	AF142621.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
5969	19155	32470	3.07	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC 14 Homo sapiens cDNA clone IMAGE:3347463 5'
5979	19164	32484	1.12	0.0E+00	BE503086.1	EST_HUMAN	hz83d11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q62084 Q62084
5984	19169	32491	2.09	0.0E+00	BF669905.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING ;
5989	19174	32495	0.99	0.0E+00	AA454942.1	EST_HUMAN	602185852F1 NIH_MGC 45 Homo sapiens cDNA clone IMAGE:4310076 5'
6021	19204	32524	2.15	0.0E+00	AF217289.1	NT	z699d06.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811883 3'
6023	19206	32526	4.63	0.0E+00	BE828144.1	EST_HUMAN	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6028	19211	32531	1.19	0.0E+00	BE698836.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
6044	19227	32550	0.98	0.0E+00	BE673986.1	EST_HUMAN	601645287F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3930453 5'
6044	19227	32551	0.98	0.0E+00	BE673986.1	EST_HUMAN	7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN
6048	19231	32555	0.8	0.0E+00	AW276760.1	EST_HUMAN	P51943 ORPHAN NUCLEAR RECEPTOR DAX-1. [1];
6058	19240	32565	0.96	0.0E+00	BF031742.1	EST_HUMAN	P51943 ORPHAN NUCLEAR RECEPTOR DAX-1. [1];
6058	19240	32566	0.96	0.0E+00	BF031742.1	EST_HUMAN	7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN
6058	19240	32568	0.96	0.0E+00	BF031742.1	EST_HUMAN	xc65f03.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335
6070	19252	32581	0.95	0.0E+00	AW470846.1	EST_HUMAN	GUANYLATE KINASE ASSOCIATED PROTEIN ;
6082	19264	32592	1.09	0.0E+00	BF155670.1	EST_HUMAN	601558060F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827775 5'
6082	19264	32593	1.09	0.0E+00	BF155670.1	EST_HUMAN	601558060F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827775 5'
6082	19264	32593	1.09	0.0E+00	BF155670.1	EST_HUMAN	ha34d06.x1 NCI_CGAP_Ku12 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q821N3
6082	19264	32593	1.09	0.0E+00	BF155670.1	EST_HUMAN	Q9Z1N3 MYOSIN-RHO GAP PROTEIN, MYR 7. ;
6082	19264	32593	1.09	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-280800-398-a10 HT0894 Homo sapiens cDNA
6082	19264	32593	1.09	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-280800-398-a10 HT0894 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6090	19271	32599	1.67	0.0E+00	W33068.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:321755 5'
6090	19271	32600	1.67	0.0E+00	W33068.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:321755 5'
6091	19272		2.3	0.0E+00	AF012818.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
6094	19275	32604	3.37	0.0E+00	BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
6100	19280	32812	2.43	0.0E+00	BE888610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3814238 5'
6102	19282	32615	0.58	0.0E+00	BE388673.1	EST_HUMAN	601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813085 5'
6117	19297	32833	0.65	0.0E+00	AW752848.1	EST_HUMAN	IL3-CT0220-111199-028-E04 CT0220 Homo sapiens cDNA
6120	19299	32635	1.72	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6120	19299	32636	1.72	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6121	19300	32637	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32638	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32639	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6137	25819	32656	10.17	0.0E+00	9789886	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6140	19318	32659	1.28	0.0E+00	AA193508.1	EST_HUMAN	zr40h01.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6140	19318	32660	1.28	0.0E+00	AA193508.1	EST_HUMAN	zr40h01.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6163	19339	32685	10.44	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6163	19339	32686	10.44	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6203	19376	32729	1.06	0.0E+00	BE258330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355565 5'
6223	19388	32737	1.15	0.0E+00	BE156561.1	EST_HUMAN	QV0-HT0388-090200-099-609 HT0368 Homo sapiens cDNA
6223	19388	32747	0.66	0.0E+00	M38107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6259	19433	32760	1.6	0.0E+00	BE379007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6265	19439	32786	1.35	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACET Homo sapiens cDNA clone PLACET1007201 5'
6287	19460	32812	3.33	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
6316	19488	32844	4.34	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.r1 Stratagene HNT neuron (R937233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6317	19489	32845	3.89	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6317	19489	32846	3.89	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6353	19523	32880	2.23	0.0E+00	11426367	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6357	19527	32885	3.15	0.0E+00	BE257173.1	EST_HUMAN	601109632F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350222 5'
6371	19540		0.98	0.0E+00	AI686048.1	EST_HUMAN	rs11f10.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2248639 3' similar to TR:Q14839 Q14839 MI-2 PROTEIN. ;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6375	19544	32902	1.32	0.0E+00	L35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6383	19552	32908	0.98	0.0E+00	BE797385.1	EST_HUMAN	601687971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6383	19552	32909	0.96	0.0E+00	BE797385.1	EST_HUMAN	601687971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6393	19562	32922	0.71	0.0E+00	AI198025.1	EST_HUMAN	q180b11.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:1859601 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT
6393	19562	32923	0.71	0.0E+00	AI198025.1	EST_HUMAN	q180b11.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:1859601 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT
6395	19564	32924	1.11	0.0E+00	BE337123.1	EST_HUMAN	MRO-HT0923-220800-102:505 HT0923 Homo sapiens cDNA
6403	19572	32934	1.3	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA
6413	19582	32943	0.59	0.0E+00	D55649.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6429	19597	32963	1.07	0.0E+00	AW178142.1	EST_HUMAN	IL3-HT0062-010999-014-A04 HT0062 Homo sapiens cDNA
6450	19617	32980	0.6	0.0E+00	BE674544.1	EST_HUMAN	7d02c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302 3' similar to SW:Y176_HUMAN Q14681 HYPOTHETICAL PROTEIN KIAA0176
6454	19621	32985	0.77	0.0E+00	7862039	NT	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6468	19635		9.28	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'
6477	19644	33006	3.46	0.0E+00	AW575598.1	EST_HUMAN	UHF-BLO-acc-g-12-Q.U1.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
6480	19647	33009	4.63	0.0E+00	H01255.1	EST_HUMAN	y27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'
6488	19655	33018	0.71	0.0E+00	11428293	NT	Homo sapiens aniloride-sensitive cation channel 1, neuronal (degenerate) (ACCN1), mRNA
6492	19658	33021	1.67	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
6494	19660	33023	1.17	0.0E+00	AA456375.1	EST_HUMAN	aa14e07.r1 Soares_NhrMPu_S1 Homo sapiens cDNA clone IMAGE:813252 5'
6495	19661	33024	1.04	0.0E+00	AI612841.1	EST_HUMAN	t257d08.x1 NCI_CGAP_Ov25 Homo sapiens cDNA clone IMAGE:2202687 3' similar to SW:NTCS_HUMAN
6501	19667	33030	4.27	0.0E+00	BE735989.1	EST_HUMAN	P53796 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2
6501	19667	33031	4.27	0.0E+00	BE735989.1	EST_HUMAN	601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6505	19671	33037	0.86	0.0E+00	AW748396.1	EST_HUMAN	MRO-BT0284-221198-002-f11 BT0284 Homo sapiens cDNA
6505	19671	33038	0.86	0.0E+00	AW748396.1	EST_HUMAN	MRO-BT0284-221198-002-f11 BT0284 Homo sapiens cDNA
6507	19673	33040	52.21	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6507	19673	33041	52.21	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6512	19677	33047	0.8	0.0E+00	BE780453.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871859 5'
6513	19678	33048	0.84	0.0E+00	X92217.1	NT	H. sapiens germline immunoglobulin heavy chain, variable region, (13-2)
6527	19691	33065	1.71	0.0E+00	AI989483.1	EST_HUMAN	ws25c07.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2498220 3'
6541	19704	33076	4.06	0.0E+00	BE283163.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887863 5'
6541	19704	33077	4.06	0.0E+00	BE283163.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887863 5'
6573	19735	33114	1.07	0.0E+00	BE867857.1	EST_HUMAN	601443176F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3847281 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6609	19769	33158	1.81	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-acc-h-02-q-U1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:305931 5'
6609	19769	33159	1.81	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-acc-h-02-q-U1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:305931 5'
6640	19799	33188	0.94	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLCEHC06 5'
6649	19808	33195	0.74	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6649	19808	33196	0.74	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6652	19811	33199	2.13	0.0E+00	AF190880.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant Cav1.1a (CACNA1G) mRNA, complete cds
6655	19814	33202	0.84	0.0E+00	L48546.1	NT	Homo sapiens tuberin (TSC2) gene, exons 38, 39, 40 and 41
6657	19818	33203	0.99	0.0E+00	11420858	NT	Homo sapiens transcription factor 10 (TF10) gene, complete cds
6664	19823	33210	3.5	0.0E+00	AW163840.1	EST_HUMAN	TR-O15390 O15390 GT24. [3] TR-O43840 TR-O43205
6664	19823	33211	3.5	0.0E+00	AW163840.1	EST_HUMAN	TR-O15390 O15390 GT24. [3] TR-O43840 TR-O43205
6668	19827	33214	1.06	0.0E+00	W37163.1	EST_HUMAN	SW:ZN45_HUMAN_Q02388 ZINC FINGER PROTEIN 45
6668	19827	33215	1.06	0.0E+00	W37163.1	EST_HUMAN	SW:ZN45_HUMAN_Q02388 ZINC FINGER PROTEIN 45
6684	19842	33232	1.21	0.0E+00	BE794953.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6681	19849	33239	5.1	0.0E+00	BE794953.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6692	19850	33240	1.38	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6692	19850	33241	1.38	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6696	19854	33244	6.83	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6696	19854	33245	6.83	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6705	19863	33253	4.51	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6710	19868	33257	2.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6710	19868	33258	2.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6716	19874	33265	3.68	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A) mRNA
6720	19877	33268	4.12	0.0E+00	AI639412.1	EST_HUMAN	131111.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
6722	19879	33270	1.46	0.0E+00	L32832.1	NT	P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR
6735	19891	33283	0.82	0.0E+00	AW505430.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
6737	19893	33284	4.11	0.0E+00	AA434584.1	EST_HUMAN	UI-HF-BND-ame-c-01-q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 6'
6751	19907		1.13	0.0E+00	BF217200.1	EST_HUMAN	2462203.11 Soares_tetral_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:773668 5'
6756	19912	33307	1.63	0.0E+00	BE925876.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6789	19944	33342	0.76	0.0E+00	11428758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6789	19944	33343	0.76	0.0E+00	11428758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6790	19945	33345	0.59	0.0E+00	AW011884.1	EST_HUMAN	ig82e04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952128 3'
6808	19962	33368	1.64	0.0E+00	AU125928.1	EST_HUMAN	AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM402430 5'
6810	19964	33368	0.58	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6810	19964	33369	0.58	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6832	19985	33393	1.27	0.0E+00	BE142363.1	EST_HUMAN	CMO-HT0143-270999-062-c08 HT0143 Homo sapiens cDNA
6854	20007	33416	2.43	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6854	20007	33417	2.43	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6876	20028	33438	7.78	0.0E+00	BE180131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6878	20030	33440	2.04	0.0E+00	BF085667.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6915	20230	33653	3.33	0.0E+00	AA180755.1	EST_HUMAN	z488c03.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:627292 5'
6926	20241	33676	0.83	0.0E+00	U39573.1	NT	Human salivary peroxidase mRNA, complete cds
6930	20245	33678	0.76	0.0E+00	BE671987.1	EST_HUMAN	7449b07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285 TEKTIN1
6940	20263	33689	5.73	0.0E+00	A1940821.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6940	20263	33690	5.73	0.0E+00	A1940821.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6951	20284	33703	2.15	0.0E+00	11435828	NT	Homo sapiens OD6 antigen (OD6), mRNA
6963	20191	33617	0.73	0.0E+00	AL042443.1	EST_HUMAN	DKFZp434D2021_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2021 5'
6964	20192	33618	11.05	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
6967	20195	33621	0.92	0.0E+00	A1168270.1	EST_HUMAN	oo10d01.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1665761 3' similar to TR:Q26823 Q26823 TEKTIN C1
6972	20200	33626	0.85	0.0E+00	BE734087.1	EST_HUMAN	601667370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
6991	18510	31502	1.28	0.0E+00	BE566381.1	EST_HUMAN	601339877F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682287 5'
6998	18517	31509	13.63	0.0E+00	BE867889.1	EST_HUMAN	601443967F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6998	18517	31510	13.63	0.0E+00	BE867889.1	EST_HUMAN	601443967F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
7004	20140	33558	1.74	0.0E+00	BE550162.1	EST_HUMAN	7b49r03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95
7004	20140	33559	1.74	0.0E+00	BE550162.1	EST_HUMAN	7b49r03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95
7030	20166	33588	1.66	0.0E+00	BF088376.1	EST_HUMAN	GM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA
7036	20172	33594	1.4	0.0E+00	AA195106.1	EST_HUMAN	z343g03.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665332 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7044	20097		11.81	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
7048	20098	33515	1.11	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7061	20114	33529	2.85	0.0E+00	BF593905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7088	20121	33535	0.88	0.0E+00	4557364	NT	Homo sapiens Bloem syndrome (BLM) mRNA
7078	20129		2.06	0.0E+00	J03069.1	NT	Human MYCL2 gene, complete cds
7083	20177	33599	2.56	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7083	20177	33600	2.56	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7084	20178	33601	1.07	0.0E+00	M38113.1	NT	Human neurofibromatosis type 1 gene, exon x8
7095	18522	31515	3.59	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7099	18526	31518	0.7	0.0E+00	BE268708.1	EST_HUMAN	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 5'
							W21C09.X1 Soares_Diagnostic_cdon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEBOX PROTEIN HOXA4 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element ;
7111	18537	31483	0.82	0.0E+00	AI65091.1	EST_HUMAN	w21c09.x1 Soares_Diagnostic_cdon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEBOX PROTEIN HOXA4 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element ;
7111	18537	31484	0.82	0.0E+00	AI65091.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003679 5'
7120	18549	31457	1.21	0.0E+00	AU118478.1	EST_HUMAN	601148954F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3501829 5'
7123	18549	31461	7.52	0.0E+00	BE262941.1	EST_HUMAN	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7124	18550	31462	2.72	0.0E+00	Z37976.1	NT	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7124	18550	31463	2.72	0.0E+00	Z37976.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7125	18551	31464	3.01	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7125	18551	31465	3.01	0.0E+00	AF257737.1	NT	Homo sapiens NALP1 mRNA, complete cds
7132	18558	31472	1.26	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7137	20272	33711	0.81	0.0E+00	BE762770.1	EST_HUMAN	QV3-NT0022-140600-223-f01 NT0022 Homo sapiens cDNA
7142	20277	33717	2.56	0.0E+00	BF568905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7144	20279	33719	0.78	0.0E+00	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7144	20279	33720	0.78	0.0E+00	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7148	20283	33725	3.25	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7153	20287	33729	0.72	0.0E+00	AW502362.1	EST_HUMAN	UHF-BF0p-aka-d-10-0-UJ.1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7153	20287	33730	0.72	0.0E+00	AW502362.1	EST_HUMAN	UHF-BF0p-aka-d-10-0-UJ.1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7182	20295	33738	0.87	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2211 5'
7182	20295	33739	0.87	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2211 5'
7171	20304	33747	5.81	0.0E+00	BF308996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7177	20309	33752	2.13	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7219	20084	33499	1.15	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7225	20089	33506	0.64	0.0E+00	AW513069.1	EST_HUMAN	xc40602.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2706458 3' similar to TR:094895 094895 KIAA0803 PROTEIN ;
7257	20340	33780	0.82	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7257	20340	33761	0.62	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7262	20345	33797	0.84	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7262	20345	33798	0.84	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7268	20351	33804	1.16	0.0E+00	AW554806.1	EST_HUMAN	EST366076 IMAGE ressequencing, MAGO Homo sapiens cDNA
7269	20352	33805	0.72	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354566 5'
7283	20366	33819	1	0.0E+00	LC1973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7291	20373	33829	1.03	0.0E+00	AB007835.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7291	20373	33830	1.03	0.0E+00	AB007835.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7297	20379	33837	1.47	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'
7313	20385	33857	1.06	0.0E+00	1142808.1	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7319	20401		2.82	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y78AA1 Homo sapiens cDNA clone Y78AA1002365 5'
7320	20402	33864	0.71	0.0E+00	4758839	NT	Homo sapiens netrin 1 (NTN1), mRNA
7329	20411	33872	1.25	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7329	20411	33873	1.25	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7350	18569	31436	2.43	0.0E+00	AF137266.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7350	18569	31437	2.43	0.0E+00	AF137266.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7361	20440	33901	0.67	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7361	20440	33902	0.67	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7371	20450	33913	4.07	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7371	20450	33914	4.07	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7385	20463	33927	0.63	0.0E+00	AF227744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform aa (CACNA1G) mRNA, complete cds
7406	20484	33952	36.37	0.0E+00	A1128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8tc9weeks_2NbhP8tc9w Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element ;
7406	20484	33953	36.37	0.0E+00	A1128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8tc9weeks_2NbhP8tc9w Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7408	20486	33955	0.74	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7408	20486	33956	0.74	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7410	20488	33958	5.41	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7410	20488	33959	5.41	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7413	20491		13.11	0.0E+00	BF337976.1	EST_HUMAN	802035089F1 NCL_CGAP_Br64 Homo sapiens cDNA clone IMAGE:4182839 5'
7415	20493	33961	3.49	0.0E+00	AA128453.1	EST_HUMAN	z60f09.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562
7420	20497	33967	0.77	0.0E+00	AL078497.1	EST_HUMAN	GS06582 NEBULIN ;
7420	20497	33968	0.77	0.0E+00	AL078497.1	EST_HUMAN	DKFZp434B0226_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7431	20508	33980	0.69	0.0E+00	ALJ70996.1	NT	DKFZp434B0226_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7461	20536	34011	1.13	0.0E+00	BE286489.1	EST_HUMAN	Homo sapiens partial mRNA for LTRPC5 protein (LTRPC5 gene)
7463	20538	34012	0.91	0.0E+00	11427866	NT	801174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794 5'
7466	20541		1.33	0.0E+00	AU118607.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20261), mRNA
7467	20542	34015	1.71	0.0E+00	AF005213.1	NT	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
7467	20542	34016	1.71	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7479	20554	34026	0.83	0.0E+00	AF245505.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7487	20562	34031	6.47	0.0E+00	X70172.1	NT	Homo sapiens DNA for ZNGP2 pseudogene, exon 4
7489	20564	34033	5.81	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7489	20564	34034	5.81	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7502	20577	34049	0.89	0.0E+00	AW955503.1	EST_HUMAN	EST368573 MAGI3 resequences, MAGI3 Homo sapiens cDNA
7604	20579	34051	2.31	0.0E+00	AW950516.1	EST_HUMAN	EST362586 MAGI3 resequences, MAGI3 Homo sapiens cDNA
7531	20604	34078	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa S.C.) Homo sapiens cDNA clone kappa_200
7531	20604	34079	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa S.C.) Homo sapiens cDNA clone kappa_200
7531	20604	34080	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa S.C.) Homo sapiens cDNA clone kappa_200
7552	20624		0.58	0.0E+00	M90354.1	NT	Human BTIF3 protein homologue gene, complete cds
7553	20626	34101	0.8	0.0E+00	BE408293.1	EST_HUMAN	801302679F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7580	20652		1.09	0.0E+00	R87430.1	EST_HUMAN	ym88h10.1 Scores adult brain N2b-4HB55Y Homo sapiens cDNA clone IMAGE:166051 5'
7581	20653	34129	1.81	0.0E+00	AW239326.1	EST_HUMAN	xb39a05.y1 NCL_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:3637434 5'
7600	20670		1.5	0.0E+00	AU117553.1	EST_HUMAN	HNF3/IFH TRANSCRIPTION FACTOR GENESIS ;
7602	20672	34146	3.8	0.0E+00	11427135	NT	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'
7622	20692	34168	0.62	0.0E+00	AA211663.1	EST_HUMAN	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7628	20698	34174	0.63	0.0E+00	BF229235.1	EST_HUMAN	z65602.1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
							MRQ-AN0083-270900-004-107 AN0083 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7634	20703	34182	0.67	0.0E+00	AW405627.1	EST_HUMAN	UHF-BLO-ab9-d-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3037469 5'
7641	20710	34189	0.8	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7667	20733	34209	0.9	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7667	20733	34210	0.9	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7675	20740	34220	1.08	0.0E+00	AU118787.1	EST_HUMAN	AU118787 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
7733	20764	34281	4.41	0.0E+00	A1752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7733	20764	34282	4.41	0.0E+00	A1752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7786	20852	34344	0.8	0.0E+00	AL048347.2	EST_HUMAN	DKFZp434J087_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J087 5'
7813	20888	34363	1.78	0.0E+00	AF064205.1	NT	Homo sapiens dynein 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7813	20888	34364	1.78	0.0E+00	AF064205.1	NT	Homo sapiens dynein 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7821	20876	34375	1.34	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7835	20890	34392	1	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaforin) 5A (SEMA5A), mRNA
7863	20817	34422	0.7	0.0E+00	A1826504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363 AIBC1.1
7863	20817	34423	0.7	0.0E+00	A1825904.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363 AIBC1.1
7871	20825	34432	1.84	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7877	20829	34435	0.88	0.0E+00	N76126.1	EST_HUMAN	za86605.s1 Soares_Tetralung_NHL19W Homo sapiens cDNA clone IMAGE:299456 3'
7881	20833	34438	6.1	0.0E+00	BF217805.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
7886	20838	34444	0.82	0.0E+00	BF569892.1	EST_HUMAN	602185808F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4310266 5'
7891	20843	34449	3.52	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2006913 5'
7911	25855	34469	0.95	0.0E+00	AW069274.1	EST_HUMAN	cr42a09.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42a09 3'
7911	25855	34470	0.95	0.0E+00	AW069274.1	EST_HUMAN	cr42a09.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42a09 3'
7915	20866	34472	6.67	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7922	20873	34479	0.92	0.0E+00	AV758467.1	EST_HUMAN	AV758467 BM Homo sapiens cDNA clone BMFBG305 5'
7924	20974	34480	5.78	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947385 5'
7924	20974	34481	5.78	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947385 5'
7925	20975	34482	0.76	0.0E+00	6912481	NT	Homo sapiens atrophin-1 interacting protein 1, actinin receptor interacting protein 1 (KIAA0706), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7926	20976	34483	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIA0705), mRNA
7928	20976	34484	1.05	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7926	20976	34485	1.05	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7948	20998	34508	12.57	0.0E+00	BF590267.1	EST_HUMAN	haz22c04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:32663214 3' similar to contains element TAR1 repetitive element;
7959	21009	34519	1.86	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
7959	21009	34520	1.86	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
7998	21048	34561	0.83	0.0E+00	Y18795.1	NT	Homo sapiens psihHaa pseudogene
7999	21049	34562	3.86	0.0E+00	AJ345148.1	EST_HUMAN	gp43f05.x1 NCI CGAP_Co8 Homo sapiens cDNA clone IMAGE:1925793 3' similar to SW:EVX1_HUMAN
8001	21051	34564	0.68	0.0E+00	W52873.1	EST_HUMAN	P49640 HOMEBOXEVEN-SKIPPED HOMOLOG PROTEIN 1;
8002	21052	34565	0.58	0.0E+00	11425128	EST_HUMAN	zc90f10.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:338443 5'
8003	21053	34566	0.59	0.0E+00	AU117333.1	EST_HUMAN	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
8004	21054		0.57	0.0E+00	BE613963.1	EST_HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001175 5'
8018	21069	34580		0.0E+00	6995995	NT	601504084F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905733 5'
8018	21069	34581	0.73	0.0E+00	6995995	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, A TP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8037	21120	34640	0.49	0.0E+00	AU133187.1	EST_HUMAN	Homo sapiens cystic fibrosis transmembrane conductance regulator, A TP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8083	21165		0.69	0.0E+00	BF217200.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
8086	21178	34695	0.61	0.0E+00	BE313013.1	EST_HUMAN	601889317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
8108	21190	34710	1.36	0.0E+00	AA149761.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
8121	21203	34724	0.72	0.0E+00	BF026628.1	EST_HUMAN	zc01c06.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:366410 5'
8135	21217	34738	0.55	0.0E+00	AA017021.1	EST_HUMAN	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
8153	21235	34756	2.08	0.0E+00	BE786046.1	EST_HUMAN	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:360831 5'
8170	21252	34772	3.19	0.0E+00	M34872.1	NT	zc33h08.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:3639903 5'
8170	21252	34773	3.19	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8200	21282	34804	0.56	0.0E+00	AW674581.1	EST_HUMAN	Human amyloid-beta protein (APP) gene, exon 11
8200	21282	34805	0.56	0.0E+00	AW674581.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O64652 O64652
8207	21289	34811	2.07	0.0E+00	AA397551.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O64652 O64652
							F17K2.26 PROTEIN;
							F17K2.26 PROTEIN;
							z81b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8209	21291	34812	0.85	0.0E+00	AW387131.1	EST_HUMAN	MRO-ST0031-061099-003-at11 ST0031 Homo sapiens cDNA
8212	21294		0.84	0.0E+00	AB020089.1	NT	Homo sapiens mRNA for KIAA0884 protein, partial cds
8213	21295	34814	0.15	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
8218	21298	34818	0.88	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8216	21298	34819	0.88	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8231	21313	34833	0.59	0.0E+00	7687276	NT	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
8233	21315	34835	0.84	0.0E+00	W95278.1	EST_HUMAN	z605001.1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:358081 5'
8233	21315	34836	0.84	0.0E+00	W95278.1	EST_HUMAN	z605001.1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:358081 5'
8235	21317		4.11	0.0E+00	BF673099.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
8239	21321		0.93	0.0E+00	AU134114.1	EST_HUMAN	AU134114 OVARG1 Homo sapiens cDNA clone OVARG1001298 5'
8253	21335	34853	0.96	0.0E+00	BF526534.1	EST_HUMAN	602069832F1 NCL_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4212127 5'
8253	21335	34854	0.95	0.0E+00	BF525534.1	EST_HUMAN	602069832F1 NCL_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4212127 5'
8285	21367	34886	1.35	0.0E+00	AL120124.1	EST_HUMAN	DKFZp781P092.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781P092 5'
8285	21367	34887	1.35	0.0E+00	AL120124.1	EST_HUMAN	DKFZp781P092.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781P092 5'
8328	21410		1.16	0.0E+00	BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3887773 5'
8351	21432	34856	1.27	0.0E+00	AW500549.1	EST_HUMAN	UI-HF-BN0-ek-F01-0-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5'
8359	21440	34882	14.12	0.0E+00	AW157233.1	EST_HUMAN	TR:060483 O60483 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
8378	21457	34981	0.68	0.0E+00	AW072395.1	EST_HUMAN	xa07012.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567639 3' similar to contains element: OFR repetitive element 1;
8394	21475	35002	1.11	0.0E+00	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8397	21478	35005	0.57	0.0E+00	W01616.1	EST_HUMAN	za36405.1 Soares_fetal_liver_spleen_1N1S Homo sapiens cDNA clone IMAGE:204633 5'
8399	21480	35007	1.3	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926988 5'
8399	21480	35008	1.3	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926988 5'
8411	21492	35022	1.13	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8431	21512	35043	0.48	0.0E+00	D45032.1	NT	Human DNA for cardiolipin, exon 5
8450	21531	35060	0.53	0.0E+00	AJ367350.1	EST_HUMAN	q96512.x1 NCL_CGAP_UJ2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN.
8462	21543	35073	2.23	0.0E+00	BE674157.1	EST_HUMAN	7u76a04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O96793 O96793 STAUFEN PROTEIN.
8464	21545	35075	1.96	0.0E+00	AJ855871.1	EST_HUMAN	w60010.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR;
8477	21558	35091	1.47	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'

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8477	21558	35092	1.47	0.0E+00	BE563650.1	EST_HUMAN	601334730F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888655 5'
8485	21566	35102	1.72	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8485	21566	35103	1.72	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8487	21568	35105	0.84	0.0E+00	AA403192.1	EST_HUMAN	z66602.1 Soares total fetus N62HF8_9w Homo sapiens cDNA clone IMAGE:788619 5' similar to TR:G1304132 G1304132 TPRD.;
8487	21568	35106	0.84	0.0E+00	AA403192.1	EST_HUMAN	z66602.1 Soares total fetus N62HF8_9w Homo sapiens cDNA clone IMAGE:788619 5' similar to TR:G1304132 G1304132 TPRD.;
8528	21609		3.61	0.0E+00	AA398511.1	EST_HUMAN	z173408.s1 Soares testis N1HT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);
8537	21618	35155	0.5	0.0E+00	BE337593.1	EST_HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sapiens cDNA
8538	21619	35156	1.34	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8538	21619	35157	1.34	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8557	21638	35176	1.24	0.0E+00	BE612886.1	EST_HUMAN	601452412F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3856179 5'
8557	21638	35177	1.24	0.0E+00	BE612886.1	EST_HUMAN	601452412F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3856179 5'
8572	21653	35194	1.16	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
8572	21653	35195	1.16	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
8581	21682	35202	0.93	0.0E+00	AI884477.1	EST_HUMAN	wm33a11.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.;
8588	21689	35208	0.71	0.0E+00	AA502294.1	EST_HUMAN	ne25d10.st NCI CGAP Cc3 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1136434 G1136434 KIAA0187 PROTEIN.;
8593	21674		0.66	0.0E+00	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
8601	21682	35220	0.52	0.0E+00	AI580780.1	EST_HUMAN	1a04f11.x1 Soares pregnant_uterus N6HPU Homo sapiens cDNA clone IMAGE:2043117 3'
8604	21685		2.08	0.0E+00	BE990797.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
8630	21710	35246	0.61	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8630	21710	35247	0.61	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8631	21711	35248	2.13	0.0E+00	4756895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8631	21711	35249	2.13	0.0E+00	4756895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8635	21715	35252	0.61	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8635	21715	35253	0.61	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8697	21777	35309	0.46	0.0E+00	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8704	21784	35317	0.7	0.0E+00	AJ251760.1	NT	Homo sapiens NESP95, GNAS1 antisense (partial) and XLalphas (partial) genes
8709	21789	35323	2.81	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8709	21789	35324	2.81	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8709	21789	35325	2.81	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8723	21803	35339	0.76	0.0E+00	U82979.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8765	21844	35385	0.81	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8765	21844	35385	0.81	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8768	21847	35388	0.67	0.0E+00	AU131671.1	EST_HUMAN	AU131671 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
8784	21863	35408	0.64	0.0E+00	11426672	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8788	21867		1.35	0.0E+00	AW513513.1	EST_HUMAN	xx46601.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4
8790	21869		0.54	0.0E+00	BE783232.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
8791	21870	35409	1.62	0.0E+00	D52850.1	EST_HUMAN	601472166F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874912 5'
8823	21902	35442	4.15	0.0E+00	BE378495.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02
8828	21908	35446	2.15	0.0E+00	AA470545.1	EST_HUMAN	5'
8831	21910		1.35	0.0E+00	BF313946.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8838	21917	35455	0.54	0.0E+00	11424387	NT	z02604.t1 Scores ovary tumor NihOT Homo sapiens cDNA clone IMAGE:724082 5'
8843	21922	35460	1.41	0.0E+00	AW139673.1	EST_HUMAN	60190057F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128741 5'
8843	21922	35461	1.41	0.0E+00	AW139673.1	EST_HUMAN	(LILRB3), mRNA
8879	21958	35493	2.16	0.0E+00	BE260272.1	EST_HUMAN	UI-H-B1t-adr-e-12-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8884	21963	35497	2.91	0.0E+00	BF700165.1	EST_HUMAN	UI-H-B1t-adr-e-12-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8884	21963	35498	2.91	0.0E+00	BF700165.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'
8884	21963	35499	2.91	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8923	22002	35541	0.84	0.0E+00	AL449770.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8930	22009	35547	3.69	0.0E+00	AA962527.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Starvades GS) Homo sapiens cDNA
8936	22015	35555	3.41	0.0E+00	10947037	NT	α80g02.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S
8936	22015	35556	3.41	0.0E+00	10947037	NT	RIBOSOMAL PROTEIN L7A (HUMAN);
8961	22040	35583	1.65	0.0E+00	Y11107.3	NT	Homo sapiens ankryrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8963	22042	35585	1.09	0.0E+00	BE278917.1	EST_HUMAN	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8973	22052		2.86	0.0E+00	AV718377.1	EST_HUMAN	601156330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
8980	22059	35600	3.12	0.0E+00	AW337277.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAT1 5'
8986	22065	35605	1.59	0.0E+00	AU124051.1	EST_HUMAN	xx73007.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587
9063	22142	35687	0.98	0.0E+00	AU140704.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
9073	22152	35696	0.64	0.0E+00	AB007923.1	NT	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
							AU140704 PLACE4 Homo sapiens cDNA clone PLACE400089 5'
							Homo sapiens mRNA for KIAA0454 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9078	22157	35700	0.88	0.0E+00	R17132.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
9078	22157	35701	0.88	0.0E+00	R17132.1	EST_HUMAN	yg09e09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
9082	22161	35703	4.78	0.0E+00	AW592233.1	EST_HUMAN	h48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
9082	22161	35704	4.78	0.0E+00	AW592233.1	EST_HUMAN	h48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
9129	22208	35751	0.93	0.0E+00	AW714764.1	EST_HUMAN	AV714764.DCB Homo sapiens cDNA clone DCBAAU06 5'
9145	22224	35766	3.17	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9145	22224	35767	3.17	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9151	22229	35773	1.32	0.0E+00	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
9153	22231	35776	2.12	0.0E+00	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9161	22239		0.61	0.0E+00	BF058289.1	EST_HUMAN	7K29b03.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476692 3' similar to TR:O36448 O36448 S GAG:
9191	22269	35608	2.79	0.0E+00	11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA
9201	22279	35818	1.59	0.0E+00	K01241.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
9209	22287	35828	5.28	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9209	22287	35829	5.28	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9214	22292	35835	1.84	0.0E+00	AV660739.1	EST_HUMAN	AV660739 GLC Homo sapiens cDNA clone GLCGKG12 3'
9220	22298	35841	3.41	0.0E+00	7706638	NT	Homo sapiens polycystin-L (PKDL), mRNA
9225	22303	35846	0.6	0.0E+00	BE79326.1	EST_HUMAN	801588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
9246	22323	35867	4.22	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9246	22323	35868	4.22	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9256	22333	35883	0.6	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
9258	22333	35884	0.6	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
9259	22336		0.54	0.0E+00	M39866.1	NT	Human polymorphic loci in Xq28
9261	22338	35888	1.65	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9279	22355	35905	0.53	0.0E+00	AU127096.1	EST_HUMAN	AU127096 NT2RP2 Homo sapiens cDNA clone NT2RP2000579 5'
9283	22359	35909	0.83	0.0E+00	A1081395.1	EST_HUMAN	an29e04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700084 3'
9288	22364	35913					wq34a12x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MGB3_HUMAN
9293	22369	35919	5.69	0.0E+00	9256595	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3;
9303	22379	35930	2.73	0.0E+00	AW85631.1	EST_HUMAN	Homo sapiens protocadherin alpha 8 (PCDHA8), mRNA
9313	22389	35940	1.32	0.0E+00	9635487	NT	Homo sapiens MAGe resequences, MAGe Homo sapiens cDNA
9328	22404	35956	0.84	0.0E+00	AU142862.1	EST_HUMAN	Human endogenous retrovirus, complete genome
9344	22420	35974	1.04	0.0E+00	11438895	NT	AU142862 Y78AA1 Homo sapiens cDNA clone Y78AA1000578 5'

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9345	22421		0.76	0.0E+00	BE410788.1	EST_HUMAN	601301878F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9359	22434	35993	1.32	0.0E+00	BF002024.1	EST_HUMAN	7g97h12.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q9UH62
9373	22448	36009	1.62	0.0E+00	AB011150.1	NT	Q9UH62 HYPOTHETICAL 42.5 KD PROTEIN. ;
9374	22449	36010	3.42	0.0E+00	BE794823.1	EST_HUMAN	Homo sapiens mRNA for KIAA0378 protein, partial cds
9378	22453	36016	0.47	0.0E+00	BE810282.1	EST_HUMAN	601989294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
9378	22453	36016	0.47	0.0E+00	BE810282.1	EST_HUMAN	RC3-PT0151-290800-011-c05 PT0151 Homo sapiens cDNA
9381	22456	36019	0.97	0.0E+00	AU136229.1	EST_HUMAN	RC3-PT0151-290800-011-c05 PT0151 Homo sapiens cDNA
9386	22461	36024	1.19	0.0E+00	BE883843.1	EST_HUMAN	AU136229 PLACE1 Homo sapiens cDNA clone IMAGE:1003804 5'
9386	22461	36025	1.19	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3911986 5'
9403	22477	36040	0.67	0.0E+00	AB011168.1	NT	601510247F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3911986 5'
9407	22481	36044	1.43	0.0E+00	AA344601.1	EST_HUMAN	Homo sapiens mRNA for KIAA0594 protein, partial cds
9407	22481	36045	1.43	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
9464	22521	36083	0.98	0.0E+00	AW673469.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
9464	22521	36084	0.96	0.0E+00	AW673469.1	EST_HUMAN	ba54408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900397 5' similar to TR:O60275 O60275
9498	22554	36116	0.99	0.0E+00	BE207083.1	EST_HUMAN	KIAA0522 PROTEIN ;
9498	22554	36117	0.99	0.0E+00	BE207083.1	EST_HUMAN	ba54408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2823873 5' similar to TR:O60275 O60275
9509	22775	36346	1.95	0.0E+00	BF348013.1	EST_HUMAN	KIAA0522 PROTEIN ;
9545	22610	36178	3.1	0.0E+00	BE712516.1	EST_HUMAN	ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gbl:35049 Mus musculus
9577	22719	36287	0.49	0.0E+00	BF034377.1	EST_HUMAN	Bcl-xL mRNA, complete cds (MOUSE);
9577	22719	36288	0.49	0.0E+00	BF034377.1	EST_HUMAN	ba0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:4158300 5'
9583	22725	36295	0.56	0.0E+00	AI908351.1	EST_HUMAN	QV2-HT0668-250700-282-508 HT0698 Homo sapiens cDNA
9586	22728	36297	0.77	0.0E+00	5803069	NT	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3656035 5'
9595	22728	36298	0.77	0.0E+00	5803069	NT	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3656035 5'
9596	22651	36223	0.85	0.0E+00	AL042278.1	EST_HUMAN	RC-BT108-040399-032 BT108 Homo sapiens cDNA
9631	22696	36257	1.3	0.0E+00	AI088043.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5
9638	21081	34592	0.87	0.0E+00	BF306802.1	EST_HUMAN	(LILRB5), mRNA
							Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5
							(LILRB5), mRNA
							DKFZp434L0120_r1_434 (synonym: hte3) Homo sapiens cDNA clone DKFZp434L0120 5'
							ow000101.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to
							TR:Q14677 Q14677 KIAA0171 PROTEIN. ;
							601892245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138066 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9640	21083	34595	2.32	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9640	21083	34596	2.32	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9642	21085	34599	6.52	0.0E+00	A1280909.1	EST_HUMAN	qm09a06.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9642	21085	34600	6.52	0.0E+00	A1280909.1	EST_HUMAN	qm09a06.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9643	21086	34601	2.15	0.0E+00	AW093836.1	EST_HUMAN	EST368026 MAGC resequenced, MAGC Homo sapiens cDNA
9670	22632	36201	3.95	0.0E+00	AF153466.1	NT	Homo sapiens polyoma-like kidney disease 2-like protein (PKD2L) gene, exon 8
9673	22635	36205	0.69	0.0E+00	BE885123.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9673	22635	36206	0.69	0.0E+00	BE885123.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9683	22732	36305	5.87	0.0E+00	BE255829.1	EST_HUMAN	601109842F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
9686	22735	36305	1.44	0.0E+00	BE781392.1	EST_HUMAN	601468828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9686	22735	36306	1.44	0.0E+00	BE781392.1	EST_HUMAN	601468828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9688	22737	36307	5.48	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072
9697	22746	36315	0.58	0.0E+00	D87675.1	NT	60S RIBOSOMAL PROTEIN L7A (HUMAN);
9709	22758	36329	3.41	0.0E+00	BE263191.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9727	22792	36364	4.49	0.0E+00	C08158.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3180477 5'
9727	22792	36365	4.49	0.0E+00	C08158.1	EST_HUMAN	C08158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9729	22784	36368	3.38	0.0E+00	BE746215.1	EST_HUMAN	C08158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9739	22804	36376	2.03	0.0E+00	11437282	NT	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9739	22804	36379	2.03	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9739	22804	36380	2.03	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9759	22897	36265	1.91	0.0E+00	BE900549.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9776	22816	36394	1.5	0.0E+00	AV701829	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958238 5'
9788	22828	36405	2.55	0.0E+00	AF019084.1	NT	AV701829 ADB Homo sapiens cDNA clone ADBBYH01 5'
9788	22828	36406	2.55	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9821	22861	36442	1.13	0.0E+00	BE082977.1	EST_HUMAN	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9841	22881	36464	1.72	0.0E+00	AW500293.1	EST_HUMAN	RC2-BT0842-130300-017-g01 BT0842 Homo sapiens cDNA
9841	22881	36465	1.72	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BND-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9850	22890	36470	1.87	0.0E+00	AF029303.1	NT	UI-HF-BND-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9850	22890	36471	1.87	0.0E+00	AF029303.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9852	22892	36472	0.52	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9852	22892	36473	0.52	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9851	22801	36485	0.63	0.0E+00	W56629.1	EST_HUMAN	z16a11.1 Scarsa_fetal Heart_NBHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9851	22901	36488	0.63	0.0E+00	W56629.1	EST_HUMAN	z16a11.1 Scarsa_fetal Heart_NBHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9874	22914	36489	0.46	0.0E+00	AF208054.1	NT	Homo sapiens non-inhibitory killer-cell Ig-like receptor KIR (KIR2DS5) mRNA, complete cds
9875	22915	36500	1.04	0.0E+00	AB036356.1	NT	Homo sapiens mRNA for neuraxin I-alpha protein, complete cds
9879	22919	36501	0.64	0.0E+00	AH24780.1	EST_HUMAN	ant6a11.1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'
9881	22921	36505	3	0.0E+00	AW500528.1	EST_HUMAN	ULHF-BNO-ek-c-07-0.U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
9825	22955	38554	2.65	0.0E+00	AF009698.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
9953	22992	38585	2.69	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9953	22992	38586	2.69	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9956	22895	36581	2.72	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888680 5'
9976	23015	36808	1.26	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301189-043-h11 CT0311 Homo sapiens cDNA
9997	23035	36827	0.88	0.0E+00	11436432	NT	Homo sapiens multimerin (MMPN), mRNA
9998	23038	36828	0.52	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
10007	23045	36838	0.91	0.0E+00	BE206710.1	EST_HUMAN	b528c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2964000 3'
10024	23092	36858	4.48	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10024	23092	36859	4.49	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10033	23071	36671	0.95	0.0E+00	AW500336.1	EST_HUMAN	ULHF-BPOp-ai-4-05-0.U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
10039	23077	36677	13.26	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10039	23077	36678	13.26	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10052	23090	36692	1.56	0.0E+00	7682067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
10069	23107	36710	1.54	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
10074	23112	36716	0.57	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2416.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2416 5'
10084	23122	36723	2.32	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10085	23123	36724	2.16	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
10112	23130	36751	2.84	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
10112	23130	36752	2.84	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
10128	23168	36785	1.13	0.0E+00	BF092898.1	EST_HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
10180	23197	36793	2.75	0.0E+00	BE280793.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138788 5'
10169	23206	36799	6.57	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10169	23208	36800	6.57	0.0E+00	BE388700.1	EST_HUMAN	601285331F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813045 5'
10178	23215	36806	0.87	0.0E+00	AW236269.1	EST_HUMAN	xn72501.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:202152_cds1 L-
10179	23216	36807	0.84	0.0E+00	AA341305.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10188	23225	36819	0.59	0.0E+00	11427235	NT	EST48740 Fetal Kidney II Homo sapiens cDNA 5' end
10208	23244	36834	0.94	0.0E+00	AW954113.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
10222	23259	36845	5.99	0.0E+00	AU143673.1	EST_HUMAN	EST376186 MAGC resequences, MAGH Homo sapiens cDNA
10222	23259	36845	5.99	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y78AA1 Homo sapiens cDNA clone Y78AA1002307 5'
10222	23259	36845	5.99	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y78AA1 Homo sapiens cDNA clone Y78AA1002307 5'
10225	23261	36849	3.31	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10228	23263	36851	2.75	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10228	23263	36852	2.76	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10231	23266	36894	3.07	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10261	23296	36895	3.07	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10277	23312	36909	2	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7importin7 and partial ZNF143 gene
10277	23312	36910	2	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7importin7 and partial ZNF143 gene
10282	23317	36917	0.73	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKGC Homo sapiens cDNA clone GKCDXA07 5'
10282	23317	36918	0.73	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKGC Homo sapiens cDNA clone GKCDXA07 5'
10288	23323	36925	0.72	0.0E+00	AF072408.1	EST_HUMAN	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10290	23325	36928	2.42	0.0E+00	AA196387.1	EST_HUMAN	zp97H11.1 Stratiogene muscle 837208 Homo sapiens cDNA clone IMAGE:628197 5'
10317	23352	36959	0.76	0.0E+00	AA131248.1	EST_HUMAN	231101.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10317	23352	36960	0.76	0.0E+00	AA131248.1	EST_HUMAN	231101.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10359	23394	37005	1.91	0.0E+00	AF178303.1	NT	Homo sapiens KLF4 (KLF4) mRNA, complete cds
10404	23439	37046	0.99	0.0E+00	BE880558.1	EST_HUMAN	601497665F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893657 5'
10417	23462	37057	5.34	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10417	23462	37058	5.34	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10422	23467	37062	0.8	0.0E+00	AU127403.1	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10432	23467	37073	0.89	0.0E+00	BE968511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:38930177 5'
10432	23467	37074	0.89	0.0E+00	BE968511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:38930177 5'
10450	23485	37094	0.48	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10460	23495	37107	0.91	0.0E+00	AA311624.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10461	23498	37108	0.55	0.0E+00	4758827	NT	Homo sapiens neurxin III (NRXN3) mRNA
10473	23508	37121	0.64	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10475	23510	37123	0.77	0.0E+00	11560161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10486	23521	37130	1.56	0.0E+00	AB029280.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10487	23522	37131	0.5	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10487	23522	37132	0.5	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10494	23528	37137	5.8	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10494	23529	37138	5.8	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10502	23537	37147	0.77	0.0E+00	AA704457.1	EST_HUMAN	219b06.s1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gb:M14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10504	23539	37148	1.08	0.0E+00	M22921.1	NT	Human beta 1,4-galactosyl-transferase mRNA, complete cds
10506	23541	37151	4.81	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bln64 Homo sapiens cDNA clone IMAGE:4184939 5'
10506	23541	37152	4.81	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bln64 Homo sapiens cDNA clone IMAGE:4184939 5'
10530	23565	37172	0.59	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10530	23565	37173	0.59	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10595	23630	37237	1.07	0.0E+00	AI631818.1	EST_HUMAN	wa38603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10595	23630	37238	1.07	0.0E+00	AI631818.1	EST_HUMAN	Q61204 NOTCH2-LIKE ;
10610	23644	37252	1.64	0.0E+00	T03078.1	EST_HUMAN	FB23A4 Fetal brain, Stratiagene Homo sapiens cDNA clone FB23A4 3' end
10638	23672	37282	0.67	0.0E+00	AU122429.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002368 5'
10644	23678	37288	0.48	0.0E+00	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10668	23702	37312	2.22	0.0E+00	BF436218.1	EST_HUMAN	na45912.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3285271 3'
10669	23703		1.71	0.0E+00	AV654765.1	EST_HUMAN	AV654765 GIC Homo sapiens cDNA clone GLOOZC07 3'
10689	23722	37328	3.08	0.0E+00	AW517960.1	EST_HUMAN	xt74501.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:MA9086 MOESIN (HUMAN);
10693	23726	37332	2.88	0.0E+00	BE548213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10709	23742	37348	0.82	0.0E+00	11436005	NT	Homo sapiens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
10735	23768	37378	0.52	0.0E+00	X89893.1	NT	H. sapiens mRNA for NK receptor (183 Act)
10736	23769	37379	3.35	0.0E+00	BE781742.1	EST_HUMAN	601487419F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870700 5'
10758	23791	37409	2.32	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0842:150200-012-003 BT0842 Homo sapiens cDNA
10758	23791	37410	2.32	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0842:150200-012-003 BT0842 Homo sapiens cDNA
10764	23797	37417	0.67	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10772	23805	37428	0.77	0.0E+00	AI656890.1	EST_HUMAN	tt54e07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2244612 3'
10779	23812	37435	9.15	0.0E+00	BE743215.1	EST_HUMAN	601573995F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10779	23812	37436	9.15	0.0E+00	BE743215.1	EST_HUMAN	601573995F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10784	23817	37439	0.63	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3845956 3'
10784	23817	37440	0.63	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3845956 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10786	23819	37442	0.46	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10786	23819	37443	0.46	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10809	23842	37465	0.51	0.0E+00	H39805.1	EST_HUMAN	yp01a10.r1 Soares breast 3NHBBat Homo sapiens cDNA clone IMAGE:186138 5'
10835	23868	37491	0.54	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10846	23879	37499	0.59	0.0E+00	BE392276.1	EST_HUMAN	601308167F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628128 5'
10863	23886	37518	0.52	0.0E+00	AU126696.1	EST_HUMAN	AU125956 NT2RM4 Homo sapiens cDNA clone NT2RM4002636 5'
10872	23957	37586	1.84	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAG005 5'
10872	23957	37587	1.84	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAG005 5'
10874	23959		2.55	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10882	23966	37595	5.5	0.0E+00	AW963583.1	EST_HUMAN	EST375636 IMAGE resequences, MAGH Homo sapiens cDNA
10885	23979	37610	2.52	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10885	23979	37611	2.52	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
							wy61f09.x1 Soares NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to
10898	23982	37614	1.7	0.0E+00	AW057621.1	EST_HUMAN	TRQ60566 Q60566 VDX;
10906	23989	37621	8.59	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project-TCAA Homo sapiens cDNA clone TCAAP0917
10907	23990	37622	2.72	0.0E+00	AI652239.1	EST_HUMAN	w528a12.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element
10907	23990	37623	2.72	0.0E+00	AI652239.1	EST_HUMAN	MSR1 MSR1 repetitive element ;
10912	23995	37628	1.48	0.0E+00	BF306642.1	EST_HUMAN	MSR1 MSR1 repetitive element ;
10913	23996	37630	1.74	0.0E+00	BE872608.1	EST_HUMAN	601451502F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122649 5'
10913	23996	37630	1.74	0.0E+00	BE872608.1	EST_HUMAN	601451502F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3855289 5'
10920	24003	37637	3.59	0.0E+00	11545911	NT	601451502F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:3855289 5'
10920	24003	37638	3.59	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10936	24018	37651	1.52	0.0E+00	AW404795.1	EST_HUMAN	Homo sapiens NOD2 protein (NOD2), mRNA
10940	24022	37656	2.85	0.0E+00	11424828	NT	U1HF-BL0-ecm-d-04-0-01.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
10941	24023	37657	8.39	0.0E+00	4504536	NT	Homo sapiens hypodermal protein FLJ20076 (FLJ20076), mRNA
10941	24023	37658	8.39	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10942	24024	37659	2.68	0.0E+00	AI991827.1	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10946	24028	37665	3.22	0.0E+00	BE982109.1	EST_HUMAN	wu32b08.x1 Soares Diethylstilbestrol (DES) receptor 1E (HTR1E) mRNA
10950	24032	37667	6.12	0.0E+00	BE891630.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
10952	24034	37668	1.55	0.0E+00	8523639	NT	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'
10952	24034	37669	1.55	0.0E+00	8523639	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA

Single Exon Probes Expressed in Placenta

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10965	24046	37680	22.14	0.0E+00	BE030304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10968	19087	32388	1.85	0.0E+00	AA196905.1	EST_HUMAN	z96b11.1 r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:927933 5' similar to gb:X03740
10969	24089	37703	4.49	0.0E+00	BE793498.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10998	24077	37710	2.4	0.0E+00	BE729708.1	EST_HUMAN	601668929F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943016 5'
10998	24077	37711	2.4	0.0E+00	BE729708.1	EST_HUMAN	601662864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3932575 5'
10999	24078	37712	11.66	0.0E+00	AV727382.1	EST_HUMAN	601662864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3932575 5'
10999	24078	37713	11.66	0.0E+00	AV727382.1	EST_HUMAN	AV727382 HTC Homo sapiens cDNA clone HTCAQH06 5'
11003	24082	37718	1.6	0.0E+00	R17132.1	EST_HUMAN	y90909.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
11003	24082	37719	1.6	0.0E+00	R17132.1	EST_HUMAN	y90909.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
11009	24088		2.62	0.0E+00	AW139414.1	EST_HUMAN	UI-H-B11-adj-q-06-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717674 3'
11014	24093	37732	11.61	0.0E+00	AW516058.1	EST_HUMAN	x04g10.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S
11020	24089	37737	4.44	0.0E+00	AU135741.1	EST_HUMAN	RIBOSOMAL PROTEIN S16 (HUMAN);
11026	24105	37741	2.56	0.0E+00	AW593333.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone PLAGE1002794 5'
11026	24105	37742	2.56	0.0E+00	AW593333.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11026	24105	37743	2.56	0.0E+00	AW593333.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11028	24107	37744	1.67	0.0E+00	F13069.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11029	24108	37745	2.78	0.0E+00	F13069.1	EST_HUMAN	H.sapiens mRNA for H1 histamine receptor
11037	24116	37760	2.35	0.0E+00	D10083.1	NT	HSC3C031 normalized infant brain cDNA Homo sapiens cDNA clone c-3lc03
11054	24131	37767	1.71	0.0E+00	AW338094.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
11055	24132	37768	3.75	0.0E+00	AW451230.1	EST_HUMAN	xw66801.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17116 IG MJU
11055	24132	37769	3.75	0.0E+00	AW451230.1	EST_HUMAN	CHAIN C REGION (HUMAN);
11058	13443		9.52	0.0E+00	4506632	NT	UI-H-B13-adj-a-01-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11060	24136	37771	1.79	0.0E+00	AB014567.1	NT	UI-H-B13-adj-a-01-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11073	24148	37787	1.92	0.0E+00	BE284449.1	EST_HUMAN	Homo sapiens ribosomal protein L31 (RPL31) mRNA
11087	24161	37797	1.47	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0687 protein, partial cds
11092	24166	37803	1.39	0.0E+00	AA377505.1	EST_HUMAN	601119245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
11106	24178	37813	3.3	0.0E+00	BE792155.1	EST_HUMAN	Homo sapiens mRNA for KIAA0648 protein, partial cds
11107	24178		76.9	0.0E+00	BF694061.1	EST_HUMAN	EST190347 Synovial sarcoma Homo sapiens cDNA 5' end similar to LERK-2, placenta
							601592046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3966539 5'
							602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11108	24180	37814	1.45	0.0E+00	BE269288.1	EST_HUMAN	601186342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544259 5'
11110	24182	37816	7.93	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
11111	24183		1.81	0.0E+00	AW236269.1	EST_HUMAN	xn72601.x1 NCI_CGAP_QML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cde1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
11116	24188	37820	5.71	0.0E+00	AI149809.1	EST_HUMAN	q43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
11116	24188	37821	5.71	0.0E+00	AI149809.1	EST_HUMAN	q43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
11117	24189	37822	2.93	0.0E+00	AW391937.1	EST_HUMAN	QV4-ST0234-121199-032-508 ST0234 Homo sapiens cDNA
11127	24189		11.83	0.0E+00	AU116808.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
11130	24202	37827	9.87	0.0E+00	11424728	NT	Homo sapiens insulin receptor (INSR), mRNA
11132	24204	37828	2.14	0.0E+00	AI357350.1	EST_HUMAN	q495c12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN. ;
11132	24204	37829	2.14	0.0E+00	AI357350.1	EST_HUMAN	q495c12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN. ;
11137	24209	37835	1.63	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184979 5'
11139	24211	37837	13.91	0.0E+00	BE281209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
11144	24216	37843	2.19	0.0E+00	AB028040.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
11147	24219	37846	1.51	0.0E+00	AB007932.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
11151	24222	37850	3.89	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
11155	24226	37855	2.43	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-407 FT0134 Homo sapiens cDNA
11155	24226	37856	2.43	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-407 FT0134 Homo sapiens cDNA
11177	24246	37879	51.22	0.0E+00	AA740782.1	EST_HUMAN	0632607.31 NCI_CGAP_K105 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element ;
11186	24255	37890	2.81	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
11199	24268	37903	1.71	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536867 5'
11199	24268	37904	1.71	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536867 5'
11201	24270	37906	4.9	0.0E+00	C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNeKamura) Homo sapiens cDNA clone 3NH4817
11208	24277	37914	2.1	0.0E+00	AA746375.1	EST_HUMAN	oa66h01.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11208	24277	37915	2.1	0.0E+00	AA746375.1	EST_HUMAN	oa66h01.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11218	24287	37926	2.69	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBC026
11218	24287	37927	2.69	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBC026
11221	24290	37930	1.76	0.0E+00	BF353523.1	EST_HUMAN	QV2-HT0696-020800-295-307 HT0698 Homo sapiens cDNA
11222	24291	37931	6.5	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761j2116.11 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761j2116 5'
11234	24303	37940	1.86	0.0E+00	BE562822.1	EST_HUMAN	601336530F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690390 5'
11236	24305	37942	6.05	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11250	24319	37959	1.75	0.0E+00	AV693696.1	EST_HUMAN	AV693696 GKX Homo sapiens cDNA clone GKCCNC03 5'
11260	24329	37969	2.97	0.0E+00	BF366553.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
11280	24354	37984	2.4	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0846-060500-002-E06 HT0846 Homo sapiens cDNA
11288	24354	37985	2.4	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0845-000500-002-E05 HT0845 Homo sapiens cDNA
11290	24356		1.51	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAD08 5'
11305	24370	38011	3.02	0.0E+00	BE896423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
11311	24375	38019	1.83	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BNO-akg-d-02-0-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
11311	24375	38020	1.83	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BNO-akg-d-02-0-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:65553 M.musculus mRNA for poly(A) binding protein (MOUSE);
11314	24378	38023	2.49	0.0E+00	BE018293.1	EST_HUMAN	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11345	26869	38058	1.45	0.0E+00	AW387766.1	EST_HUMAN	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11345	26869	38059	1.45	0.0E+00	AW387766.1	EST_HUMAN	MR4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11363	24415	38070	3.23	0.0E+00	BE897953.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924403 5'
11355	24417	38073	2.24	0.0E+00	AH59545.1	EST_HUMAN	ac086111.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11355	24417	38074	2.24	0.0E+00	AH59545.1	EST_HUMAN	ac086111.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11368	24430	38087	1.89	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: htas3) Homo sapiens cDNA clone DKFZp434L0120 5'
11390	24451	38112	1.37	0.0E+00	A073917.1	EST_HUMAN	ou61d04.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
11390	24451	38113	1.37	0.0E+00	A073917.1	EST_HUMAN	ou61d04.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
11390	24451	38114	1.37	0.0E+00	A073917.1	EST_HUMAN	ou61d04.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
11404	24465	38130	3.8	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11405	24466	38131	24.41	0.0E+00	BF206931.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
11411	24472	38137	11.85	0.0E+00	AW207734.1	EST_HUMAN	UI-H-BI2-sge-h-01-0-JL1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11416	24477	38141	3.93	0.0E+00	AB016260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11416	24477	38142	3.93	0.0E+00	AB016260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11418	24479	38144	2.63	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B 65KDA-ASSOCIATED PROTEIN ;

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11418	24479	38145		2.83	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-
11428	24480	38155		2.37	11526408	NT	58KDA-ASSOCIATED PROTEIN ; Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
11438	24489	38168		1.88	A075915.1	EST_HUMAN	ov46g07.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640412 3' similar to TR:Q14507
11445	24508	38172		1.73	11024711	NT	Q14507 EPIDIDYMIS-SPECIFIC GENE PRODUCT, ALPHA ; Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11448	24509	38176		1.98	BF093687.1	EST_HUMAN	QV0-JM0091-120900-385-b12 UM0091 Homo sapiens cDNA
11448	20710	34189		1.94	0.0E+00 L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11452	24512	38178		4.81	0.0E+00 SE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11452	24512	38179		4.61	0.0E+00 BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11475	24534	38204		1.66	0.0E+00 AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
11475	24534	38205		1.66	0.0E+00 AW673469.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
11480	24549	38223		4.84	0.0E+00 BF507876.1	EST_HUMAN	U1H-B14-ack-b-10-U1.s1 NCI_GGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11490	24549	38224		4.84	0.0E+00 BF507876.1	EST_HUMAN	U1H-B14-ack-b-10-U1.s1 NCI_GGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11488	24554	38229		4.65	0.0E+00 AU135170.1	EST_HUMAN	AU135170 PLAGE1 Homo sapiens cDNA clone PLACE1001381 5'
11501	24559	38234		2.07	0.0E+00 BF576138.1	EST_HUMAN	802132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11501	24559	38235		2.07	0.0E+00 BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11503	24561	38238		4.06	0.0E+00 BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11503	24561	38239		4.06	0.0E+00 BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11511	24569	38246		1.61	0.0E+00 D87982.1	NT	Human mRNA for KIAA0241 gene, partial cds
11518	24573			3.87	0.0E+00 BF240636.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089710 5'
11531	24587	38262		1.81	0.0E+00 AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11531	24587	38263		1.81	0.0E+00 AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11536	24591	38266		3.09	0.0E+00	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11536	24591	38267		3.09	0.0E+00	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11563	24601	38287		6.13	0.0E+00	NT	Homo sapiens eukaryotic translation initiation factor 6A (EIF5A) mRNA
11560	24615	38294		2.08	0.0E+00 BF576267.1	EST_HUMAN	802134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11562	24617	38297		3.53	0.0E+00 AW328173.1	EST_HUMAN	dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11567	24622			42.5	0.0E+00 M55093.1	NT	Human gamma actin-like pseudogene, complete cds
11571	24628	38305		1.75	0.0E+00 AI860968.1	EST_HUMAN	wf20e11.x1 Soares Dialectraef. cdor, NIHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
11574	24629	38307		3.37	0.0E+00 BF306996.1	EST_HUMAN	601898823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11874	24629	38308	3.37	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:412948 5'
11581	24635	38315	47.2	0.0E+00	BF362462.1	EST_HUMAN	QV2-NN0054-230800-333-604 NN0054 Homo sapiens cDNA
11601	24654	38338	2.32	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11601	24654	38339	2.32	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11608	24659		4.33	0.0E+00	BE897051.1	EST_HUMAN	601439603F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11607	24660		2.37	0.0E+00	4503786	NT	Homo sapiens fyn-related kinase (FRK) mRNA
11621	24672	38361	2.34	0.0E+00	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11623	24674		2.07	0.0E+00	BF207662.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11636	24718	38407	4.53	0.0E+00	BE206846.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN ;
11636	24716	38408	4.53	0.0E+00	BE206846.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN ;
11638	24718	38410	3.59	0.0E+00	AW763028.1	EST_HUMAN	QV0-CT0225-101299-071-06 CT0225 Homo sapiens cDNA
11643	24723		3.01	0.0E+00	AA558707.1	EST_HUMAN	ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11644	18590	31562	2.56	0.0E+00	AB34954.1	EST_HUMAN	wp06g08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
11645	24724	38416	7.51	0.0E+00	AW327895.1	EST_HUMAN	df02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11684	25870	38435	1.78	0.0E+00	AW292776.1	EST_HUMAN	UI-H-8W0-adj-07-0-UJ.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729509 3'
11671	23899	37622	1.93	0.0E+00	4758827	NT	Homo sapiens neurxin III (NRXN3) mRNA
11677	24076	38367	1.35	0.0E+00	BE284088.1	EST_HUMAN	601113003F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354600 5'
11680	24879	38369	1.79	0.0E+00	BE985909.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3886916 3'
11680	24879	38370	1.79	0.0E+00	BE866909.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3886916 3'
11681	24880	38371	3.81	0.0E+00	BE185656.1	EST_HUMAN	IL5-H10731-020500-077-05 HT0731 Homo sapiens cDNA
11682	24881		1.39	0.0E+00	BF513963.1	EST_HUMAN	UIH-BW1-amy-a-05-0-UJ.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071121 3'
11686	24893	38384	7.19	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11696	24893	38385	7.19	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11706	24703	38395	10.19	0.0E+00	AI923116.1	EST_HUMAN	wn83g03.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11708	24748	38440	4.47	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11708	24748	38441	4.47	0.0E+00	AA760913.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN ;
11713	24763	38447	2.21	0.0E+00	BE910546.1	EST_HUMAN	nz11c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
							Q13686 ALKB HOMOLOG PROTEIN ;
							801501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11723	23909	37533	11.64	0.0E+00	BE676347.1	EST_HUMAN	712712.x1 NCL_CGAP_C111 Homo sapiens cDNA clone IMAGE:3295919.3' similar to TR:Q00409 Q00409 CHECKPOINT SUPPRESSOR 1.;
11725	23911	37535	1.47	0.0E+00	AI683358.1	EST_HUMAN	b66009.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2274521.3' similar to gb:M55542 INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (HUMAN);
11727	23913	37537	3.13	0.0E+00	BE616666.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144.5'
11729	23915	37539	3.13	0.0E+00	BE616666.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144.5'
11734	23920	37545	1.59	0.0E+00	AV757420.1	EST_HUMAN	AV757420 BM Homo sapiens cDNA clone BMFAGH03.5'
11739	23925	37550	7.33	0.0E+00	AL037746.1	EST_HUMAN	DKFZp564C187_r1 964 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564C187.5'
11740	23926	37551	4.2	0.0E+00	U62769.1	NT	Human oxytocinase variant 2 mRNA, complete cds
11745	23931	37557	1.33	0.0E+00	BE883388.1	EST_HUMAN	601509139F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910833.5'
11766	24759	38454	1.75	0.0E+00	Y18880.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
11769	24761	38456	3.69	0.0E+00	L30891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11769	24761	38456	3.59	0.0E+00	L30891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11784	24774	38470	2.03	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1009077.5'
11787	24787	38485	6.43	0.0E+00	BE623317.1	EST_HUMAN	601441086F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270.5'
11833	24822	38512	17.72	0.0E+00	BE748899.1	EST_HUMAN	601672186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012.3'
11833	24822	38513	17.72	0.0E+00	BE748899.1	EST_HUMAN	601672186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012.3'
11845	24834	38527	4.58	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398.5'
11845	24834	38528	4.58	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398.5'
11848	24837	38531	2.7	0.0E+00	AW006022.1	EST_HUMAN	wz91h01.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566225.3' similar to WP:F53H10.2 CE11040 ZINC FINGER, C2H2 TYPE 1
11853	25671	38537	2.73	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCL_CGAP_C016 Homo sapiens cDNA clone IMAGE:3316699.3' similar to TR:Q13458 Q13458 TRIO.1
11864	24852	38548	1.32	0.0E+00	C06264.1	EST_HUMAN	C06264 Human pancreatic islet Homo sapiens cDNA similar to Insulin receptor
11868	24856		1.56	0.0E+00	BE727811.1	EST_HUMAN	601564180F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833730.5'
11872	24860	38555	2.36	0.0E+00	AI472010.1	EST_HUMAN	ib00a10.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2147802.3' similar to gb:M31681 PROLACTIN RECEPTOR TYPE 2 PRECURSOR (HUMAN);
11878	24866	38563	2.84	0.0E+00	AW387776.1	EST_HUMAN	MR4-S10118-261099-012-b03 S10118 Homo sapiens cDNA
11878	24866	38564	2.84	0.0E+00	AW387776.1	EST_HUMAN	MR4-S10118-261099-012-b03 S10118 Homo sapiens cDNA
11889	24877		1.8	0.0E+00	AW863777.1	EST_HUMAN	MR4-SN0010-310300-107-h03 SN0010 Homo sapiens cDNA
11901	24889	38589	3.67	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11901	24889	38590	3.67	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11907	24894	38596	4.39	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
11911	24898	38600	26.74	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623.5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11911	24898	38601	26.74	0.0E+00	BE379254.1	EST_HUMAN	601237681F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11917	24903	38606	4.87	0.0E+00	AW 500056.1	EST_HUMAN	UI-HF-BNO-ak-b-03-0-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077332 5'
11932	24918	38621	2.05	0.0E+00	BE794788.1	EST_HUMAN	601690588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11934	24920	38622	65.18	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11935	24921	38623	1.6	0.0E+00	ME0676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11941	24927	38629	1.38	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11941	24927	38629	1.38	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11946	24932	38635	1.58	0.0E+00	AF053543.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7
11953	24939	38642	7.29	0.0E+00	BE409993.1	EST_HUMAN	601269403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
11954	24940	38643	2.22	0.0E+00	BE148650.1	EST_HUMAN	MRO-HT0241-150500-011-02 HT0241 Homo sapiens cDNA Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11955	24941	38644	2.89	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11955	24941	38645	2.89	0.0E+00	AF223391.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11956	16785	31831	1.48	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11956	16785	31832	1.48	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11958	24943	38647	11.38	0.0E+00	BF681841.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286725 5'
11958	24943	38648	11.38	0.0E+00	BF681841.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286725 5'
11964	24949	38655	1.79	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000929 5'
11967	24952	38657	4.99	0.0E+00	BE903372.1	EST_HUMAN	601876357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3658935 5'
11983	24958	38671	1.56	0.0E+00	BF312552.1	EST_HUMAN	601897624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11983	24958	38672	1.56	0.0E+00	BF312552.1	EST_HUMAN	601897624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11986	24971	38675	3.4	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11986	24971	38676	3.4	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11998	24983		1.96	0.0E+00	BE906402.1	EST_HUMAN	601488553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900396 5'
12013	24987	38700	1.46	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12028	25872		8.57	0.0E+00	BF309120.1	EST_HUMAN	601800534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
12029	25012	38713	2.37	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-507 NN0025 Homo sapiens cDNA
12029	25012	38714	2.37	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-507 NN0025 Homo sapiens cDNA
12032	25015	38717	60.96	0.0E+00	BE267175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632868 5'
12046	25027	38733	1.42	0.0E+00	BE744311.1	EST_HUMAN	601576625F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12046	25027	38734	1.42	0.0E+00	BE744311.1	EST_HUMAN	601576625F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12054	25035	38741	2.02	0.0E+00	BE257612.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'
12054	25035	38742	2.02	0.0E+00	BE257612.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12084	25084	38770	2.85	0.0E+00	BE545535.1	EST_HUMAN	601070391F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456407 5'
12087	25087	38773	1.34	0.0E+00	AA399001.1	EST_HUMAN	283501.1 Soares testis NIH Homo sapiens cDNA clone IMAGE:728912 5' similar to SW:PM11_SCHPO
12088	25088	38774	1.59	0.0E+00	AU117974.1	EST_HUMAN	P40990 DNA METHYLTRANSFERASE PMT1 ;
12088	25088	38775	1.55	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002812 5'
12091	25071	38778	1.72	0.0E+00	BE780463.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002812 5'
12108	25088	38792	2.15	0.0E+00	AW259990.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12118	25098	38803	1.99	0.0E+00	AU132394.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12131	25111	38815	1.35	0.0E+00	BE292840.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12147	26185	31540	9.34	0.0E+00	BE312542.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12160	26005		3.02	0.0E+00	AL163246.2	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12162	26013		5.49	0.0E+00	AI190993.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12172	25134		3.73	0.0E+00	AB011399.1	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12192	25149		8.87	0.0E+00	AL163246.2	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12194	25151		1.35	0.0E+00	AB018195.1	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12201	25156		3.2	0.0E+00	11417862	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12220	25170		4.95	0.0E+00	5802973	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12254	25973	31787	1.47	0.0E+00	AF240786.1	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12267	25983		3.47	0.0E+00	AL041931.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12285	26146		3.39	0.0E+00	11418318	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12304	25222		4.77	0.0E+00	AL046644.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12317	28017		2.92	0.0E+00	AI903497.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12366	28172		1.88	0.0E+00	N54484.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12371	25265		4.08	0.0E+00	AF106658.1	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12374	14042	27106	5.36	0.0E+00	4507500	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12374	14042	27107	5.36	0.0E+00	4507500	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12383	26021		3.07	0.0E+00	10092587	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12415	13754		4.88	0.0E+00	AF003528.1	NT	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12450	25781	31937	3.95	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12510	25950	31765	1.64	0.0E+00	AW590892.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
12542	25982		1.34	0.0E+00	L20493.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
12573	26015		2.73	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12618	25418		4.61	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12638	25428		1.19	0.0E+00	AV720878.1	EST_HUMAN	AV720878 GLC Homo sapiens cDNA clone GLCPE08 5'
12660	26008		3.51	0.0E+00	A1204914.1	EST_HUMAN	en05h04.x1 Sirelagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884759 3'
12684	25462		1.33	0.0E+00	A1904846.1	EST_HUMAN	QV-BT085-020399-103 BT085 Homo sapiens cDNA
12702	26006		2.29	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
12714	15187	28207	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12714	15187	28208	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12739	25490	32027	1.21	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12751	14869	27960	3.26	0.0E+00	H30132.1	EST_HUMAN	yo56e08.r1 Soares breast 3NhbBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:IM64089
12751	14869	27961	3.26	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN);
12755	13978	27031	1.6	0.0E+00	AB011399.1	NT	GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN);
12766	25509		33.13	0.0E+00	D50859.1	NT	Homo sapiens gene for AF-8, complete cds
12771	25514	31997	5.44	0.0E+00	11418189	NT	Human gamma-cytoplasmic actin (ACTGP8) pseudogene
12771	25514	31998	5.44	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12776	25518		7.88	0.0E+00	AB028898.1	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12776	15294	28420	1.7	0.0E+00	4758489	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12837	25557		2.11	0.0E+00	AW564899.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12847	25553	31988	1.43	0.0E+00	11430460	NT	h88e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979154 3'
12892	14409	27471	1.74	0.0E+00	8922593	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12927	16558	28573	3.11	0.0E+00	4885312	NT	Homo sapiens hypodermal protein FLJ10897 (FLJ10897), mRNA
12935	18494	31832	2.3	0.0E+00	6906918	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12938	25517		1.88	0.0E+00	AB029900.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12981	25639	31983	1.82	0.0E+00	9558724	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
13010	26197		2.93	0.0E+00	AL163246.2	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
13017	13828	28851	2.46	0.0E+00	6906918	NT	Homo sapiens chromosome 21 segment HS21C046
13113	25726	31943	1.17	0.0E+00	11417882	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
							Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13118	25728		1.4	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13119	25731		3.11	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
13140	25740		5.96	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
13151	26207		1.16	0.0E+00	AW505178.1	EST_HUMAN	U1-HF-BNO-aly-g-08-0-U1.r1 NIH_MGC, 50 Homo sapiens cDNA clone IMAGE-3081399 5'
13190	25774		1.51	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE-1 (ERV8)
13209	16135	28151	1.37	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13209	16135	28152	1.37	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13215	14345	27402	1.29	0.0E+00	9969844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human placenta comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,233 - 26,232.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,232 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human placenta.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,233 - 26,232 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
- 10 of SEQ ID NOs.: 26,233 - 38,837, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human placenta.
- 15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one
- 25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human placenta, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human placenta; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the placenta of said eukaryote, said probe
is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 26,232 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 26,232.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,233 - 38,837.

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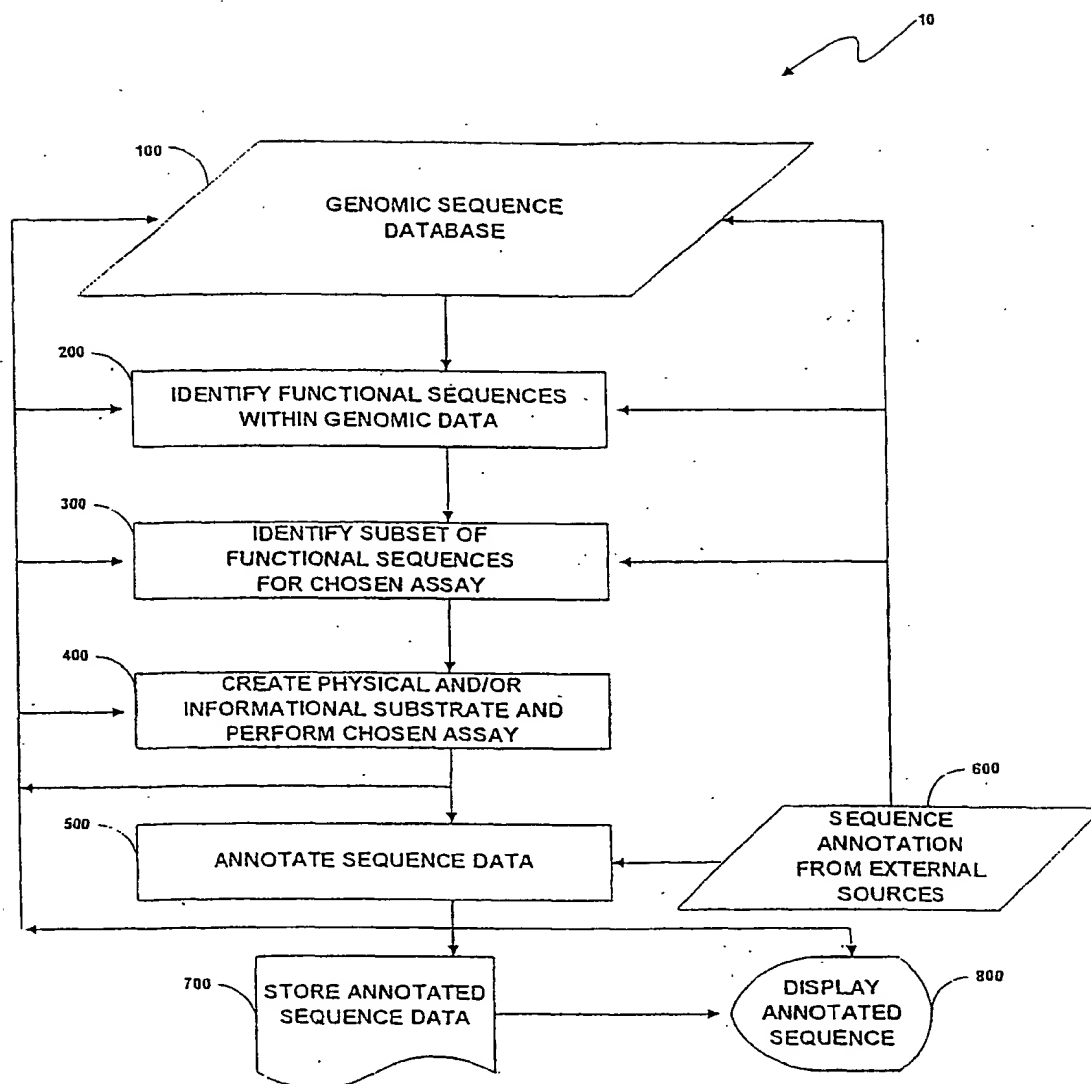


Fig. 1

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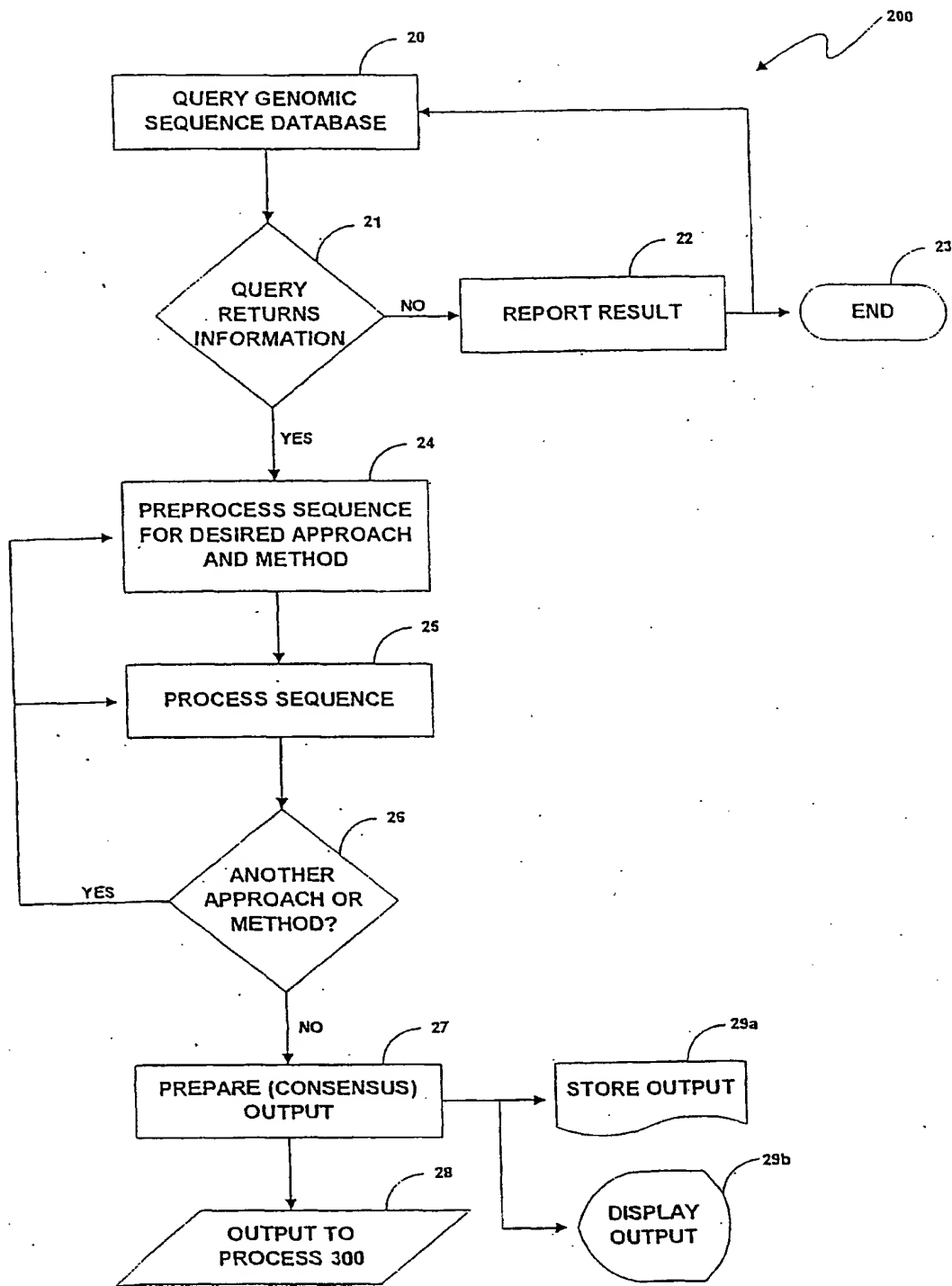


Fig. 2

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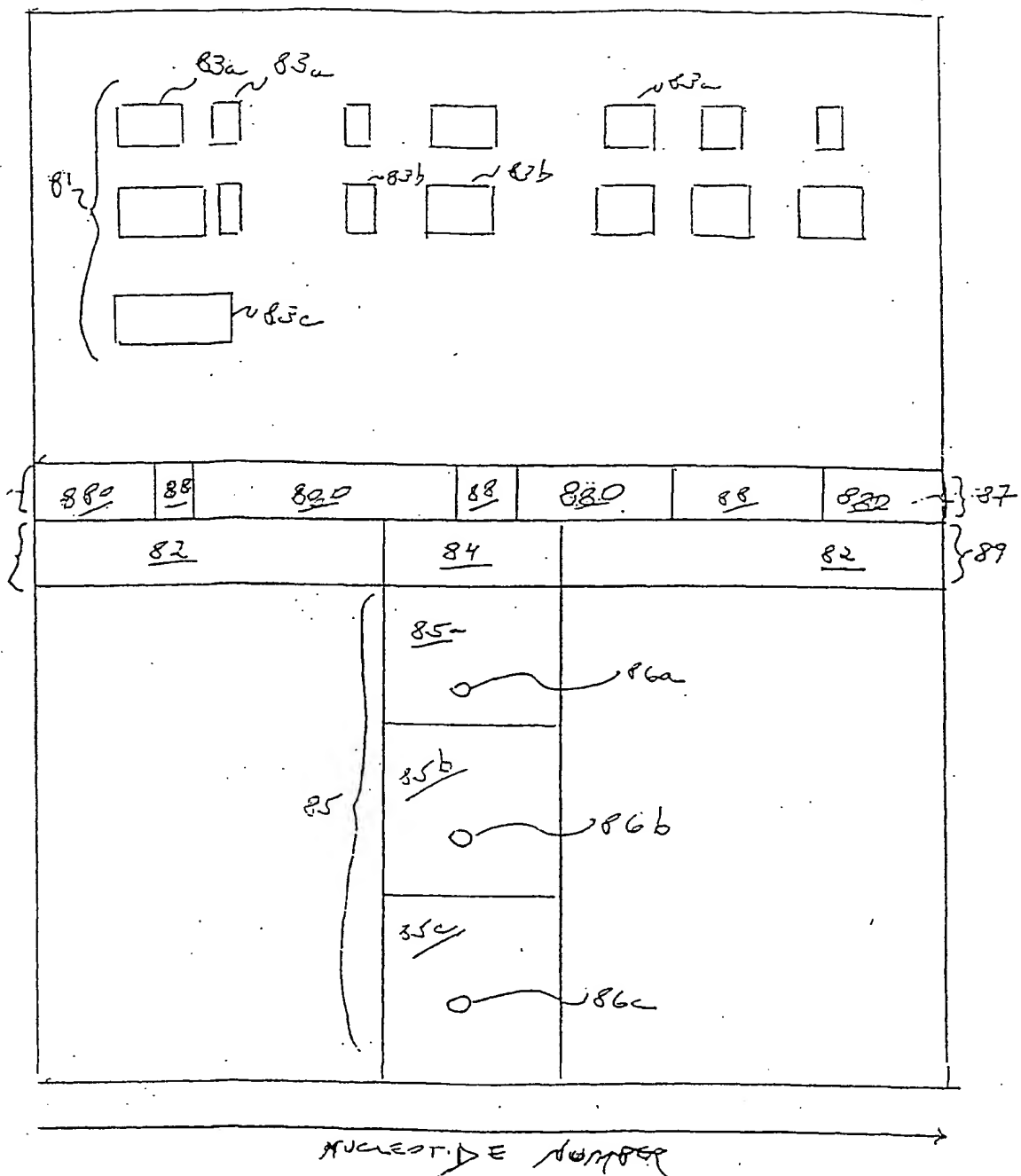


Fig. 3

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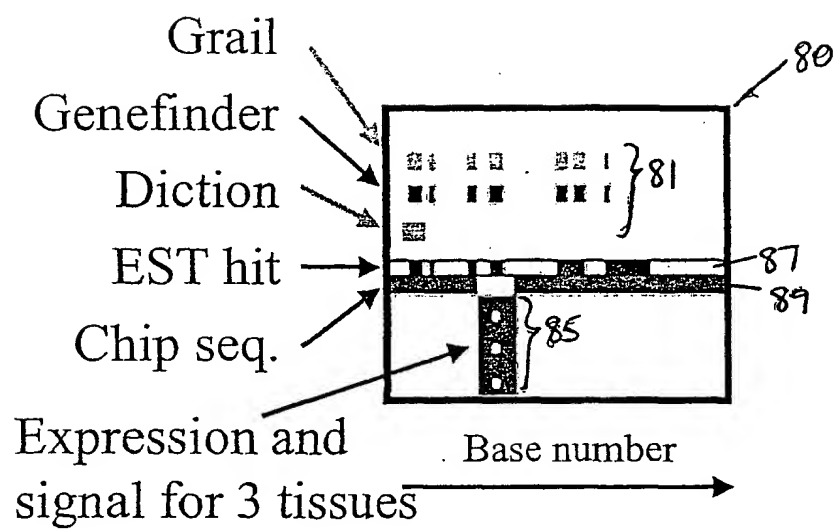


Fig. 4

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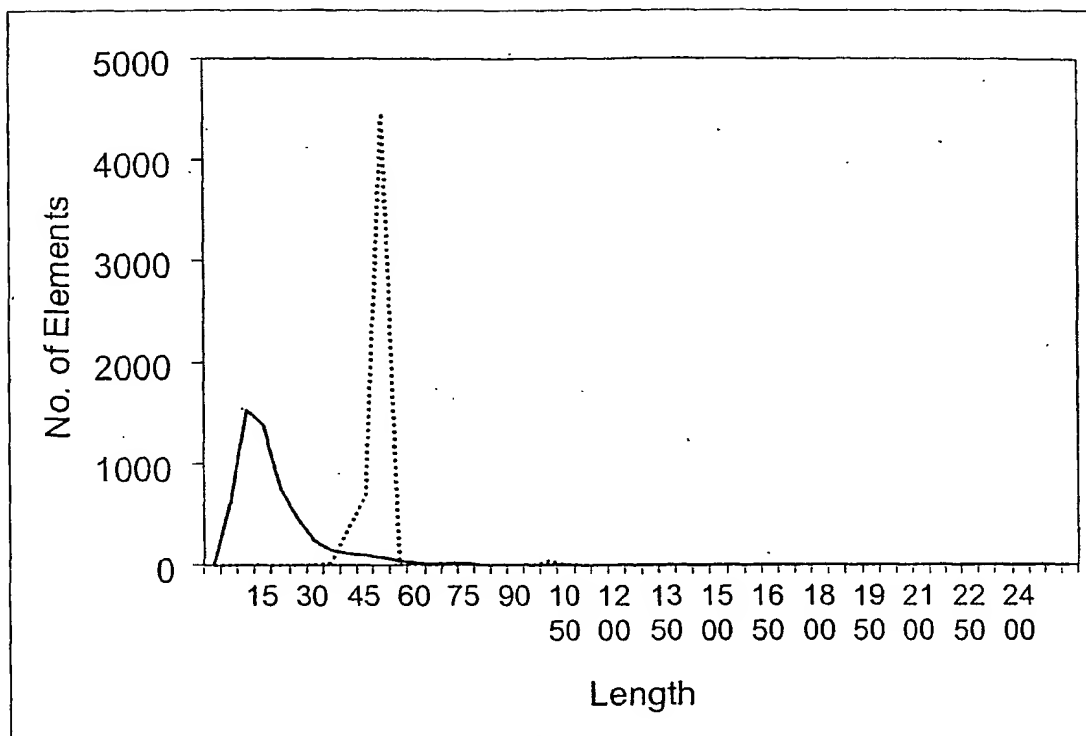


Fig. 5

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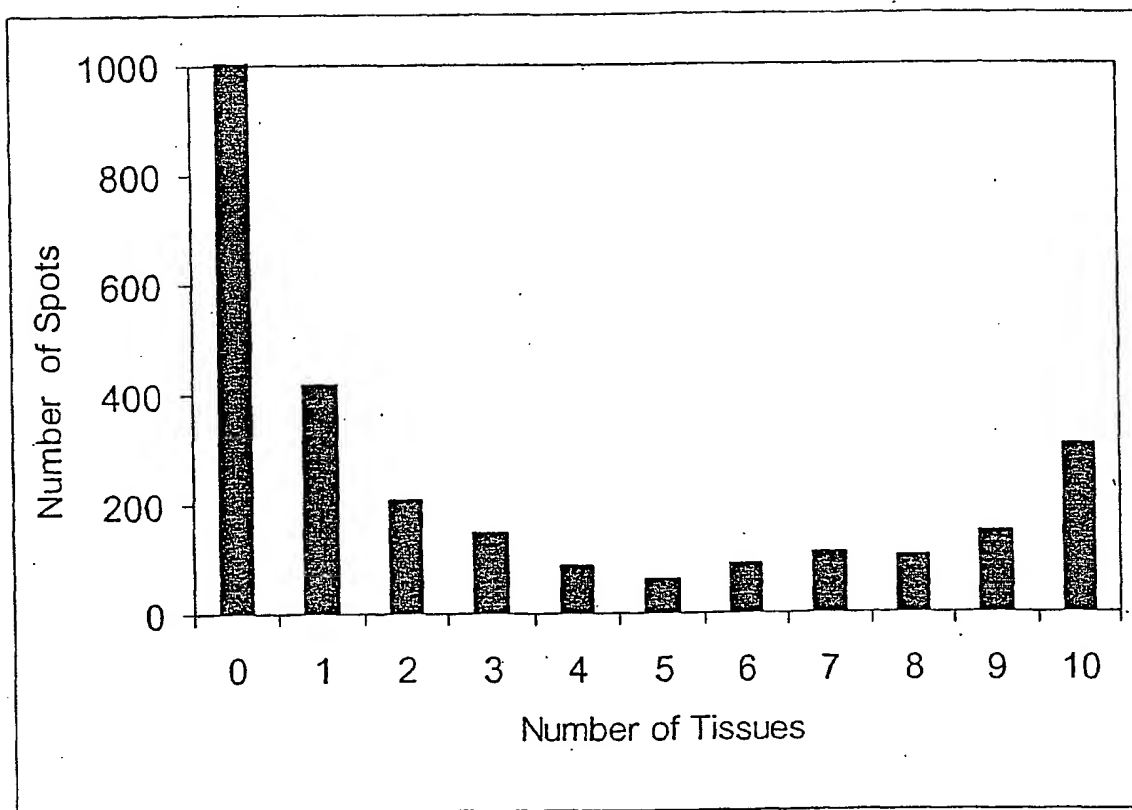


Fig. 6

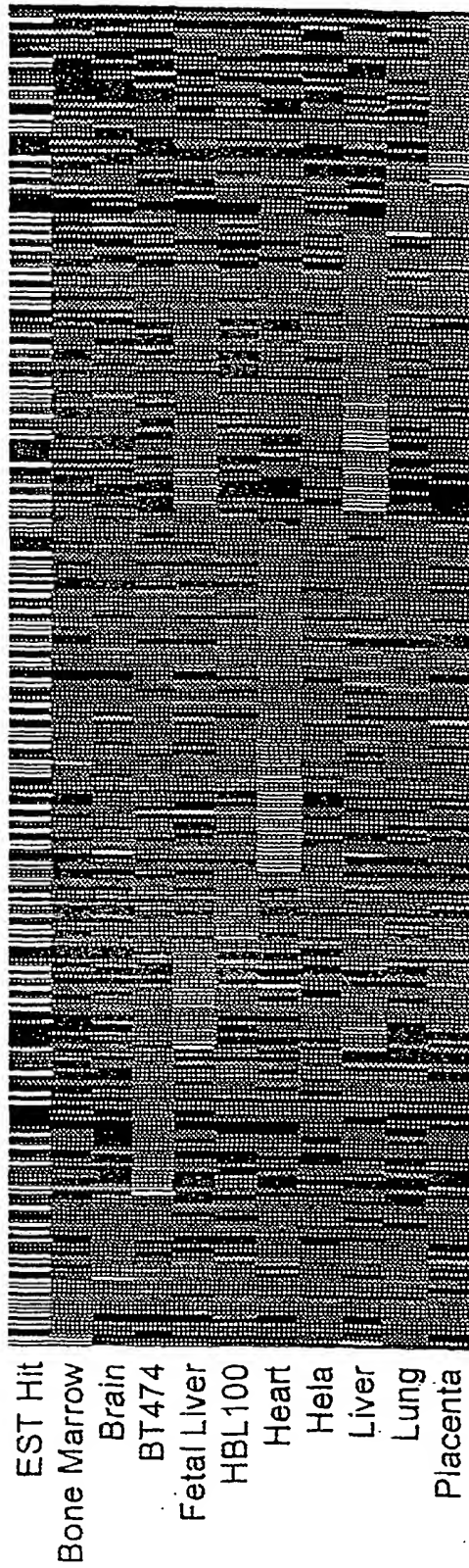


Fig. 7a

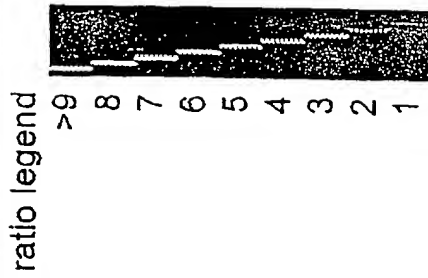


Fig. 7b

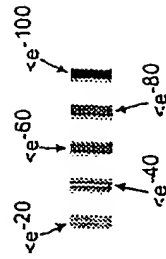


Fig. 7c

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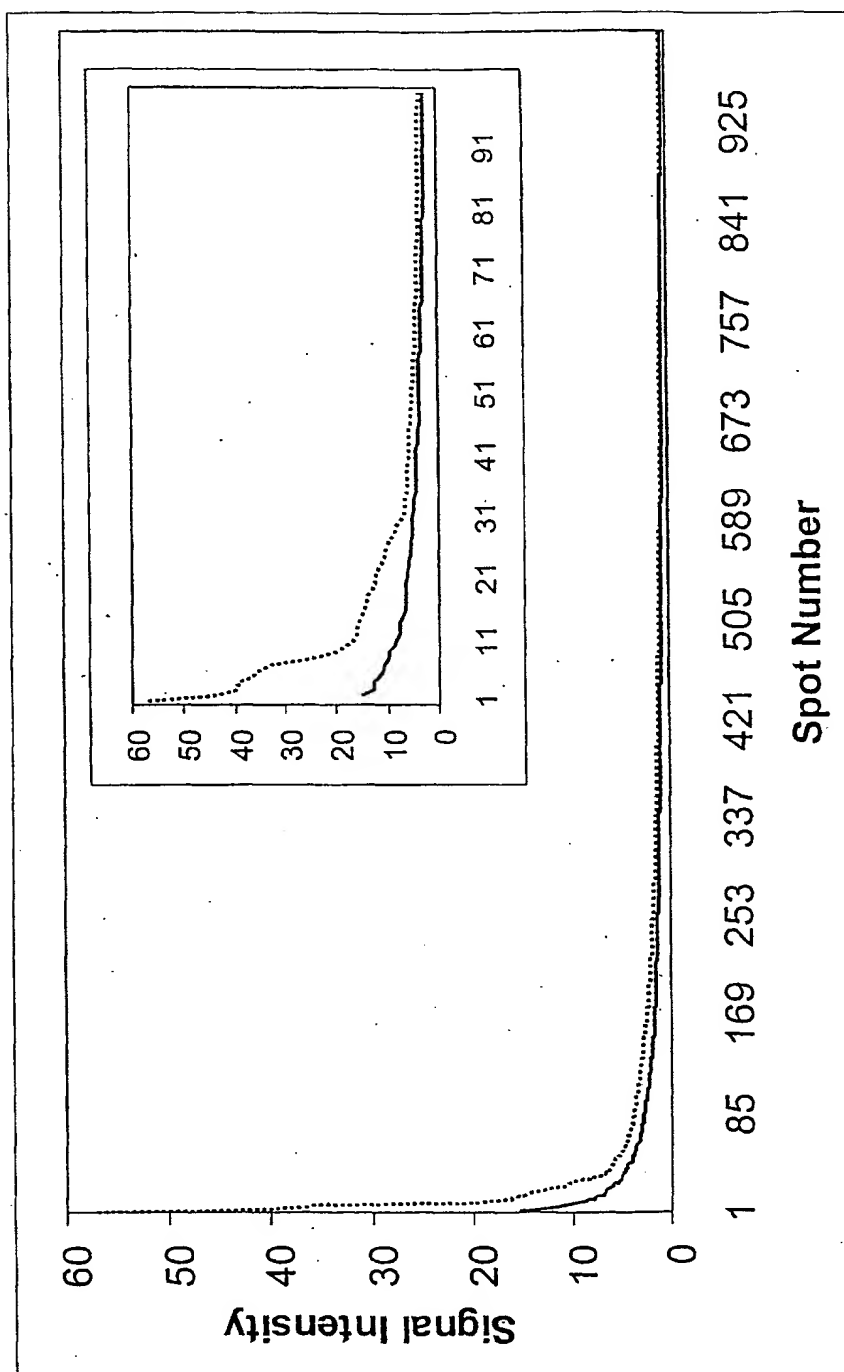


Fig. 8

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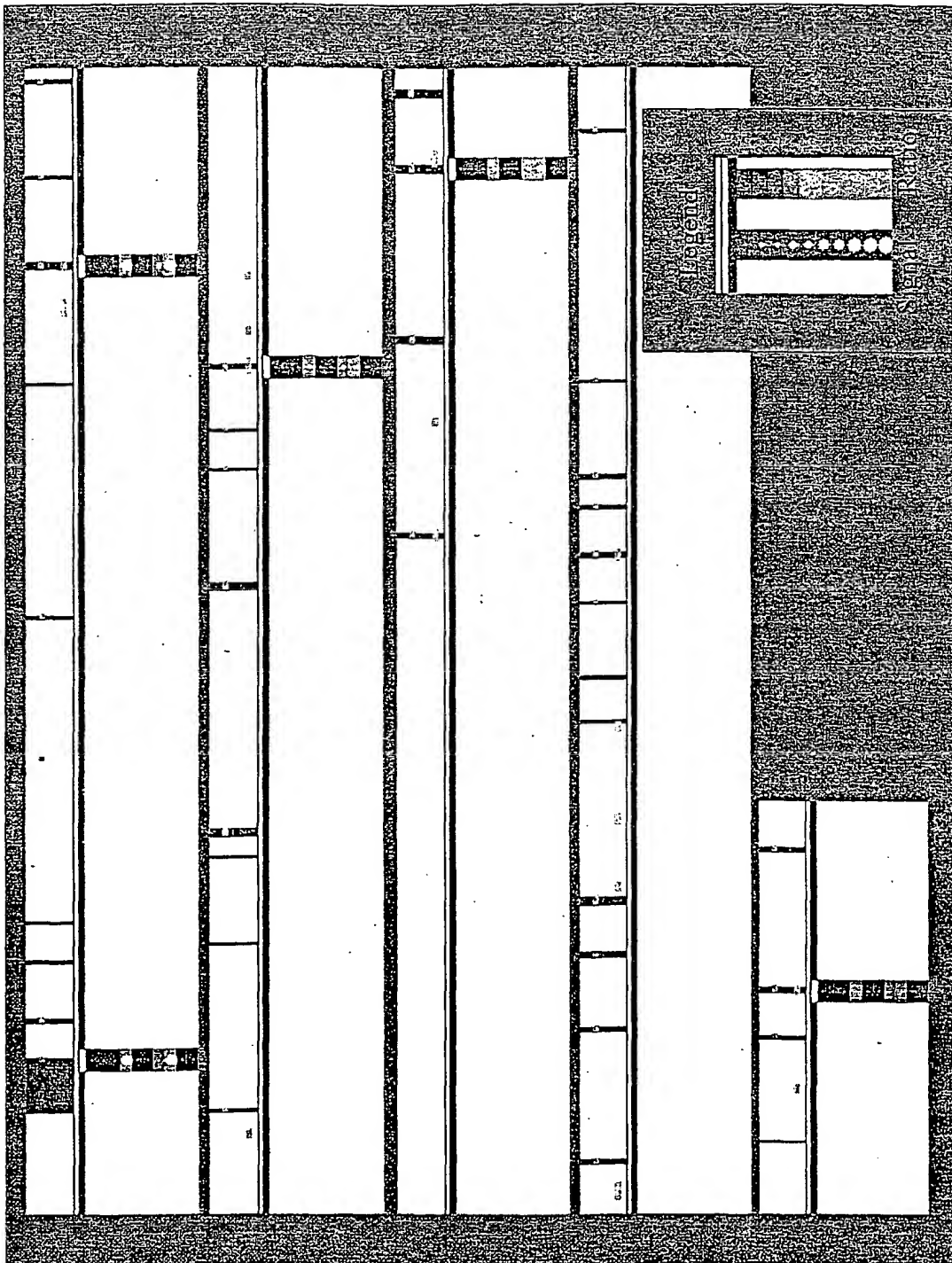
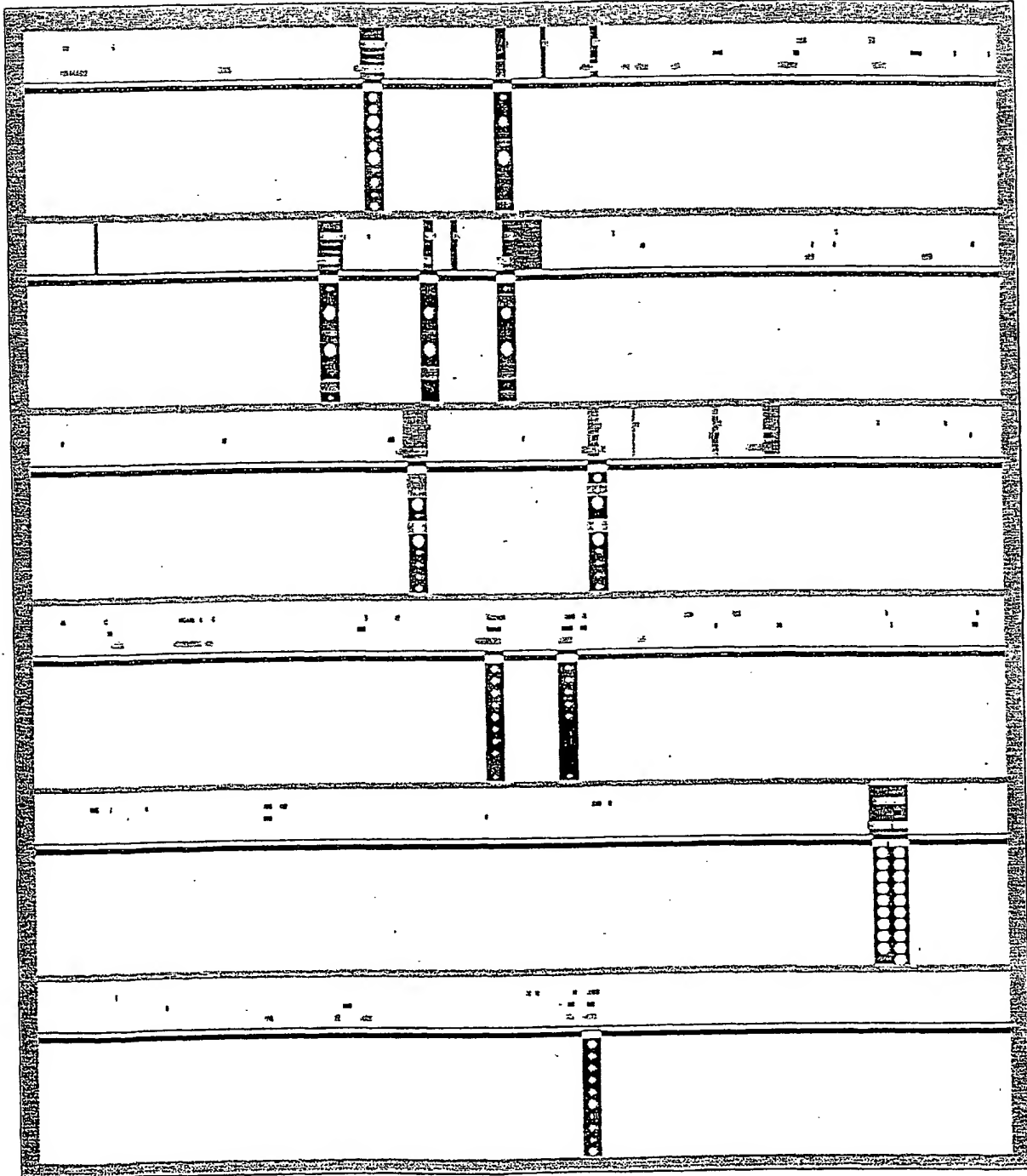


Fig. 9

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Fig. 10



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